

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2004, 11:11:40 ; Search time 42 Seconds
(without alignments)
79.363 Million cell updates/sec

Title: US-10-002-884A-2

Perfect score: 113
Sequence: 1 RRRRRWGRRRRRPKKRRKV 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 19Jun03:*

- 1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	76.1	405	22	Novel human diago
2	80	70.8	280	23	Biomembrane permea
3	78	69.0	54	22	Synthetic protamin
4	78	69.0	56	22	Novel human diago
5	78	69.0	761	22	Novel human diago
6	76	67.3	91	22	Novel human diago
7	76	67.3	808	22	Novel human diago
8	75	66.4	86	22	Human liver peptid
9	75	66.4	86	22	Human peptide #544

10	75	66.4	86	22	ABB33064	Peptide #570 enco
11	75	66.4	86	22	ABB18534	Protein #333 enco
12	75	66.4	86	22	AAW53862	Human brain expre
13	75	66.4	86	22	AAW66249	Human bone marrow
14	75	66.4	86	22	AAW14119	Peptide #553 enco
15	75	66.4	86	22	AAW26526	Peptide #563 enco
16	75	66.4	86	22	AAW01857	Peptide #539 enco
17	75	66.4	86	22	ABG35896	Human peptide enco
18	74	65.5	109	22	ABG26507	Novel human diago
19	73.5	65.0	762	21	AAW11546	SEN virus protein
20	73	64.6	57	22	AAW82958	Human immune/haema
21	73	64.6	130	22	ABG49651	Human liver peptid
22	73	64.6	130	22	ABG29645	Peptide #2296 enco
23	73	64.6	130	22	ABG34819	Peptide #2325 enco
24	73	64.6	130	22	ABG20238	Protein #2237 enco
25	73	64.6	130	22	AAW55623	Human brain expre
26	73	64.6	130	22	AAW68007	Human bone marrow
27	73	64.6	130	22	AAW15826	Peptide #2260 enco
28	73	64.6	130	22	AAW28336	Peptide #2373 enco
29	73	64.6	130	22	AAW03564	Peptide #2246 enco
30	72	63.7	80	22	ABG59141	Human liver peptid
31	72	63.7	80	22	ABB43770	Peptide #11276 enc
32	72	63.7	80	22	ABB26713	Protein #8712 enc
33	72	63.7	80	22	AAW64732	Human brain expre
34	72	63.7	80	22	AAW77502	Human bone marrow
35	72	63.7	80	22	AAW21431	Peptide #7865 enco
36	72	63.7	80	22	AAW37674	Peptide #11711 enc
37	72	63.7	80	22	ABG46527	Human peptide enco
38	72	63.7	99	22	ABG26520	Novel human diago
39	71	62.8	54	22	AAW51399	Synthetic protamin
40	71	62.8	78	22	ABG26500	Novel human diago
41	71	62.8	109	22	ABG26491	Novel human diago
42	71	62.8	115	22	ABG26526	Novel human diago
43	70	61.9	48	22	AAW51397	Synthetic protamin
44	70	61.9	57	22	ABG58055	Human liver peptid
45	70	61.9	57	22	ABB42642	Peptide #10148 enc

ALIGNMENTS

RESULT 1
ABG26543
ID ABG26543 standard; Protein; 405 AA.
XX ABG26543;
XX AC
XX XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #26534.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS90730.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in

Thu Jan 29 10:08:38 2004

us-10-002-884a-2.rag

PT diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID NO 56902; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 405 AA;

Query Match 76.1%; Score 86; DB 22; Length 405;
 Best Local Similarity 80.0%; Pred. No. 0.0024; Indels 0; Gaps 0;
 Matches 16; Conservative 2; Mismatches 2;

QY 1 RRRRRWGRRRRRPPKKKK 20
 ||||| ||||| :|||
 Db 257 RRRRRWGRRRRRPPKKKK 276

RESULT 2

AAU99807

AAU99807 standard; Protein; 280 AA.

XX AC AAU99807;

XX DT 07-OCT-2002 (first entry)

XX DE Biomembrane permeable compound associated NLS-11R-GFP fusion protein.

XX KW Biomembrane permeating signal sequence; nucleus-transfer signal;

XX KW postsynapse transfer signal sequence; biomembrane permeable compound;

XX KW PCR; primer; ss; NLS-11R-GFP; nuclear localisation signal;

XX KW green fluorescent protein.

XX OS Synthetic.

XX PN JP2002153288-A.

XX PD 28-MAY-2002.

XX PF 24-NOV-2000; 2000JP-0358442.

XX PR 24-NOV-2000; 2000JP-0358442.

XX XX (MATS/) MATSUI H.

XX PA (MATS/) MATSUSHITA M.

XX XX WPI; 2002-552745/59.

XX XX Compound for introducing a substance to a specific site in a cell, a

XX PT PAK inhibitor, a transcription inhibitor, a vector

XX XX Disclosure; Page 17-18; 25pp; Japanese.

PS

XX The invention describes a compound containing a biomembrane permeating
 CC signal sequence and a selectively introduced signal sequence to a
 CC specific site in a cell and which can be localised in the specific site
 CC in the cell. The biomembrane permeating signal sequence consists of
 CC 9-13 arginine residues and the selectively introduced signal sequence
 CC to a specific site in a cell is a nucleus-transfer or postsynapse
 CC transfer signal sequence. The compound is used for localising a peptide
 CC acting as a drug in a cell nucleus. This is the amino acid sequence of
 CC the NUS (nuclear localisation signal)-11R-GFP (green fluorescent protein)
 CC fusion protein used in the development of a biomembrane permeable
 CC compound.

XX Sequence 280 AA;

Query Match 70.8%; Score 80; DB 23; Length 280;

Best Local Similarity 90.0%; Pred. No. 0.01; Indels 2; Gaps 1;

Matches 18; Conservative 0; Mismatches 0;

QY 2 RRRRWGRRRRRPPKKKKV 21

||||| ||||| |||||

Db 2 RRRRWGRRRRRPPKKKKV 19

RESULT 3

AAMS1398

ID AAMS1398 standard; Peptide; 54 AA.

XX AC AAMS1398;

XX DT 15-JAN-2002 (first entry)

XX DE Synthetic procaine family consensus kink motif derived peptide 8.

XX KW Hybridisation device; single base pair difference; diagnostic test;

XX KW protein purification; nucleic acid purification; secondary structure;

XX KW Salmine A1; protamine.

XX OS Synthetic.

XX Key Location/Qualifiers

XX Duplication 1.8

XX /label= Direct repeat

XX /note= "Unit comprising [(Arg)n-Pro-Gly] repeated at

XX positions 9-16, 17-24, 25-32, 33-40 and 41-48"

XX FT Misc-difference 1..6

XX /note= "1-4 arginine residues of each repeat unit are

XX optionally absent"

XX FT Misc-difference 17..48

XX /note= "Repeat units 17-24, 25-32, 33-40 and 41-48

XX optionally absent"

XX FT Misc-difference 49..54

XX /note= "1-4 arginine residues are optionally absent"

XX FT WO200166687-A1.

XX PN 13-SEP-2001.

XX PD 24-AUG-2000; 2000WO-US23438.

XX PF 09-MAR-2000; 2000US-052240.

XX PR 10-AUG-2000; 2000US-0636268.

XX XX (GENO-) GENOMETRIX GENOMIX INC.

XX XX Hogan M, Powdrill T, Iverson B, Belosludtsev YY, Belosludtsev IY;

XX XX WPI; 2001-611328/70.

XX XX Association device for nucleic acid-based diagnostic test, isolation of

XX PT nucleic acids, comprises oligonucleotide probe and solid substrate

XX PT having support surface comprising association surface for linking probe

XX PT to substrate

XX PT

XX PS Claim 55; Page -; 101pp; English.

XX CC The invention relates to an association/hybridisation device comprising

XX CC nucleic acid and polypeptide probes, or combinations of these, linked to

XX CC a porous solid substrate, comprising an external substrate surface and

XX CC several internal pores. The pore surfaces comprise an association surface

XX CC which is charged with net positive or negative charge density where the

XX CC pH is lower or higher than the pI of association surface. The device is

XX CC useful for associating a nucleic acid or a polypeptide in a sample to a

XX CC nucleic acid or a polypeptide probe. The device is also useful for

XX CC detecting a single base pair difference between a nucleic acid in a test

XX CC sample and an oligonucleotide probe. The device finds application in

XX CC nucleic acid-based diagnostic tests, isolation and purification of

XX CC nucleic acids or polypeptides from a sample. The device can be used at

XX CC any temperature and the kinetics of association between the

XX CC oligonucleotide probe and the nucleic acid in the test sample are 10 fold

XX CC more rapid than the kinetics of association under conditions when the

XX CC substrate surface or association surface has a neutral or net negative

XX CC charge density. The device and the method can be used for hybridisation

XX CC of probes to target DNA or RNA at low bulk ion concentrations. The

XX CC present sequence is that of a synthetic peptide. Known members of the

XX CC protamine family, including Salmine A1, are defined by the consensus

XX CC sequence [(Arg)n-bendin-Argn, where n=3-5, m=3-5 and bend = 1-3 amino

XX CC acid sequence capable of inducing a "kink" in the peptide backbone.

XX CC Note: The present peptide sequence is not given in the specification but

XX CC is derived from a consensus sequence given in Claim 55 as

XX CC [(Arg)n-Pro-Gly)n-Argn, where n is the integer 2, 3, 4, 5 or 6.

XX SQ Sequence 54 AA;

Query Match 69.0%; Score 78; DB 22; Length 54;

Best Local Similarity 75.0%; Pred. No. 0.0045;

Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RRRRRGRRRRRPPKRRK 20

Db 1 RRRRRPGRRRRRPPGRRR 20

RESULT 4

ABG11732

ID ABG11732 standard; Protein; 56 AA.

XX AC ABG11732;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #11723.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX DR N-PSDB; AAS75919.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity -

Claim 20; SEQ ID No 42091; 103pp; English.

The invention relates to isolated polynucleotide (I) and

polypeptide (II) sequences. (I) is useful as hybridisation probes,

polymerase chain reaction (PCR) primers, oligomers, and for chromosome

and gene mapping, and in recombinant production of (II). The

polynucleotides are also used in diagnostics as expressed sequence tags

for identifying expressed genes. (I) is useful in gene therapy techniques

to restore normal activity of (II) or to treat disease states involving

(II). (II) is useful for generating antibodies against it, detecting or

quantitating a polypeptide in tissue, as molecular weight markers and as

a food supplement. (II) and its binding partners are useful in medical

imaging of sites expressing (II). (I) and (II) are useful for treating

disorders involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in

diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits to assess biodiversity

and to produce other types of data and products dependent on DNA and

amino acid sequences. ABG0010-ABG30377 represent novel human

diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed

specification, but was obtained in electronic format directly from WIPO

at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 56 AA;

Query Match 69.0%; Score 78; DB 22; Length 56;

Best Local Similarity 80.0%; Pred. No. 0.0047;

Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RRRRRGRRRRRPPKRRK 20

Db 19 RRRRRRRRRRRRPPKRRK 38

RESULT 5

ABG26518

ID ABG26518 standard; Protein; 761 AA.

XX AC ABG26518;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #26509.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX DR N-PSDB; AAS90705.

XX PT New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity -

XX Claim 20; SEQ ID No 56877; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG30377 represent novel human

CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 91 AA;

Query Match 67.3%; Score 76; DB 22; Length 91;

Best Local Similarity 80.0%; Pred. No. 0.013; 3; Indels 0; Gaps 0;

Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20

DB 48 RRRRRRRRRRRPKKKRK 67

RESULT 7

ABG05367

ID ABG05367 standard; Protein; 808 AA.

XX AC ABG05367;

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #5358.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder;

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS69554.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits and to assess

XX biodiversity -

XX Claim 20; SEQ ID No 35726; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

XX Claim 20; SEQ ID No 56877; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG30377 represent novel human

CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 761 AA;

Query Match 69.0%; Score 78; DB 22; Length 761;

Best Local Similarity 85.0%; Pred. No. 0.043; 3; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20

DB 740 RRRRRRRRRRRPKKKRK 759

RESULT 6

ABG26516

ID ABG26516 standard; Protein; 91 AA.

XX AC ABG26516;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #26507.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AAS90703.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits and to assess

XX biodiversity -

XX Claim 20; SEQ ID No 56875; 103pp; English.

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 808 AA;
 CC Query Match 67.3%; Score 76; DB 22; Length 808;
 CC Best Local Similarity 80.0%; Pred. No. 0.081; 3; Indels 0; Gaps 0;
 CC Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 CC QY 1 RRRRRWGRRRRRPKKKK 20
 CC DB 231 RRRRRRRRRRRPKKKK 250

RESULT 8
 ABG47914
 ID ABG47914 standard; Peptide; 86 AA.
 XX AC ABG47914;
 XX DT 25-FEB-2003 (first entry)
 XX DE Human liver peptide, SEQ ID No 26562.
 XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 XX KW hypercholesterolaemia; coronary heart disease.
 XX OS Homo sapiens.
 XX PN WO200157273-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US00664.
 XX PR 04-FEB-2000; 2000US-0180312.
 XX PR 26-MAY-2000; 2000US-0207456.
 XX PR 30-JUN-2000; 2000US-0608408.
 XX PR 03-AUG-2000; 2000US-0632366.
 XX PR 21-SEP-2000; 2000US-0234687.
 XX PR 27-SEP-2000; 2000US-0236359.
 XX PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX PI WPI; 2001-48898/53.
 XX DR Human genome-derived single exon nucleic acid probes useful for
 XX PT analysing gene expression in human adult liver -
 XX PS Claim 27; SEQ ID No 26562; 650pp; English.
 XX The invention relates to a single exon nucleic acid probe (SENP) (I) for

CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult
 CC liver. (I) may be used for predicting, measuring and displaying gene
 CC expression in samples derived from human adult liver. The genes
 CC identified may be involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
 CC is associated with coronary heart disease. ABG47348-ABG5930 represent
 CC human liver single exon encoded peptides of the invention.
 CC Note: The sequence information for this patent does not appear in the
 CC printed specification but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 86 AA;
 CC Query Match 66.4%; Score 75; DB 22; Length 86;
 CC Best Local Similarity 70.0%; Pred. No. 0.016; 2; Indels 0; Gaps 0;
 CC Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 CC QY 1 RRRRRWGRRRRRPKKKK 20
 CC DB 7 RRRRRRRRRRRPKKKKAR 26

RESULT 9
 ABB27893
 ID ABB27893 standard; Peptide; 86 AA.
 XX AC ABB27893;
 XX DT 01-FEB-2002 (first entry)
 XX DE Human peptide #544 encoded by breast cell single exon nucleic acid probe.
 XX KW Human; microarray; single exon probe; gene expression; breast;
 XX KW disease; cancer.
 XX OS Homo sapiens.
 XX PN WO200157271-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US00662.
 XX PR 04-FEB-2000; 2000US-0180312.
 XX PR 26-MAY-2000; 2000US-0207456.
 XX PR 30-JUN-2000; 2000US-0608408.
 XX PR 03-AUG-2000; 2000US-0632366.
 XX PR 21-SEP-2000; 2000US-0234687.
 XX PR 27-SEP-2000; 2000US-0236359.
 XX PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX PI WPI; 2001-496933/54.
 XX DR New spatially-addressable set of single exon nucleic acid probes,
 XX PT useful for measuring gene expression in sample derived from human
 XX PT breast, comprises number of single exon nucleic acid probes -
 XX PT Claim 27; SEQ ID No 10861; 327pp + sequence listing; English.
 XX PS The invention relates to a spatially-addressable set of single exon
 XX CC nucleic acid probes for measuring gene expression in a sample derived
 XX CC from human breast and BT 474 cells. The method involves contacting
 XX CC the probes with a collection of detectably labelled nucleic acids
 XX CC derived from mRNA of human breast, and then measuring the label
 XX CC bound to each probe of the microarray. The probes are useful for
 XX CC verifying the expression of regions of genomic DNA predicted to

X

Qy
1 RRRRRWRRRRRRPKKKRK 20

1 RRRRRWGRRRRRPCKKK 20

Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.

Homo sapiens.

WO200157276-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00668.

04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488900/53.

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -

Example 4; SEQ ID NO: 26555; 659pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.

Sequence 86 AA;

Query Match 66.4%; Score 75; DB 22; Length 86;

Best Local Similarity 70.0%; Pred. No. 0.016; 2; Indels 0; Gaps 0;

Matches 14; Conservative 4; Mismatches 2;

Qy 1 RRRRRWGRRRRRPKKKRK 20

Db 7 KRRRRGRRRRRKKKKR 26

RESULT 14

AAM4119

ID AAM14119 standard; Protein; 86 AA.

AC AAM14119;

XX

XX

DT 12-OCT-2001 (first entry)

XX

DE Peptide #553 encoded by probe for measuring cervical gene expression.

XX Probe; human; microarray; gene expression; cervical epithelial cell; cervical cancer.

XX

OS Homo sapiens.

XX

PN WO200157278-A2.

XX

PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US00670.

XX

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX

Human brain expressed single exon probe encoded protein SEQ ID NO: 25967.

Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

Homo sapiens.

WO200157275-A2.

09-AUG-2001.

30-JAN-2001; 2001WO-US00667.

04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-483446/52.

Single exon nucleic acid probes for analyzing gene expression in human brains -

Example 4; SEQ ID NO: 25967; 650pp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.

Sequence 86 AA;

Query Match 66.4%; Score 75; DB 22; Length 86;

Best Local Similarity 70.0%; Pred. No. 0.016; 2; Indels 0; Gaps 0;

Matches 14; Conservative 4; Mismatches 2;

Qy 1 RRRRRWGRRRRRPKKKRK 20

Db 7 KRRRRGRRRRRKKKKR 26

RESULT 13

AAM6249

ID AAM66249 standard; Protein; 86 AA.

AC AAM66249;

XX

XX

DT 06-NOV-2001 (first entry)

XX

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26555.

XX

Thu Jan 29 10:08:38 2004

PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human placenta -
 XX
 PS Claim 27; SEQ ID No 26795; 654pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP;
 CC see AA131315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 XX
 SQ Sequence 86 AA;
 Query Match 66.4%; Score 75; DB 22; Length 86;
 Best Local Similarity 70.0%; Pred. No. 0.016; 2; Indels 0; Gaps 0;
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RRRRRGRRRRRRPKKKRK 20
 Db 7 KRRRRGRRRRRRPKKKRK 26
 RESULT 16
 AAM01857
 ID AAM01857 standard; Protein; 86 AA.
 XX
 AC AAM01857;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Peptide #539 encoded by probe for measuring human breast gene expression.
 XX
 KW Probe; human; breast disease; breast cancer; development disorder;
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200157270-A2.
 XX
 PD 09-AUG-2001.
 XX
 XX 29-JAN-2001; 2001WO-US00661.
 XX
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-476286/51.
 XX
 XX Novel single exon nucleic acid probe used to measuring gene expression
 PT in a human breast -
 XX
 XX Claim 27; SEQ ID No 10597; 322pp; English.
 XX
 CC The present invention relates to novel single exon nucleic acid probes
 CC (see AA100010-AA110067). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for measuring human gene expression in
 CC a human breast sample, where the probe hybridises at high stringency to a
 CC nucleic acid expressed in the human breast. The probes are useful for
 CC predicting, diagnosing, grading, staging, monitoring and prognosing
 CC diseases of the human breast, particularly those diseases with polygenic
 CC aetiology. The diseases include: breast cancer, disorders of development,
 CC inflammatory diseases of the breast, fibrocystic changes, proliferative
 CC breast disease and non-carcinoma tumours.

PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488901/53.
 XX
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human cervical epithelial cells -
 XX
 PS Claim 27; SEQ ID No 18945; 487pp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENP; see AA110068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 86 AA;
 Query Match 66.4%; Score 75; DB 22; Length 86;
 Best Local Similarity 70.0%; Pred. No. 0.016; 2; Indels 0; Gaps 0;
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RRRRRGRRRRRRPKKKRK 20
 Db 7 KRRRRGRRRRRRPKKKRK 26
 RESULT 15
 AAM26526
 ID AAM26526 standard; Protein; 86 AA.
 XX
 AC AAM26526;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #563 encoded by probe for measuring placental gene expression.
 XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US00663.
 XX
 XX 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488901/53.
 XX
 XX WPI; 2001-488901/53.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 86 AA;
 Query Match 66.4%; Score 75; DB 22; Length 86;
 CC Best Local Similarity 70.0%; Pred. No. 0.016; 2; Indels 0; Gaps 0;
 CC Matches 14; Conservative 4; Mismatches 4

QY 1 RRRRRWGRRRRRPKKKK 20
 DB 7 KRRRRRGRRRRRKKKKR 26

RESULT 17
 ABG35896
 ID ABG35896 standard; Peptide; 86 AA.
 XX AC ABG35896;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 25561.

XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.

XX OS Homo sapiens.
 XX PN WO200186003-A2.
 XX PD 15-NOV-2001.
 XX PF 30-JAN-2001; 2001WO-US00665.
 XX PR 04-FEB-2000; 2000US-180312P.
 XX PR 26-MAY-2000; 2000US-207456P.
 XX PR 30-JUN-2000; 2000US-0608408.
 XX PR 03-AUG-2000; 2000US-0632366.
 XX PR 21-SEP-2000; 2000US-234687P.
 XX PR 27-SEP-2000; 2000US-236359P.
 XX PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX PI WPI; 2002-114183/15.
 XX DR Spatially-addressable set of single exon nucleic acid probes, used to
 XX measure gene expression in human lung samples -
 XX Claim 27; SEQ ID No 25561; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridise at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of

CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 86 AA;

Query Match 66.4%; Score 75; DB 23; Length 86;
 CC Best Local Similarity 70.0%; Pred. No. 0.016; 2; Indels 0; Gaps 0;
 CC Matches 14; Conservative 4; Mismatches 4

QY 1 RRRRRWGRRRRRPKKKK 20
 DB 7 KRRRRRGRRRRRKKKKR 26

RESULT 18
 ABG26507
 ID ABG26507 standard; Protein; 109 AA.
 XX AC ABG26507;
 XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #26498.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US08631.
 XX PR 31-MAR-2000; 2000US-0540217.
 XX PR 23-AUG-2000; 2000US-0649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX DR N-PSDB; AAS90694.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in

XX

PR 14-AUG-2000; 2000US=0225268
PR 14-AUG-2000; 2000US=0225270
PR 14-AUG-2000; 2000US=0225270

PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 06-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234597.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.

PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-483426/52.
 XX N-PSDB; AAK55739.
 DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 XX useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 PT Claim 11; SEQ ID NO 10551; 3071pp + Sequence Listing; English.
 PS AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent;
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX Sequence 57 AA;
 SQ Query Match 64.6%; Score 73; DB 22; Length 57;
 Best Local Similarity 75.0%; Pred. No. 0.02;

Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
||||: || |||| ||||: |||
Db 35 RRRRRKGRGRRRRGKKKK 54

RESULT 21
ABG49651
ID ABG49651 standard; Peptide; 130 AA.
XX AC ABG49651;
XX DT 25-FEB-2003 (first entry)
XX DE Human liver peptide, SEQ ID No 28299.
XX KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX OS Homo sapiens.
XX PN W0200157273-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00664.
XX PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX FA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analysing gene expression in human adult liver -
PS Claim 27; SEQ ID No 28299; 658pp; English.
XX The invention relates to a single exon nucleic acid probe (SENP) (i) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult
CC liver. (i) may be used for predicting, measuring and displaying gene
CC expression in samples derived from human adult liver. The genes
CC identified may be involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
CC is associated with coronary heart disease. ABG47348-ABG59930 represent
CC human liver single exon encoded peptides of the invention.
CC Note: The sequence information for this patent does not appear in the
CC printed specification but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 130 AA;

Query Match 64.6%; Score 73; DB 22; Length 130;
Best Local Similarity 75.0%; Pred. No. 0.041;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
||||: || |||| ||||: |||
Db 54 RRRRRKGRGRRRRGKKKK 73

RESULT 22
ABB29645
ID ABB29645 standard; Peptide; 130 AA.
XX AC ABB29645;
XX DT 01-FEB-2002 (first entry)
XX DE Peptide #2296 encoded by breast cell single exon nucleic acid probe.
XX KW Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer.
XX OS Homo sapiens.
XX PN W0200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00662.
XX PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX FA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-496933/54.
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX Claim 27; SEQ ID NO 12613; 327pp + sequence listing; English.
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing the toxicity of chemical
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a peptide encoded by a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 130 AA;

Query Match 64.6%; Score 73; DB 22; Length 130;
Best Local Similarity 75.0%; Pred. No. 0.041;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
||||: || |||| ||||: |||
Db 54 RRRRRKGRGRRRRGKKKK 73

```

OS Homo sapiens.
XX
XX WO200157274-A2.
XX
XX
XX 09-AUG-2001.
XX
XX
XX 30-JAN-2001; 2001WO-US00666.
XX
XX
XX 04-FEB-2000; 2000US-0180312.
XX
XX 26-MAY-2000; 2000US-0207456.
XX
XX 30-JUN-2000; 2000US-0608408.
XX
XX 03-AUG-2000; 2000US-0632366.
XX
XX 21-SEP-2000; 2000US-0234687.
XX
XX 27-SEP-2000; 2000US-0236359.
XX
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
XX Claim 15; SEQ ID No 22008; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 130 AA;
XX
XX Query Match 64.6%; Score 73; DB 22; Length 130;
XX Best Local Similarity 75.0%; Pred. No. 0.041;
XX Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 RRRRRWGGRRRRRPPKKKK 20
XX |||||: |||||: |||||:
XX 54 RRRRRKKRRRRKKKKKK 73
XX
XX Db
XX
XX RESULT 25
XX AAM55623
XX ID AAM55623 standard; Protein; 130 AA.
XX
XX AC AAM55623;
XX
XX XX
XX DT 05-NOV-2001 (first entry)
XX
XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27728.
XX
XX KW Human; brain expressed exon; gene expression analysis; probe;
XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
XX KW epilepsy; cancer.
XX
XX OS Homo sapiens.
XX
XX XX WO200157275-A2.
XX
XX
XX 09-AUG-2001.
XX
XX
XX 30-JAN-2001; 2001WO-US00667.
XX
XX

```

PT Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human bone marrow -
 PS Example 4; SEQ ID NO: 28313; 659pp + Sequence Listing; English.
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.
 XX
 SQ Sequence 130 AA;
 Query Match 64.6%; Score 73; DB 22; Length 130;
 Best Local Similarity 75.0%; Pred. NO. 0.041;
 Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RRRRRGWRGRRRRPKKKRK 20
 Db 54 RRRRRKRRRRRRKKKKK 73
 RESULT 27
 RAN15826
 ID AM15826 standard; Protein; 130 AA.
 XX
 AC AM15826;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Peptide #2260 encoded by probe for measuring cervical gene expression.
 XX
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 XX
 OS Homo sapiens.
 XX
 FN WO200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00670.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human cervical epithelial cells -
 XX
 PS Claim 27; SEQ ID No 20652; 487pp; English.
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENP: see AAI10068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO

PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483446/52.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT brains -
 XX
 PS Example 4; SEQ ID NO: 27728; 650pp + Sequence Listing; English.
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention.
 XX
 SQ Sequence 130 AA;
 Query Match 64.6%; Score 73; DB 22; Length 130;
 Best Local Similarity 75.0%; Pred. NO. 0.041;
 Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RRRRRGWRGRRRRPKKKRK 20
 Db 54 RRRRRKRRRRRRKKKKK 73
 RESULT 26
 AAM68007
 ID AAM68007 standard; Protein; 130 AA.
 XX
 AC AAM68007;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28313.
 XX
 KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX
 OS Homo sapiens.
 XX
 FN WO200157276-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00668.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488900/53.
 XX

```

CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 130 AA;
    Query Match 64.6%; Score 73; DB 22; Length 130;
    Best Local Similarity 75.0%; Pred. No. 0.041;
    Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPPKKKK 20
    |||||: |||||: |||||:
Db 54 RRRRRKKRRRRRRKKKKK 73

RESULT 28
ID AAM28336
AA AAM28336 standard; Protein; 130 AA.
XX
AC AAM28336;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #2373 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0623366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0623366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
    analyzing gene expression in human placenta -
XX
XX Claim 27; SEQ ID No 28605; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
    see A131315-AA157546). The present sequence is a peptide encoded by one
    such probe. The probes are useful for producing a microarray for
    predicting, measuring and displaying gene expression in samples derived
    from human placenta. The probes are useful for antenatal diagnosis of
    human genetic disorders.
XX
SQ Sequence 130 AA;
    Query Match 64.6%; Score 73; DB 22; Length 130;
    Best Local Similarity 75.0%; Pred. No. 0.041;
    Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPPKKKK 20
    |||||: |||||: |||||:
Db 54 RRRRRKKRRRRRRKKKKK 73

RESULT 29
AAM03564
AA AAM03564 standard; Protein; 130 AA.
XX
AC AAM03564;
XX
DT 09-OCT-2001 (first entry)
XX
DE Peptide #2246 encoded by probe for measuring breast gene expression.
XX
KW Probe; human; breast disease; breast cancer; development disorder;
    inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
XX Homo sapiens.
XX
PN WO200157270-A2.
XX
PD 09-AUG-2001.
XX
PF 29-JAN-2001; 2001WO-US00661.
XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0623366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-476286/51.
XX
PT Novel single exon nucleic acid probe used to measuring gene expression
    in a human breast -
XX
XX Claim 27; SEQ ID No 12304; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes
    (see A100010-AA110067). The present sequence is a peptide encoded by one
    such probe. The probes are useful for measuring human gene expression in
    a human breast sample, where the probe hybridises at high stringency to a
    nucleic acid expressed in the human breast. The probes are useful for
    predicting, diagnosing, grading, staging, monitoring and prognosing
    diseases of the human breast, particularly those diseases with polygenic
    aetiology. The diseases include: breast cancer, disorders of development,
    inflammatory diseases of the breast, fibrocystic changes, proliferative
    breast disease and non-carcinoma tumours.
XX
CC Note: The sequence data for this patent did not form part of the printed
    specification, but was obtained in electronic format directly from WIPO
    at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 130 AA;
    Query Match 64.6%; Score 73; DB 22; Length 130;
    Best Local Similarity 75.0%; Pred. No. 0.041;
    Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPPKKKK 20
    |||||: |||||: |||||:
Db 54 RRRRRKKRRRRRRKKKKK 73

RESULT 30
ABG59141
ID ABG59141 standard; Peptide; 80 AA.
XX
AC ABG59141;
XX
XX 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID No 37789.
XX

```

KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX Homo sapiens.

OS WO200157273-A2.
XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00664.
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for
XX analysing gene expression in human adult liver -
XX Claim 27; SEQ ID NO 37789; 659pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult
XX liver. (I) may be used for predicting, measuring and displaying gene
XX expression in samples derived from human adult liver. The genes
XX identified may be involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
XX is associated with coronary heart disease. ABG47348-ABG5930 represent
XX human liver single exon encoded peptides of the invention.

XX Note: The sequence information for this patent does not appear in the
XX printed specification but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 80 AA;

Query Match 63.7%; Score 72; DB 22; Length 80;
Best Local Similarity 88.2%; Pred. No. 0.036; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 1 RRRRRRGWRRRRRPPK 17
Db 62 RRRRRRGWRRRRRPPK 78

RESULT 31
ABB43770
ID ABB43770 standard; Peptide; 80 AA.

XX ABB43770;

XX 04-FEB-2002 (first entry)

XX Peptide #11276 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX Homo sapiens.
XX WO200157277-A2.
XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00669.

XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for
XX analysing gene expression in human foetal liver -
XX Claim 27; SEQ ID NO 36405; 639pp + sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a peptide encoded by a single exon
XX nucleic acid probe of the invention.
XX Note: The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 80 AA;

Query Match 63.7%; Score 72; DB 22; Length 80;
Best Local Similarity 88.2%; Pred. No. 0.036; 2; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 1 RRRRRRGWRRRRRPPK 17
Db 62 RRRRRRGWRRRRRPPK 78

RESULT 32
ABB26713
ID ABB26713 standard; Protein; 80 AA.

XX ABB26713;

XX 23-JAN-2002 (first entry)

XX Protein #8712 encoded by probe for measuring heart cell gene expression.
XX Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.

XX Homo sapiens.

XX WO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00666.

XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-48899/53.
 DR Single exon nucleic acid probes for analyzing gene expression in human
 XX hearts -
 XX Claim 15; SEQ ID No 28483; 530pp; English.
 XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX SQ Sequence 80 AA;
 Query Match 63.7%; Score 72; DB 22; Length 80;
 Best Local Similarity 88.2%; Pred. No. 0.036;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RRRRRWGRRRRRPKK 17
 DB 62 RRRRRRGRRRRRKKK 78
 RESULT 33
 AAM64732
 ID AAM64732 standard; Protein; 80 AA.
 XX
 AC AAM64732;
 XX
 DT 05-NOV-2001 (first entry)
 XX Human brain expressed single exon probe encoded protein SEQ ID NO: 36837.
 XX Human; brain expressed exon; gene expression analysis; probe;
 XX microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 XX epilepsy; cancer.
 XX Homo sapiens.
 XX WO200157275-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US00667.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0632366.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-483446/52.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 XX brains -
 XX Claim 15; SEQ ID No 28483; 530pp; English.
 XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX SQ Sequence 80 AA;
 Query Match 63.7%; Score 72; DB 22; Length 80;
 Best Local Similarity 88.2%; Pred. No. 0.036;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RRRRRWGRRRRRPKK 17
 DB 62 RRRRRRGRRRRRKKK 78
 RESULT 34
 AAM77502
 ID AAM77502 standard; Protein; 80 AA.
 XX
 AC AAM77502;
 XX
 DT 06-NOV-2001 (first entry)
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 37808.
 XX Human; bone marrow expressed exon; gene expression analysis; probe;
 XX microarray; cancer; leukaemia; lymphoma; myeloma.
 XX Homo sapiens.
 XX WO200157276-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US00668.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0632366.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488990/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human bone marrow -
 XX Example 4; SEQ ID NO: 37808; 650pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.
 XX
 XX SQ Sequence 80 AA;
 Query Match 63.7%; Score 72; DB 22; Length 80;
 Best Local Similarity 88.2%; Pred. No. 0.036;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RRRRRWGRRRRRPKK 17
 DB 62 RRRRRRGRRRRRKKK 78
 RESULT 35
 AAM77502
 ID AAM77502 standard; Protein; 80 AA.
 XX
 AC AAM77502;
 XX
 DT 06-NOV-2001 (first entry)
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 37808.
 XX Human; bone marrow expressed exon; gene expression analysis; probe;
 XX microarray; cancer; leukaemia; lymphoma; myeloma.
 XX Homo sapiens.
 XX WO200157276-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 30-JAN-2001; 2001WO-US00668.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 30-JUN-2000; 2000US-0608408.
 XX 03-AUG-2000; 2000US-0632366.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488990/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human bone marrow -
 XX Example 4; SEQ ID NO: 37808; 650pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.
 XX
 XX SQ Sequence 80 AA;
 Query Match 63.7%; Score 72; DB 22; Length 80;
 Best Local Similarity 88.2%; Pred. No. 0.036;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RRRRRWGRRRRRPKK 17
 DB 62 RRRRRRGRRRRRKKK 78

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKK 17
 ||||| ||||| ||
 Db 62 RRRRRRGRRRRRKKK 78

RESULT 35
 AAM21431
 ID AAM21431 standard; Protein; 80 AA.
 XX AC AAM21431;
 XX DT 12-OCT-2001 (first entry)
 XX DE Peptide #7865 encoded by probe for measuring cervical gene expression.
 XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
 XX KW cervical cancer.
 XX OS Homo sapiens.
 XX PN WO200157278-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US00670.
 XX PR 04-FEB-2000; 2000US-0180312.
 XX PR 26-MAY-2000; 2000US-0207456.
 XX PR 30-JUN-2000; 2000US-0608408.
 XX PR 03-AUG-2000; 2000US-0632366.
 XX PR 21-SEP-2000; 2000US-0234687.
 XX PR 27-SEP-2000; 2000US-0236359.
 XX PR 04-OCT-2000; 2000GB-0024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488901/53.
 XX DR Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human cervical epithelial cells -
 XX Claim 27; SEQ ID No 26257; 487pp; English.
 XX PS The present invention relates to human single exon nucleic acid probes
 CC (SENP: see AAT10068-AA128459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 80 AA;
 Query Match 63.7%; Score 72; DB 22; Length 80;
 Best Local Similarity 88.2%; Pred. No. 0.036;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKK 17
 ||||| ||||| ||
 Db 62 RRRRRRGRRRRRKKK 78

RESULT 36
 AAM37674
 ID AAM37674 standard; Protein; 80 AA.

XX AAM37674;
 AC 17-OCT-2001 (first entry)
 DT Peptide #11711 encoded by probe for measuring placental gene expression.
 DE Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 KW OS Homo sapiens.
 XX PN WO200157272-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US00663.
 XX PR 04-FEB-2000; 2000US-0180312.
 XX PR 26-MAY-2000; 2000US-0207456.
 XX PR 30-JUN-2000; 2000US-0608408.
 XX PR 03-AUG-2000; 2000US-0632366.
 XX PR 21-SEP-2000; 2000US-0234687.
 XX PR 27-SEP-2000; 2000US-0236359.
 XX PR 04-OCT-2000; 2000GB-0024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-48897/53.
 XX DR Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human placenta -
 XX Claim 27; SEQ ID No 37943; 654pp; English.
 XX PS The present invention relates to single exon nucleic acid probes (SENP:
 CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 XX SQ Sequence 80 AA;
 Query Match 63.7%; Score 72; DB 22; Length 80;
 Best Local Similarity 88.2%; Pred. No. 0.036;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKK 17
 ||||| ||||| ||
 Db 62 RRRRRRGRRRRRKKK 78

RESULT 37
 ABG46527
 ID ABG46527 standard; Peptide; 80 AA.
 XX AC ABG46527;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 36192.
 XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;

KW hyaline membrane disease.
 XX Homo sapiens.
 XX WO200186003-A2.
 PN 15-NOV-2001.
 XX 30-JAN-2001; 2001WO-US00665.
 XX 04-FEB-2000; 2000US-180312P.
 PR 26-MAY-2000; 2000US-207456P.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-236359P.
 PR 04-OCT-2000; 2000GB-0024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.
 XX Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples -
 XX Claim 27; SEQ ID No 36192; 634pp; English.
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of
 CC probes; the novel set of probes which hybridize at high stringency to a
 CC nucleic acid expressed in the human lung; measuring gene expression in a
 CC sample derived from human lung, comprising (a) contacting the array with
 CC a collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of
 CC the array; identifying exons in a eukaryotic genome, comprising
 CC (a) algorithmically predicting at least one exon from genomic sequences
 CC of the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene
 CC expression analysis, and for identifying exons in a gene, particularly
 CC using human lung derived mRNA and for the study of lung diseases
 CC such as asthma, lung cancer, chronic obstructive pulmonary disease
 CC (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
 CC fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
 CC Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary
 CC haemangioendothelioma, pulmonary histiocytosis, lymphangioleiomyomatosis,
 CC pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic
 CC pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension
 CC and hyaline membrane disease. The present sequence is a peptide/protein
 CC encoded by a single exon probe of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

Best Local Similarity 88.2%; Pred. No. 0.036;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RRRRRWGRRRRRPKK 17
 DB 62 RRRRRRGRRRRRKKK 78
 RESULT 38
 ABG26520
 ID ABG26520 standard; Protein; 99 AA.
 XX AC ABG26520;
 XX 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #26511.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US08631.
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX (HYSE-) HYSEQ INC.
 XX Dmanac RT, Liu C, Tang YT;
 PI WPI; 2001-639362/73.
 XX N-PSDB; AAS90707.
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 20; SEQ ID No 56879; 103pp; English.
 PS The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 99 AA;
 SQ Query Match 63.7%; Score 72; DB 22; Length 99;
 Best Local Similarity 66.7%; Pred. No. 0.044;
 Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPCKKRV 21
||||| ||||| :|||:
Db .79 RRRRRRRRRRRRRRRRKI 99

RESULT 39
AAM51399
ID AAM51399 standard; Peptide; 54 AA.
AC AAM51399;
XX
XX 15-JAN-2002 (first entry)
DT Synthetic protamine family consensus kink motif derived peptide 9.
DE
DE Synthetic protamine family consensus kink motif derived peptide 9.
XX
XX Hybridisation device; single base pair difference; diagnostic test;
KW protein purification; nucleic acid purification; secondary structure;
KW Saline Al; protamine.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Duplication 1..8
FT /label= Direct_repeat
FT /note= "Unit comprising [(Arg)n-Gly-Gly] repeated at
FT positions 9-16, 17-24, 25-32, 33-40 and 41-48"
FT Misc-difference 1..6
FT /note= "1-4 arginine residues of each repeat unit are
FT optionally absent"
FT Misc-difference 17..48
FT /note= "Repeat units 17-24, 25-32, 33-40 and 41-48
FT optionally absent"
FT Misc-difference 49..54
FT /note= "1-4 arginine residues are optionally absent"
FT
XX WO200166687-A1.
FN
XX
XX 13-SEP-2001.
PD
XX
XX 24-AUG-2000; 2000WO-US23438.
PF
XX
XX 09-MAR-2000; 2000US-0522240.
PR
XX 10-AUG-2000; 2000US-0636268.
PR
XX (GENO-) GENOMETRIX GENOMIX INC.
PA
XX
XX Hogan M, Powderill T, Iverson B, Belosludtsev YY, Belosludtsev IY;
PI
XX
XX WPI; 2001-611328/70.
DR
XX
XX Association device for nucleic acid-based diagnostic test, isolation of
PT nucleic acids, comprises oligonucleotide probe and solid substrate
PT having support surface comprising association surface for linking probe
PT to substrate -
XX
XX Claim 55; Page -; 101pp; English.
PS
XX
XX The invention relates to an association/hybridisation device comprising
CC nucleic acid and polypeptide probes, or combinations of these, linked to
CC a porous solid substrate, comprising an external substrate surface and
CC several internal pores. The pore surfaces comprise an association surface
CC which is charged with net positive or negative charge density where the
CC pH is lower or higher than the pI of association surface. The device is
CC useful for associating a nucleic acid or a polypeptide in a sample to a
CC nucleic acid or a polypeptide probe. The device is also useful for
CC detecting a single base pair difference between a nucleic acid in a test
CC sample and an oligonucleotide probe. The device finds application in
CC nucleic acid-based diagnostic tests, isolation and purification of
CC nucleic acids or polypeptides from a sample. The device can be used at
CC any temperature and the kinetics of association between the
CC oligonucleotide probe and the nucleic acid in the test sample are 10 fold
CC more rapid than the kinetics of association under conditions when the

CC substrate surface or association surface has a neutral or net negative
CC charge density. The device and the method can be used for hybridisation
CC of probes to target DNA or RNA at low bulk ion concentrations. The
CC present sequence is that of a synthetic peptide. Known members of the
CC protamine family, including Saline Al, are defined by the consensus
CC sequence [(Arg)n-bend]m-Argn, where n=3-5, m=3-5 and bend = 1-3 amino
CC acid sequence capable of inducing a "kink" in the peptide backbone.
CC Note: The present peptide sequence is not given in the specification but
CC is derived from a consensus sequence given in Claim 55 as
CC [(Arg)n-Gly-Gly]n-Argn, where n is the integer 2, 3, 4, 5 or 6.
XX
SQ Sequence 54 AA;
Query Match 52.8%; Score 71; DB 22; Length 54;
Best Local Similarity 70.0%; Pred. No. 0.035; 3; Indels 0; Gaps 0;
Matches 14; Conservative 3; Mismatches 3;
Qy 1 RRRRRWGRRRRRPCKKRV 20
||||| ||||| :|||:
Db 1 RRRRRGGRRRRRRGRRR 20
||||| ||||| :|||:
RESULT 40
ABG26500
ID ABG26500 standard; Protein; 78 AA.
XX
XX ABG26500;
AC
XX 18-FEB-2002 (first entry)
DT
XX Novel human diagnostic protein #26491.
DE
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
FN
XX
XX 11-OCT-2001.
PD
XX
XX 30-MAR-2001; 2001WO-US08631.
PF
XX
XX 31-MAR-2000; 2000US-0540217.
PR
XX 23-AUG-2000; 2000US-0649167.
PR
XX (HYSE-) HYSEQ INC.
PA
XX
XX Drmanac RT, Liu C, Tang YT;
PI
XX
XX WPI; 2001-639362/73.
DR
XX N-PSDB; AAS90687.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 56859; 103pp; English.
PS
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG0377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX
 SQ Sequence 78 AA;

Query Match 62.8%; Score 71; DB 22; Length 78;
 Best Local Similarity 77.8%; Pred. No. 0.048;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWRRRRRRPKKK 18
 ||||| |||||:
 Db 61 RRRRRRGRRRKKKKK 78

Search completed: January 23, 2004, 11:17:40
 Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2004, 11:18:11 ; Search time 177 Seconds
(without alignments)
107.956 Million cell updates/sec

Title: US-10-002-884A-2

Perfect score: 113

Sequence: 1 RRRRRGRRRRRRPKKKRKV 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:*

- 1: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
- 2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
- 3: /cgn2_6/ptodata/1/paa/US07 COMB.pcp.*
- 4: /cgn2_6/ptodata/1/paa/US080 COMB.pcp.*
- 5: /cgn2_6/ptodata/1/paa/US081 COMB.pcp.*
- 6: /cgn2_6/ptodata/1/paa/US082 COMB.pcp.*
- 7: /cgn2_6/ptodata/1/paa/US083 COMB.pcp.*
- 8: /cgn2_6/ptodata/1/paa/US084 COMB.pcp.*
- 9: /cgn2_6/ptodata/1/paa/US085 COMB.pcp.*
- 10: /cgn2_6/ptodata/1/paa/US086 COMB.pcp.*
- 11: /cgn2_6/ptodata/1/paa/US087 COMB.pcp.*
- 12: /cgn2_6/ptodata/1/paa/US088 COMB.pcp.*
- 13: /cgn2_6/ptodata/1/paa/US089 COMB.pcp.*
- 14: /cgn2_6/ptodata/1/paa/US090 COMB.pcp.*
- 15: /cgn2_6/ptodata/1/paa/US091 COMB.pcp.*
- 16: /cgn2_6/ptodata/1/paa/US092 COMB.pcp.*
- 17: /cgn2_6/ptodata/1/paa/US093 COMB.pcp.*
- 18: /cgn2_6/ptodata/1/paa/US094 COMB.pcp.*
- 19: /cgn2_6/ptodata/1/paa/US095 COMB.pcp.*
- 20: /cgn2_6/ptodata/1/paa/US096 COMB.pcp.*
- 21: /cgn2_6/ptodata/1/paa/US097A COMB.pcp.*
- 22: /cgn2_6/ptodata/1/paa/US097B COMB.pcp.*
- 23: /cgn2_6/ptodata/1/paa/US098 COMB.pcp.*
- 24: /cgn2_6/ptodata/1/paa/US099A COMB.pcp.*
- 25: /cgn2_6/ptodata/1/paa/US099B COMB.pcp.*
- 26: /cgn2_6/ptodata/1/paa/US100 COMB.pcp.*
- 27: /cgn2_6/ptodata/1/paa/US101 COMB.pcp.*
- 28: /cgn2_6/ptodata/1/paa/US102 COMB.pcp.*
- 29: /cgn2_6/ptodata/1/paa/US103 COMB.pcp.*
- 30: /cgn2_6/ptodata/1/paa/US104 COMB.pcp.*
- 31: /cgn2_6/ptodata/1/paa/US106 COMB.pcp.*
- 32: /cgn2_6/ptodata/1/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB ID	Description
1	113	100.0	21	1 PCT-US02-34980-2 Sequence 2, Appli

113	100.0	21	26	US-10-002-884A-2	Sequence 2, Appli
106	93.8	21	1	PCT-US02-34980-3	Sequence 3, Appli
106	93.8	21	26	US-10-002-884A-3	Sequence 3, Appli
90	79.6	32	1	PCT-US02-34980-1	Sequence 1, Appli
90	79.6	32	26	US-10-002-884A-1	Sequence 1, Appli
7	76.1	405	1	PCT-US01-08631-56902	Sequence 56902, A
7	76.1	405	1	PCT-US01-08631-42091	Sequence 42091, A
8	69.0	56	1	PCT-US01-08631-56877	Sequence 56877, A
78	69.0	761	1	PCT-US01-08631-176818	Sequence 176818, A
76.5	67.7	342	30	US-10-437-963-176818	Sequence 23590, A
11	76.5	342	30	US-10-438-246-23590	Sequence 4, Appli
12	76.7	31	1	PCT-US02-34980-4	Sequence 4, Appli
13	76.7	31	26	US-10-002-884A-4	Sequence 4, Appli
14	76.7	31	26	PCT-US01-08631-56875	Sequence 56875, A
15	76.7	808	1	PCT-US01-08631-35726	Sequence 35726, A
16	75.6	86	1	PCT-US01-00563-26795	Sequence 26795, A
17	75.6	86	23	US-09-864-761-33832	Sequence 33832, A
18	75.6	86	27	US-10-182-993-25967	Sequence 25967, A
19	75.6	86	27	US-10-182-995-20304	Sequence 20304, A
20	75.6	86	27	US-10-182-997-18945	Sequence 18945, A
21	75.6	86	27	US-10-182-998-10597	Sequence 10597, A
22	75.6	86	28	US-10-203-134-26555	Sequence 26555, A
23	75.6	86	28	US-10-203-135-25561	Sequence 25561, A
24	75.6	86	28	US-10-203-136-26562	Sequence 26562, A
25	75.6	86	28	US-10-203-137-26795	Sequence 26795, A
26	75.6	86	28	US-10-203-138-10861	Sequence 10861, A
27	75.6	86	28	US-10-203-138A-10861	Sequence 10861, A
28	75.6	86	28	US-10-203-139-25699	Sequence 25699, A
29	75.6	86	32	US-60-236-359-15217	Sequence 15217, A
30	74.5	109	1	PCT-US01-08631-56866	Sequence 56866, A
31	73.5	762	23	US-09-831-578-196	Sequence 196, App
32	73.5	57	1	PCT-US01-01354-10551	Sequence 10551, A
33	73.5	57	22	US-09-764-905-10551	Sequence 10551, A
34	73.5	57	26	US-10-092-399-10551	Sequence 10551, A
35	73.5	71	26	US-10-029-386-31410	Sequence 31410, A
36	73.5	130	1	PCT-US01-00663-28605	Sequence 28605, A
37	73.5	130	23	US-09-864-761-35536	Sequence 35536, A
38	73.5	130	27	US-10-182-993-27728	Sequence 27728, A
39	73.5	130	27	US-10-182-995-22008	Sequence 22008, A
40	73.5	130	27	US-10-182-997-20652	Sequence 20652, A
41	73.5	130	27	US-10-182-998-12304	Sequence 12304, A
42	73.5	130	28	US-10-203-134-28313	Sequence 28313, A
43	73.5	130	28	US-10-203-136-28299	Sequence 28299, A
44	73.5	130	28	US-10-203-137-28605	Sequence 28605, A
45	73.5	130	28	US-10-203-138-12613	Sequence 12613, A

ALIGNMENTS

RESULT 1
PCT-US02-34980-2
; Sequence 2, Application PC/TUS0234980
; GENERAL INFORMATION:
; APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
; TITLE OF INVENTION: PEPTIDES THAT DELIVER ANTISENSE OLIGONUCLEOTIDES WHICH DOWNREGU
; TITLE OF INVENTION: PROTEIN EXPRESSION IN CELLS
; FILE REFERENCE: 0575/63293-pct
; CURRENT APPLICATION NUMBER: PCT/US02/34980
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: us 10/002,884
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: NOVEL PEPTIDE - SV40/PROTAMINE SOURCE
PCT-US02-34980-2

Query Match 100.0%; Score 113; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;

Sequence 3, Application JS/10002884A
CRYPTIC INFORMATION

```
; LENGTH: 32
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: NOVEL PEPTIDE - SV40/PROTAMINE SOURCE
US-10-002-884A-1

Query Match      79.6%; Score 90; DB 26; Length 32;
Best Local Similarity 74.1%; Pred. No. 0.0047;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 1;

QY 1 RRRRWGRR-----RRRPKKKKK 21
Db 6 RRRRRFGRRRRRVWRRRPKKKKK 32

RESULT 7
PCT-US01-08631-56902
; Sequence 56902, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56902
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (29)..(51)
; OTHER INFORMATION: Domain in SPLA and the Ryanodine Receptor domain identified
; OTHER INFORMATION: by eMATRIX, accession number PF00622B, p-value=1.783e-16, raw score
PCT-US01-08631-56902

Query Match      76.1%; Score 86; DB 1; Length 405;
Best Local Similarity 80.0%; Pred. No. 0.13;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRRRPKKKKK 20
Db 257 RRRRWRRRRRRRRKKKK 276

RESULT 8
PCT-US01-08631-42091
; Sequence 42091, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 42091
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN

; LENGTH: 32
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: NOVEL PEPTIDE - SV40/PROTAMINE SOURCE
US-10-002-884A-1

Query Match      79.6%; Score 90; DB 26; Length 32;
Best Local Similarity 74.1%; Pred. No. 0.0047;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 1;

QY 1 RRRRWGRR-----RRRPKKKKK 21
Db 6 RRRRRFGRRRRRVWRRRPKKKKK 32

RESULT 7
PCT-US01-08631-56902
; Sequence 56902, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56902
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (29)..(51)
; OTHER INFORMATION: Domain in SPLA and the Ryanodine Receptor domain identified
; OTHER INFORMATION: by eMATRIX, accession number PF00622B, p-value=1.783e-16, raw score
PCT-US01-08631-56902

Query Match      76.1%; Score 86; DB 1; Length 405;
Best Local Similarity 80.0%; Pred. No. 0.13;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRRRPKKKKK 20
Db 257 RRRRWRRRRRRRRKKKK 276

RESULT 8
PCT-US01-08631-42091
; Sequence 42091, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 42091
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN

; LOCATION: (6)..(41)
; OTHER INFORMATION: Matrix protein (MA) p15. domain identified by eMATRIX,
; OTHER INFORMATION: accession number PF01140D, p-value=7.625e-12, raw score of 15.54
PCT-US01-08631-42091

Query Match      69.0%; Score 78; DB 1; Length 56;
Best Local Similarity 80.0%; Pred. No. 0.18;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRRRPKKKKK 20
Db 19 RRRRRRRRRRRRPKKKKK 38

RESULT 9
PCT-US01-08631-56877
; Sequence 56877, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56877
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (725)..(752)
; OTHER INFORMATION: Protamine P1 proteins domain identified by eMATRIX, accession
; OTHER INFORMATION: number BL00048, p-value=6.667e-28, raw score of 6.39
PCT-US01-08631-56877

Query Match      69.0%; Score 78; DB 1; Length 761;
Best Local Similarity 85.0%; Pred. No. 2;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRRRPKKKKK 20
Db 740 RRRRRRRRRRRRPKKKKK 759

RESULT 10
US-10-437-963-176818
; Sequence 176818, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176818
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MBT4530_74530C.1.pap
```

US-10-437-963-176818

Query Match 67.7%; Score 76.5; DB 30; Length 342;
Best Local Similarity 57.7%; Pred. No. 1.4;
Matches 15; Conservative 3; Mismatches 5; Gaps 1;

QY 1 RRRRRWGR-----RRRRPPKKRKV 21
DB 295 RRRRRWGRNSQRRRRPPSPERRI 320

RESULT 11

US-10-438-246-23590
; Sequence 23590, Application US/10438246
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Transcription in Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53333)B
; CURRENT APPLICATION NUMBER: US/10/438,246
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 39516
; SEQ ID NO 23590
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: TF_OsC4338_1.pep
US-10-438-246-23590

Query Match 67.7%; Score 76.5; DB 30; Length 342;
Best Local Similarity 57.7%; Pred. No. 1.4;
Matches 15; Conservative 3; Mismatches 5; Gaps 1;

QY 1 RRRRRWGR-----RRRRPPKKRKV 21
DB 295 RRRRRWGRNSQRRRRPPSPERRI 320

RESULT 12

PCT-US02-34980-4
; Sequence 4, Application PC/TUS0234980
; GENERAL INFORMATION:
; APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
; TITLE OF INVENTION: PEPTIDES THAT DELIVER ANTISENSE OLIGONUCLEOTIDES WHICH DOWNREGULATE
; TITLE OF INVENTION: PROTEIN EXPRESSION IN CELLS
; FILE REFERENCE: 0575/63293-pct
; CURRENT APPLICATION NUMBER: PCT/US02/34980
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: us 10/002,884
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 31
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: CONTROL PEPTIDE
PCT-US02-34980-4

Query Match 67.3%; Score 76; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 0.18;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRNSQRRRRPPKKRKV 20

DB 6 RRRRRFGRRRRRVVRRRK 25

RESULT 13

US-10-002-884A-4
; Sequence 4, Application US/10002884A
; GENERAL INFORMATION:
; APPLICANT: Stein, Cy A
; APPLICANT: Benimetskaya, Lyuba
; APPLICANT: Guzzo-Pernell, Nancy
; TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DOWN
; TITLE OF INVENTION: PKC-PROTEIN EXPRESSION IN CELLS
; FILE REFERENCE: 0575/63293
; CURRENT APPLICATION NUMBER: US/10/002,884A
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 31
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: CONTROL PEPTIDE
US-10-002-884A-4

Query Match 67.3%; Score 76; DB 26; Length 31;
Best Local Similarity 75.0%; Pred. No. 0.18;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRNSQRRRRPPKKRKV 20
DB 6 RRRRRFGRRRRRVVRRRK 25

RESULT 14

PCT-US01-08631-56875
; Sequence 56875, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56875
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)..(59)
; OTHER INFORMATION: Troponin domain identified by eMATRIX, accession number
; OTHER INFORMATION: PF00992A, p-value=2.775e-10, raw score of 16.67
PCT-US01-08631-56875

Query Match 67.3%; Score 76; DB 1; Length 91;
Best Local Similarity 80.0%; Pred. No. 0.48;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRNSQRRRRPPKKRKV 20
DB 48 RRRRRRRRRRRRRKKKKK 67

RESULT 15

PCT-US01-08631-35726
; Sequence 35726, Application PC/TUS0108631

```

; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 35726
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (209)..(220)
; OTHER INFORMATION: PROTEIN REPEAT MUSCLE CALCIUM-BI domain identified by
; OTHER INFORMATION: eMATRIX, accession number PD0301A, p-value=2.800e-09, raw score
; OTHER INFORMATION: 10.24
; NAME/KEY: DOMAIN
; LOCATION: (470)..(673)
; OTHER INFORMATION: FtsK/SpoIIIE family domain identified by Pfam, accession name
; OTHER INFORMATION: FtsK_SpoIIIE, E-value=0.097, Pfam score of -41.0
PCT-US01-08631-35726

```

```

Query Match      67.3%; Score 76; DB 1; Length 808;
Best Local Similarity 80.0%; Pred. No. 3.5;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 RRRRRRGGRRRRRPPKKRK 20
    ||||| ||||| |||||
DB 231 RRRRRRRRRRRRRKKKKK 250

```

```

RESULT 16
PCT-US01-00663-26795
; Sequence 26795, Application PC/TUS0100663
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: PCT/US01/00663
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 26795
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1

```

```

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 13
PCT-US01-00663-26795
Query Match      66.4%; Score 75; DB 1; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 RRRRRRGGRRRRRPPKKRK 20
    :||||| ||||| |||||
DB 7 KRRRRRRRRRRRRKKKKK 26

```

```

RESULT 17
US-09-864-761-33832
; Sequence 33832, Application US/09864761
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33832
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.8

```


OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 13
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.5
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.3
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.1
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.1
 US-09-864-761-33832

Query Match 66.4%; Score 75; DB 23; Length 86;
 Best Local Similarity 70.0%; Pred. No. 0.59;
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRRPPKKKK 20
 :|||||:|||||:|||||:
 Db 7 KRRRRRGRRRRRRKKKKKK 26

RESULT 18
 US-10-182-993-25967
 Sequence 25967, Application US/10182993
 GENERAL INFORMATION:
 APPLICANT: Molecular Dynamics, Inc.
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN
 FILE REFERENCE: PB 0004 WO 2
 CURRENT APPLICATION NUMBER: US/10/182,993
 CURRENT FILING DATE: 2002-08-02
 PRIOR FILING DATE: 04 February 2000 (04.02.00)
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 26 May 2000 (26.05.00)
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 03 August 2000 (03.08.00)
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 03 October 2000 (03.10.00)
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 27 September 2000 (27.09.00)
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 30 June 2000 (30.06.00)
 NUMBER OF SEQ ID NOS: 37811
 SOFTWARE: Molecular Dynamics Sequence Listing Engine
 SEQ ID NO 25967
 LENGTH: 86
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC007857.1
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.3
 US-10-182-993-25967

Query Match 66.4%; Score 75; DB 27; Length 86;
 Best Local Similarity 70.0%; Pred. No. 0.59;
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRRPPKKKK 20
 :|||||:|||||:|||||:
 Db 7 KRRRRRGRRRRRRKKKKKK 26

RESULT 19
 US-10-182-995-20304
 Sequence 20304, Application US/10182995
 GENERAL INFORMATION:
 APPLICANT: Molecular Dynamics, Inc.
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN HEART
 FILE REFERENCE: PB 0004 WO 1
 CURRENT APPLICATION NUMBER: US/10/182,995
 CURRENT FILING DATE: 2002-08-02
 PRIOR FILING DATE: 04 February 2000 (04.02.00)
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 26 May 2000 (26.05.00)
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 03 August 2000 (03.08.00)
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 03 October 2000 (03.10.00)
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 27 September 2000 (27.09.00)
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 21 September 2000 (21.09.00)
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 30 June 2000 (30.06.00)
 NUMBER OF SEQ ID NOS: 29119
 SOFTWARE: Molecular Dynamics Sequence Listing Engine
 SEQ ID NO 20304
 LENGTH: 86
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AC007857.1
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.8
 US-10-182-995-20304

Query Match 66.4%; Score 75; DB 27; Length 86;
 Best Local Similarity 70.0%; Pred. No. 0.59;
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRRPPKKKK 20
 :|||||:|||||:|||||:
 Db 7 KRRRRRGRRRRRRKKKKKK 26

RESULT 20
 US-10-182-997-18945
 Sequence 18945, Application US/10182997
 GENERAL INFORMATION:
 APPLICANT: Molecular Dynamics, Inc.
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HELA
 FILE REFERENCE: PB 0004 WO 10
 CURRENT APPLICATION NUMBER: US/10/182,997
 CURRENT FILING DATE: 2002-08-02
 PRIOR FILING DATE: 04 February 2000 (04.02.00)
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 26 May 2000 (26.05.00)
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 03 August 2000 (03.08.00)
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 03 October 2000 (03.10.00)
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 27 September 2000 (27.09.00)
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 21 September 2000 (21.09.00)
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 30 June 2000 (30.06.00)
 NUMBER OF SEQ ID NOS: 26941
 SOFTWARE: Molecular Dynamics Sequence Listing Engine
 SEQ ID NO 18945

```

; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; FEATURE: EXPRESSED IN HELA, SIGNAL = 8.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.7
US-10-182-997-18945

Query Match          66.4%; Score 75; DB 27; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
   :|||||:|||||:|||||:
Db 7 KRRRRRGRRRRRKKKKKKR 26

RESULT 21
US-10-182-998-10597
; Sequence 10597, Application US/10182998
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HBL 100
; FILE REFERENCE: PB 0004 WO 9
; CURRENT APPLICATION NUMBER: US/10/182,998
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15009
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 10597
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; FEATURE: EXPRESSED IN HELA, SIGNAL = 8.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.7
US-10-182-998-10597

Query Match          66.4%; Score 75; DB 27; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
   :|||||:|||||:|||||:
Db 7 KRRRRRGRRRRRKKKKKKR 26

RESULT 22
US-10-203-134-26555
; Sequence 26555, Application US/10203134
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
```

```

; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BONE MARROW
; FILE REFERENCE: PB 0004 WO 6
; CURRENT APPLICATION NUMBER: US/10/203,134
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38628
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 26555
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; FEATURE: EXPRESSED IN BONE MARROW, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12
US-10-203-134-26555

Query Match          66.4%; Score 75; DB 28; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
   :|||||:|||||:|||||:
Db 7 KRRRRRGRRRRRKKKKKKR 26

RESULT 23
US-10-203-135-25561
; Sequence 25561, Application US/10203135
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN LUNG
; FILE REFERENCE: PB 0004 WO 5
; CURRENT APPLICATION NUMBER: US/10/203,135
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37012
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
```

```

; SEQ ID NO 25561
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.1
US-10-203-135-25561

```

```

Query Match 66.4%; Score 75; DB 28; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 RRRRRGRRRRRPPKKKK 20
   :|||||:|||||:|||||:
DB 7 KRRRRRGRRRRRKKKKK 26

```

```

RESULT 24
US-10-203-136-26562
; Sequence 10861, Application US/10203136
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 3
; CURRENT APPLICATION NUMBER: US/10/203,136
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38578
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 26562
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.8
US-10-203-136-26562

```

```

Query Match 66.4%; Score 75; DB 28; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 RRRRRGRRRRRPPKKKK 20
   :|||||:|||||:|||||:
DB 7 KRRRRRGRRRRRKKKKK 26

```

```

RESULT 25
US-10-203-137-26795
; Sequence 10861, Application US/10203137
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.

```

```

; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 7
; CURRENT APPLICATION NUMBER: US/10/203,137
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 38837
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 26795
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 13
US-10-203-137-26795

```

```

Query Match 66.4%; Score 75; DB 28; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 RRRRRGRRRRRPPKKKK 20
   :|||||:|||||:|||||:
DB 7 KRRRRRGRRRRRKKKKK 26

```

```

RESULT 26
US-10-203-138-10861
; Sequence 10861, Application US/10203138
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438

```

```
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 10861
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.5
US-10-203-138-10861
```

```
Query Match          66.4%; Score 75; DB 28; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 RRRRRWGRRRRRPKKKR 20
   :|||||:|||||:|||||:
Db 7 KRRRRRGRRRRRPKKKR 26
```

RESULT 27

```
US-10-203-138A-10861
; Sequence 10861, Application US/10203138A
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 8
; CURRENT APPLICATION NUMBER: US/10/203,138A
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 15438
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 10861
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.5
US-10-203-138A-10861
```

```
Query Match          66.4%; Score 75; DB 28; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 RRRRRWGRRRRRPKKKR 20
   :|||||:|||||:|||||:
Db 7 KRRRRRGRRRRRPKKKR 26
```

RESULT 28

```
US-10-203-139-25699
; Sequence 25699, Application US/10203139
; GENERAL INFORMATION:
```

```
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: PB 0004 WO 4
; CURRENT APPLICATION NUMBER: US/10/203,139
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37156
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 25699
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.3
US-10-203-139-25699
```

```
Query Match          66.4%; Score 75; DB 28; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 RRRRRWGRRRRRPKKKR 20
   :|||||:|||||:|||||:
Db 7 KRRRRRGRRRRRPKKKR 26
```

RESULT 29

```
US-60-236-359-15217
; Sequence 15217, Application US/60236359
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: MDHMRP-4P
; CURRENT APPLICATION NUMBER: US/60/236,359
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 21709
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 15217
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 13
```

```
Query Match          66.4%; Score 75; DB 28; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 RRRRRWGRRRRRPKKKR 20
   :|||||:|||||:|||||:
Db 7 KRRRRRGRRRRRPKKKR 26
```

```
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.1
US-60-236-359-15217

Query Match          66.4%; Score 75; DB 32; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.59;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
   :||||| :||||| :|||:
Db 7 KRRRRRGRRRRRKKKKRK 26

RESULT 30
PCT-US01-08631-56866
; Sequence 56866, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56866
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (18)..(61)
; OTHER INFORMATION: p53 tumor antigen proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00348F, p-value=7.407e-10, raw score of 23.19
PCT-US01-08631-56866

Query Match          65.5%; Score 74; DB 1; Length 109;
Best Local Similarity 80.0%; Pred. No. 0.96;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
   :||||| :||||| :|||:
Db 68 KRRRRRGRRRRRKKKKRK 87

RESULT 31
US-09-831-578-196
; Sequence 196, Application US/09831578
; GENERAL INFORMATION:
; APPLICANT: Priml, Daniele
; APPLICANT: Fiordalisi, Gianfranco
; APPLICANT: Mantero, Giovanni Lorenzo
; APPLICANT: Mattioli, Sonia
; APPLICANT: Bonelli, Fabrizio
; APPLICANT: Sottini, Alessandra
; APPLICANT: Vaglini, Laura
; APPLICANT: Olivero, Paolo
; APPLICANT: Dal Corso, Andrea
; APPLICANT: Bonelli, Marco
; TITLE OF INVENTION: IDENTIFICATION OF SENV GENOTYPES
; FILE REFERENCE: HO-P021580S0 (10103530 / OTA 01-104)
; CURRENT APPLICATION NUMBER: US/09/831,578
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: PCT/EP99/08566
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: IT MI98A002437
; PRIOR FILING DATE: 1998-11-10
```

```
; PRIOR APPLICATION NUMBER: IT MI99A000923
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: EP 99113932.0
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: WO 00/28039
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: EP 99830298.8
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 196
; LENGTH: 762
; TYPE: PRT
; ORGANISM: SENV
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(762)
; OTHER INFORMATION: X represents unknown.
US-09-831-578-196

Query Match          65.0%; Score 73.5; DB 23; Length 762;
Best Local Similarity 50.0%; Pred. No. 6.4;
Matches 16; Conservative 3; Mismatches 2; Indels 11; Gaps 1;

QY 1 RRRRRWGRRRRRRRPKKKRK 21
   :||||| :||||| :|||:
Db 41 RRRRRRGRRRRRRGYRRRLRLRRRRRRKKKI 72

RESULT 32
PCT-US01-01354-10551
; Sequence 10551, Application PC/TUS0101354
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC004PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01354
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 42506
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10551
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (57)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-01354-10551

Query Match          64.6%; Score 73; DB 1; Length 57;
Best Local Similarity 75.0%; Pred. No. 0.69;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRRRPKKKRK 20
   :||||| :||||| :|||:
Db 35 RRRRRRGRRRRRKKKKRK 54

RESULT 33
US-09-764-905-10551
; Sequence 10551, Application US/09764905
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC004
; CURRENT APPLICATION NUMBER: US/09/764,905
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
```

1 PRIOR FILING DATE: 2000-06-28
2 PRIOR APPLICATION NUMBER: 60/217,487
3 PRIOR FILING DATE: 2000-07-11
4 PRIOR APPLICATION NUMBER: 60/225,758
5 PRIOR FILING DATE: 2000-08-14
6 PRIOR APPLICATION NUMBER: 60/220,963
7 PRIOR FILING DATE: 2000-07-26
8 PRIOR APPLICATION NUMBER: 60/217,496
9 PRIOR FILING DATE: 2000-07-11
10 PRIOR APPLICATION NUMBER: 60/225,447
11 PRIOR FILING DATE: 2000-08-14
12 PRIOR APPLICATION NUMBER: 60/218,290
13 PRIOR FILING DATE: 2000-07-14
14 PRIOR APPLICATION NUMBER: 60/225,757
15 PRIOR FILING DATE: 2000-08-14
16 PRIOR APPLICATION NUMBER: 60/226,868
17 PRIOR FILING DATE: 2000-08-22
18 PRIOR APPLICATION NUMBER: 60/216,647
19 PRIOR FILING DATE: 2000-07-07
20 PRIOR APPLICATION NUMBER: 60/225,267
21 PRIOR FILING DATE: 2000-08-14
22 PRIOR APPLICATION NUMBER: 60/251,869
23 PRIOR FILING DATE: 2000-12-08
24 PRIOR APPLICATION NUMBER: 60/235,834
25 PRIOR FILING DATE: 2000-09-27
26 PRIOR APPLICATION NUMBER: 60/234,274
27 PRIOR FILING DATE: 2000-09-21
28 PRIOR APPLICATION NUMBER: 60/234,223
29 PRIOR FILING DATE: 2000-09-21
30 PRIOR APPLICATION NUMBER: 60/228,924
31 PRIOR FILING DATE: 2000-08-30
32 PRIOR APPLICATION NUMBER: 60/224,518
33 PRIOR FILING DATE: 2000-08-14
34 PRIOR APPLICATION NUMBER: 60/236,369
35 PRIOR FILING DATE: 2000-09-29
36 PRIOR APPLICATION NUMBER: 60/224,519
37 PRIOR FILING DATE: 2000-08-14
38 PRIOR APPLICATION NUMBER: 60/220,964
39 PRIOR FILING DATE: 2000-07-26
40 PRIOR APPLICATION NUMBER: 60/241,809
41 PRIOR FILING DATE: 2000-10-20
42 PRIOR APPLICATION NUMBER: 60/249,299
43 PRIOR FILING DATE: 2000-11-17
44 PRIOR APPLICATION NUMBER: 60/236,327
45 PRIOR FILING DATE: 2000-09-29
46 PRIOR APPLICATION NUMBER: 60/241,785
47 PRIOR FILING DATE: 2000-10-20
48 PRIOR APPLICATION NUMBER: 60/244,617
49 PRIOR FILING DATE: 2000-11-01
50 PRIOR APPLICATION NUMBER: 60/225,268
51 PRIOR FILING DATE: 2000-08-14
52 PRIOR APPLICATION NUMBER: 60/236,368
53 PRIOR FILING DATE: 2000-09-29
54 PRIOR APPLICATION NUMBER: 60/251,856
55 PRIOR FILING DATE: 2000-12-08
56 PRIOR APPLICATION NUMBER: 60/251,868
57 PRIOR FILING DATE: 2000-12-08
58 PRIOR APPLICATION NUMBER: 60/229,344
59 PRIOR FILING DATE: 2000-09-01
60 PRIOR APPLICATION NUMBER: 60/234,997
61 PRIOR FILING DATE: 2000-09-25
62 PRIOR APPLICATION NUMBER: 60/229,343
63 PRIOR FILING DATE: 2000-09-01
64 PRIOR APPLICATION NUMBER: 60/229,345
65 PRIOR FILING DATE: 2000-09-01
66 PRIOR APPLICATION NUMBER: 60/229,287
67 PRIOR FILING DATE: 2000-09-01
68 PRIOR APPLICATION NUMBER: 60/229,513
69 PRIOR FILING DATE: 2000-09-05
70 PRIOR APPLICATION NUMBER: 60/231,413
71 PRIOR FILING DATE: 2000-09-08
72 PRIOR APPLICATION NUMBER: 60/229,509
73 PRIOR FILING DATE: 2000-09-05
74 PRIOR APPLICATION NUMBER: 60/236,367
75 PRIOR FILING DATE: 2000-09-29
76 PRIOR APPLICATION NUMBER: 60/237,039
77 PRIOR FILING DATE: 2000-10-02
78 PRIOR APPLICATION NUMBER: 60/237,038
79 PRIOR FILING DATE: 2000-10-02
80 PRIOR APPLICATION NUMBER: 60/236,370
81 PRIOR FILING DATE: 2000-09-29
82 PRIOR APPLICATION NUMBER: 60/236,802
83 PRIOR FILING DATE: 2000-10-02
84 PRIOR APPLICATION NUMBER: 60/237,037
85 PRIOR FILING DATE: 2000-10-02
86 PRIOR APPLICATION NUMBER: 60/237,040
87 PRIOR FILING DATE: 2000-10-02
88 PRIOR APPLICATION NUMBER: 60/240,960
89 PRIOR FILING DATE: 2000-10-20
90 PRIOR APPLICATION NUMBER: 60/239,935
91 PRIOR FILING DATE: 2000-10-13
92 PRIOR APPLICATION NUMBER: 60/239,937
93 PRIOR FILING DATE: 2000-10-13
94 PRIOR APPLICATION NUMBER: 60/241,787
95 PRIOR FILING DATE: 2000-10-20
96 PRIOR APPLICATION NUMBER: 60/246,474
97 PRIOR FILING DATE: 2000-11-08
98 PRIOR APPLICATION NUMBER: 60/246,532
99 PRIOR FILING DATE: 2000-11-08
100 PRIOR APPLICATION NUMBER: 60/249,216
101 PRIOR FILING DATE: 2000-11-17
102 PRIOR APPLICATION NUMBER: 60/249,210
103 PRIOR FILING DATE: 2000-11-17
104 PRIOR APPLICATION NUMBER: 60/226,681
105 PRIOR FILING DATE: 2000-08-22
106 PRIOR APPLICATION NUMBER: 60/225,759
107 PRIOR FILING DATE: 2000-08-14
108 PRIOR APPLICATION NUMBER: 60/225,213
109 PRIOR FILING DATE: 2000-08-14
110 PRIOR APPLICATION NUMBER: 60/227,182
111 PRIOR FILING DATE: 2000-08-22
112 PRIOR APPLICATION NUMBER: 60/225,214
113 PRIOR FILING DATE: 2000-08-14
114 PRIOR APPLICATION NUMBER: 60/235,836
115 PRIOR FILING DATE: 2000-09-27
116 PRIOR APPLICATION NUMBER: 60/230,438
117 PRIOR FILING DATE: 2000-09-06
118 PRIOR APPLICATION NUMBER: 60/215,135
119 PRIOR FILING DATE: 2000-06-30
120 PRIOR APPLICATION NUMBER: 60/225,266
121 PRIOR FILING DATE: 2000-08-14
122 PRIOR APPLICATION NUMBER: 60/249,218
123 PRIOR FILING DATE: 2000-11-17
124 PRIOR APPLICATION NUMBER: 60/249,208
125 PRIOR FILING DATE: 2000-11-17
126 PRIOR APPLICATION NUMBER: 60/249,213
127 PRIOR FILING DATE: 2000-11-17
128 PRIOR APPLICATION NUMBER: 60/249,212
129 PRIOR FILING DATE: 2000-11-17
130 PRIOR APPLICATION NUMBER: 60/249,207
131 PRIOR FILING DATE: 2000-11-17
132 PRIOR APPLICATION NUMBER: 60/249,245
133 PRIOR FILING DATE: 2000-11-17
134 PRIOR APPLICATION NUMBER: 60/249,244
135 PRIOR FILING DATE: 2000-11-17
136 PRIOR APPLICATION NUMBER: 60/249,217
137 PRIOR FILING DATE: 2000-11-17
138 PRIOR APPLICATION NUMBER: 60/249,211
139 PRIOR FILING DATE: 2000-11-17
140 PRIOR APPLICATION NUMBER: 60/249,215
141 PRIOR FILING DATE: 2000-11-17
142 PRIOR APPLICATION NUMBER: 60/249,264

PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/249,214
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/249,297
 PRIOR FILING DATE: 2000-11-17
 PRIOR APPLICATION NUMBER: 60/232,400
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/231,242
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: 60/232,081
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: 60/232,080
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: 60/231,414
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: 60/231,244
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: 60/233,064
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/233,063
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/232,397
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/232,399
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/232,401
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/241,808
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/241,826
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/241,786
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/241,221
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/246,475
 PRIOR FILING DATE: 2000-11-08
 PRIOR APPLICATION NUMBER: 60/231,243
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: 60/233,065
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: 60/232,398

Query Match 64.6%; Score 73; DB 22; Length 57;
 Best Local Similarity 75.0%; Pred. No. 0.69;
 Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGRRRRRRPKKKK 20
 Db 35 RRRRRGRRRRRRPKKKK 54

RESULT 34
 US-10-092-399-10551
 ; Sequence 10551, Application US/10092399
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC004C1
 ; CURRENT APPLICATION NUMBER: US/10/092,399
 ; CURRENT FILING DATE: 2002-03-07
 ; NUMBER OF SEQ ID NOS: 42506
 ; Prior Application removed - See File Wrapper or Palm
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10551
 ; LENGTH: 57
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (57)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-092-399-10551

Query Match 64.6%; Score 73; DB 26; Length 57;
 Best Local Similarity 75.0%; Pred. No. 0.69;
 Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGRRRRRRPKKKK 20
 Db 35 RRRRRGRRRRRRPKKKK 54

RESULT 35
 US-10-029-386-31410
 ; Sequence 31410, Application US/10029386
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: AEOMICA-X-2
 ; CURRENT APPLICATION NUMBER: US/10/029,386
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 34288
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 31410
 ; LENGTH: 71
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC016943.7
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.99
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.86
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.52

US-10-029-386-31410
 Query Match 64.6%; Score 73; DB 26; Length 71;
 Best Local Similarity 71.4%; Pred. No. 0.85;
 Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGRRRRRRPKKKK 21
 Db 50 RRRRRGRRRRRRPKKKK 70

RESULT 36
 PCT-US01-00663-28605
 ; Sequence 28605, Application PC/TUS0100663
 ; GENERAL INFORMATION:
 ; APPLICANT: Molecular Dynamics, Inc.
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: PB 0004 WO 7
 ; CURRENT APPLICATION NUMBER: PCT/US01/00663
 ; CURRENT FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 04 February 2000 (04.02.00)
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 26 May 2000 (26.05.00)
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 03 August 2000 (03.08.00)
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 03 October 2000 (03.10.00)
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 27 September 2000 (27.09.00)
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 21 September 2000 (21.09.00)
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 30 June 2000 (30.06.00)

```

; NUMBER OF SEQ ID NOS: 38637
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 28605
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006391.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL =
PCT-US01-00663-28605

```

Query Match 64.6%; Score 73; DB 1; Length 130;
Best Local Similarity 75.0%; Pred. No. 1.5;
Matches 15: Conservative 2; Mismatches 3; Indels

```

Qy 1 RRRRRWGRRRRRRPKKKK 20
    ||||: ||||| |||:|
pb 54 RRRRRKKRRRRRRKKKKK 73

```

RESULT, T 37

```

US-09-864-761-35536
RESOLU 1 37
SEQUENCE 35536, Application US/09864761
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rankel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED
TITLE OF INVENTION: GENE EXPRESSION ANAL
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine
SEQ ID NO 35536
LENGTH: 130

```

```

/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC006391.7
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
/ OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.6
/ OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 2.2
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
/ US-09-864-761-35536

```

Query Match 64.6%; Score 73; DB 23; Length 130;
Best Local Similarity 75.0%; Pred. No. 1.5;
Matches 15: Conservative 2; Mismatches 3; Indels

```

QY 1 RRRRRGRRRRRRPPKKRK 20
    ||||: ||||| |||: |
Db 54 RRRRRKKRRRRRRKKKKK 73

```

RESIT.T 38

```

US-10-182-993-27728
; Sequence 27728, Application US/10182993
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN BRAIN
; FILE REFERENCE: PB 0004 WO 2
; CURRENT APPLICATION NUMBER: US/10/182,993
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 37811
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 27728
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006391.7
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
US-10-182-993-27728

```

Query Match 64.6%; Score 73; DB 27; Length 130;
Best Local Similarity 75.0%; Pred. No. 1.5;
Matches 15: Conservative 2; Mismatches 3; Indels

```

Qy      1 RRRRRWGRRRRRRPPKKRK 20
        |||||: ||||| |||:|
Db     54 RRRRRKKRRRRRRKKKKK 73

```


Thu Jan 29 10:08:39 2004

us-10-002-884a-2.rapm

```

RESULT 39
US-10-182-995-22008
; Sequence 22008, Application US/10182997
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN HEART
; FILE REFERENCE: PB 0004 WO 1
; CURRENT APPLICATION NUMBER: US/10/182,995
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 29119
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 22008
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006391.7
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
US-10-182-995-22008

Query Match 64.6%; Score 73; DB 27; Length 130;
Best Local Similarity 75.0%; Pred. No. 1.5;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGRRRRRPPKXK 20
   |||||: ||||| |||||
Db 54 RRRRRKRRRRRKKKKK 73

Search completed: January 23, 2004, 11:23:48
Job time : 178 secs

US-10-182-997-20652
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 21 September 2000 (21.09.00)
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 30 June 2000 (30.06.00)
; NUMBER OF SEQ ID NOS: 26941
; SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 20652
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006391.7
; FEATURE:
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
US-10-182-997-20652

Query Match 64.6%; Score 73; DB 27; Length 130;
Best Local Similarity 75.0%; Pred. No. 1.5;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGRRRRRPPKXK 20
   |||||: ||||| |||||
Db 54 RRRRRKRRRRRKKKKK 73

Search completed: January 23, 2004, 11:23:48
Job time : 178 secs

US-10-182-997-20652
; Sequence 20652, Application US/10182997
; GENERAL INFORMATION:
; APPLICANT: Molecular Dynamics, Inc.
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HELA
; FILE REFERENCE: PB 0004 WO 10
; CURRENT APPLICATION NUMBER: US/10/182,997
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 04 February 2000 (04.02.00)
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 26 May 2000 (26.05.00)
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 03 August 2000 (03.08.00)
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 03 October 2000 (03.10.00)
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 27 September 2000 (27.09.00)

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2004, 11:17:45 ; Search time 23 Seconds

(without alignments)
68.233 Million cell updates/sec

Title: US-10-002-884a-2

Perfect score: 113

Sequence: 1 RRRRRWGRRRRRPPKRRKV 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 361565 seqs, 74731050 residues

Total number of hits satisfying chosen parameters: 361565

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71.5	63.3	488	6	US-10-679-063-3796
2	71.5	63.3	516	6	US-10-679-063-3797
3	68	60.2	550	5	US-09-614-150A-32376
4	66.5	58.8	336	6	US-10-425-114A-38775
5	66.5	58.8	337	6	US-10-425-114A-53493
6	66	58.4	20	5	US-09-199-524A-10
7	66	58.4	25	5	US-09-199-524A-11
8	66	58.4	30	5	US-09-199-524A-20
9	66	58.4	41	5	US-09-910-432-16
10	66	58.4	43	5	US-09-910-432-17
11	66	58.4	45	5	US-09-910-432-18
12	66	58.4	271	6	US-10-425-114A-53733
13	64	56.6	39	5	US-09-910-432-15
14	63	55.8	803	1	PCT-US03-38193-2578
15	63	55.8	803	6	US-10-723-860-2578
16	62	54.9	557	6	US-10-425-114A-63856
17	61	54.0	129	6	US-10-739-930-8952
18	60	53.1	193	7	US-60-495-114-1247
19	60	53.1	373	1	PCT-US02-18638A-79
20	60	53.1	373	1	PCT-US03-38193-2796
21	60	53.1	373	6	US-10-723-860-2796
22	60	53.1	385	6	US-10-425-114A-50702
23	59.5	52.7	261	6	US-10-425-114A-63205
24	59.5	52.7	323	6	US-10-425-114A-67908
25	59	52.2	175	6	US-10-425-114A-42033
26	59	52.2	176	6	US-10-425-114A-48319

27	59	52.2	255	1	PCT-US03-30720-2504	Sequence 2504, Ap
28	59	52.2	259	6	US-10-425-114A-69249	Sequence 69249, A
29	59	52.2	316	6	US-10-425-114A-63866	Sequence 63866, A
30	58.5	51.8	144	6	US-10-425-114A-68862	Sequence 68862, A
31	58	51.3	22	5	US-09-910-432-7	Sequence 7, Appli
32	58	51.3	33	6	US-10-471-074-2	Sequence 2, Appli
33	58	51.3	37	5	US-09-910-432-14	Sequence 14, Appli
34	58	51.3	75	1	PCT-US03-33947-952	Sequence 952, App
35	58	51.3	162	6	US-10-425-114A-47461	Sequence 47461, A
36	58	51.3	163	6	US-10-425-114A-60931	Sequence 60931, A
37	58	51.3	183	6	US-10-425-114A-49344	Sequence 49344, A
38	58	51.3	441	6	US-10-425-114A-61244	Sequence 61244, A
39	58	51.3	507	6	US-10-425-114A-59210	Sequence 59210, A
40	58	51.3	870	6	US-10-322-281-358	Sequence 358, App
41	58	51.3	19725	6	US-10-084-846A-4	Sequence 4, Appli
42	57.5	50.9	206	6	US-10-425-114A-59176	Sequence 59176, A
43	57	50.4	33	6	US-10-471-074-1	Sequence 1, Appli
44	57	50.4	120	6	US-10-425-114A-36640	Sequence 36640, A
45	57	50.4	140	6	US-10-425-114A-61776	Sequence 61776, A

ALIGNMENTS

RESULT 1

US-10-679-063-3796
; Sequence 3796, Application US/10679063
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52054)B
; CURRENT APPLICATION NUMBER: US/10/679,063
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/415,758
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 3796
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(488)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-679-063-3796

Query Match 63.3%; Score 71.5; DB 6; Length 488;
Best Local Similarity 88.2%; Pred. No. 5.5;
Matches 15; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 RRRRRWGRRRRRPPK 17

DB 190 RRRRRWGRRRRRPPK 205

RESULT 2

US-10-679-063-3797
; Sequence 3797, Application US/10679063
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52054)B
; CURRENT APPLICATION NUMBER: US/10/679,063
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/415,758
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 3797
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure

Thu Jan 29 10:08:39 2004

us-10-002-884a-2.rapn

```
; LOCATION: (1)...(516)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-679-063-3797

Query Match      63.3%; Score 71.5; DB 6; Length 516;
Best Local Similarity 88.2%; Pred. No. 5.7;
Matches 15; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 RRRRRWGRRRRRPKK 17
Db 216 RRRRRW-RRRRRRPTK 231

RESULT 3
US-09-614-150A-32376
; Sequence 32376, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/09/614,150A
; CURRENT FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32376
; LENGTH: 550
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150A-32376

Query Match      60.2%; Score 68; DB 5; Length 550;
Best Local Similarity 73.7%; Pred. No. 12;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKR 19
Db 240 RRRRRW-RRRRRRPKKR 258

RESULT 4
US-10-425-114A-38775
; Sequence 38775, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 38775
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700201601_FLI.pep
US-10-425-114A-38775

Query Match      58.8%; Score 66.5; DB 6; Length 336;
Best Local Similarity 60.9%; Pred. No. 13;
Matches 14; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 1 RRRRRWGRRRRR---PKKKK 20
Db 181 RRRRRW-RRRRRTPTPTGR 203

RESULT 5
US-10-425-114A-53493
; Sequence 53493, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 53493
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700239811_FLI.pep
US-10-425-114A-53493

Query Match      58.8%; Score 66.5; DB 6; Length 337;
Best Local Similarity 60.9%; Pred. No. 13;
Matches 14; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 1 RRRRRWGRRRRR---PKKKK 20
Db 188 RRRRRW-RRRRRTPTPTGR 210

RESULT 6
US-09-199-524A-10
; Sequence 10, Application US/09199524A
; GENERAL INFORMATION:
; APPLICANT: ROTHBARD, JONATHAN B.
; APPLICANT: WENDER, PAUL A.
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR ENHANCING TRANSPORT ACROSS
; TITLE OF INVENTION: BIOLOGICAL MEMBRANES
; FILE REFERENCE: 8400-0005.20
; CURRENT APPLICATION NUMBER: US/09/199,524A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 09/083,259
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 60/047,345
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-199-524A-10

Query Match 58.4%; Score 66; DB 5; Length 20;
Best Local Similarity 65.0%; Pred. No. 3.8;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPPKKRK 20
||||| ||||| :||:
Db 1 RRRRRRRRRRRRRRRR 20

RESULT 7

US-09-199-524A-11
; Sequence 11, Application US/09199524A
; GENERAL INFORMATION:
; APPLICANT: ROTHBARD, JONATHAN B.
; APPLICANT: WENDER, PAUL A.
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR ENHANCING TRANSPORT ACROSS
; TITLE OF INVENTION: BIOLOGICAL MEMBRANES
; FILE REFERENCE: 8400-0005.20
; CURRENT APPLICATION NUMBER: US/09/199,524A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 09/083,259
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 60/047,345
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-199-524A-11

Query Match 58.4%; Score 66; DB 5; Length 25;
Best Local Similarity 65.0%; Pred. No. 4.2;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPPKKRK 20
||||| ||||| :||:
Db 1 RRRRRRRRRRRRRRRR 20

RESULT 8

US-09-199-524A-20
; Sequence 20, Application US/09199524A
; GENERAL INFORMATION:
; APPLICANT: ROTHBARD, JONATHAN B.
; APPLICANT: WENDER, PAUL A.
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR ENHANCING TRANSPORT ACROSS
; TITLE OF INVENTION: BIOLOGICAL MEMBRANES
; FILE REFERENCE: 8400-0005.20
; CURRENT APPLICATION NUMBER: US/09/199,524A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 09/083,259
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 60/047,345
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-199-524A-20

Query Match 58.4%; Score 66; DB 5; Length 30;
Best Local Similarity 65.0%; Pred. No. 4.6;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPPKKRK 20
||||| ||||| :||:
Db 1 RRRRRRRRRRRRRRRR 20

RESULT 9

US-09-910-432-16
; Sequence 16, Application US/09910432
; GENERAL INFORMATION:
; APPLICANT: Waugh, Jacob
; APPLICANT: Dake, Michael
; APPLICANT: Essentia Biosystems, Inc.
; TITLE OF INVENTION: Multi-Component Biological Transport Systems
; FILE REFERENCE: 020154-000110US
; CURRENT APPLICATION NUMBER: US/09/910,432
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/220,244
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: positively
; OTHER INFORMATION: charged branching group (efficiency group)
; OTHER INFORMATION: attached to solid backbone
; NAME/KEY: MOD_RES
; LOCATION: (1)-(20)
; OTHER INFORMATION: Gly at positions 1-20 may be present or absent
US-09-910-432-16

Query Match 58.4%; Score 66; DB 5; Length 41;
Best Local Similarity 65.0%; Pred. No. 5.3;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPPKKRK 20
||||| ||||| :||:
Db 21 RRRRRRRRRRRRRRRR 40

RESULT 10

US-09-910-432-17
; Sequence 17, Application US/09910432
; GENERAL INFORMATION:
; APPLICANT: Waugh, Jacob
; APPLICANT: Dake, Michael
; APPLICANT: Essentia Biosystems, Inc.
; TITLE OF INVENTION: Multi-Component Biological Transport Systems
; FILE REFERENCE: 020154-000110US
; CURRENT APPLICATION NUMBER: US/09/910,432
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/220,244
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: positively
; OTHER INFORMATION: charged branching group (efficiency group)
; OTHER INFORMATION: attached to solid backbone
; NAME/KEY: MOD_RES
US-09-910-432-17

Thu Jan 29 10:08:39 2004

us-10-002-884a-2.rapn

US-10-425-114A-53733

; LOCATION: (1)..(20)
; OTHER INFORMATION: Gly at positions 1-20 may be present or absent
US-09-910-432-17

Query Match 58.4%; Score 66; DB 5; Length 43;

Best Local Similarity 65.0%; Pred. No. 5.4;

Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKXK 20

||||| ||||| ::|||

Db 21 RRRRRRRRRRRRRRRR 40

RESULT 11

US-09-910-432-18

; Sequence 18, Application US/09910432

; GENERAL INFORMATION:

; APPLICANT: Waugh, Jacob

; APPLICANT: Dake, Michael

; APPLICANT: Essentia Biosystems, Inc.

; TITLE OF INVENTION: Multi-Component Biological Transport Systems

; FILE REFERENCE: 020154-000110US

; CURRENT APPLICATION NUMBER: US/09/910,432

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/220,244

; PRIOR FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 18

; LENGTH: 45

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:positively

; OTHER INFORMATION: charged branching group (efficiency group)

; OTHER INFORMATION: attached to solid backbone

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (1)..(20)

; OTHER INFORMATION: Gly at positions 1-20 may be present or absent

US-09-910-432-18

Query Match 58.4%; Score 66; DB 5; Length 45;

Best Local Similarity 65.0%; Pred. No. 5.5;

Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKXK 20

||||| ||||| ::|||

Db 21 RRRRRRRRRRRRRRRR 40

RESULT 12

US-10-425-114A-53733

; Sequence 53733, Application US/10425114A

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114A

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 53733

; LENGTH: 271

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3245-491-F1_FLI.pep

Query Match 58.4%; Score 66; DB 6; Length 271;

Best Local Similarity 75.0%; Pred. No. 13;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKK 16

||||| ||||| ::|||

Db 124 RRRRRWGRRRRRSR 139

RESULT 13

US-09-910-432-15

; Sequence 15, Application US/09910432

; GENERAL INFORMATION:

; APPLICANT: Waugh, Jacob

; APPLICANT: Dake, Michael

; APPLICANT: Essentia Biosystems, Inc.

; TITLE OF INVENTION: Multi-Component Biological Transport Systems

; FILE REFERENCE: 020154-000110US

; CURRENT APPLICATION NUMBER: US/09/910,432

; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/220,244

; PRIOR FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 15

; LENGTH: 39

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:positively

; OTHER INFORMATION: charged branching group (efficiency group)

; OTHER INFORMATION: attached to solid backbone

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (1)..(20)

; OTHER INFORMATION: Gly at positions 1-20 may be present or absent

US-09-910-432-15

Query Match 56.6%; Score 64; DB 5; Length 39;

Best Local Similarity 68.4%; Pred. No. 7.7;

Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKXK 19

||||| ||||| ::|||

Db 21 RRRRRRRRRRRRRRRR 39

RESULT 14

PCT-US03-38193-2578

; Sequence 2578, Application PC/TUS0338193

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsburg, Wendy M.

; APPLICANT: Zlornik, Albert

; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &

; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

; FILE REFERENCE: 05882.0193.00PC00

; CURRENT APPLICATION NUMBER: PCT/US03/38193

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: 60/429,739

; PRIOR FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 8393

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2578

; LENGTH: 803

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US03-38193-2578

Query Match 55.8%; Score 63; DB 1; Length 803;

Best Local Similarity 56.5%; Pred. No. 38;

Thu Jan 29 10:08:39 2004

```

Matches 13; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 2 RRRRWGRRRRR-----PKKKRK 20
Db 32 RRRRWGRRRRRDRPGPEKRE 54

RESULT 15
US-10-723-860-2578
; Sequence 2578, Application US/10723860
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2578
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-2578

Query Match 55.8%; Score 63; DB 6; Length 803;
Best Local Similarity 56.5%; Pred. No. 38;
Matches 13; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 2 RRRRWGRRRRR-----PKKKRK 20
Db 32 RRRRWGRRRRRDRPGPEKRE 54

RESULT 16
US-10-425-114A-63856
; Sequence 63856, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63856
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB189-025-G10_FLI.pep
US-10-425-114A-63856

Query Match 54.9%; Score 62; DB 6; Length 557;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRRWGRRRRR 14
Db 286 RRRRWGRRRRRRR 299

RESULT 17
US-10-739-930-8952
; Sequence 8952, Application US/10739930
; GENERAL INFORMATION: David K.
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 8952
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: GLYMA-23APR03-C264449_1.p
US-10-739-930-8952

Query Match 54.0%; Score 61; DB 6; Length 129;
Best Local Similarity 47.4%; Pred. No. 24;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 3 RRRRWGRRRRRPPKKRK 21
Db 111 RRRRWGRRRRRPPKKRK 129

RESULT 18
US-60-495-114-1247
; Sequence 1247, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO01480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1247
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-495-114-1247

Query Match 53.1%; Score 60; DB 7; Length 193;
Best Local Similarity 72.2%; Pred. No. 35;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 RRRRWGRRRRRPPKKRK 20
Db 127 RRRRWGRRRRRPPKKRK 144

RESULT 19
PCT-US02-18638A-79
; Sequence 79, Application PC/TUS0218638A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035PC
; CURRENT APPLICATION NUMBER: PCT/US02/18638A
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0

```

```
; SEQ ID NO 79
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18638A-79

Query Match      53.1%; Score 60; DB 1; Length 373;
Best Local Similarity 55.6%; Pred. No. 48;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRGRRRRRRPPKK 18
Db 348 KQRRRYGKKRSTKK 365

RESULT 20
PCT-US03-38193-2796
; Sequence 2796, Application PC/TUS0338193
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.00PC00
; CURRENT APPLICATION NUMBER: PCT/US03/38193
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2796
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-38193-2796

Query Match      53.1%; Score 60; DB 1; Length 373;
Best Local Similarity 55.6%; Pred. No. 48;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRGRRRRRRPPKK 18
Db 348 KQRRRYGKKRSTKK 365

RESULT 21
US-10-723-860-2796
; Sequence 2796, Application US/10723860
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2796
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-2796

Query Match      53.1%; Score 60; DB 6; Length 373;
Best Local Similarity 55.6%; Pred. No. 48;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRGRRRRRRPPKK 18
Db 348 KQRRRYGKKRSTKK 365

RESULT 22
US-10-425-114A-50702
; Sequence 50702, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 50702
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: L1B3689-212-P9_FLI.pep
US-10-425-114A-50702

Query Match      53.1%; Score 60; DB 6; Length 385;
Best Local Similarity 68.4%; Pred. No. 49;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRGRRRRRRPPKK 19
Db 346 RRRRGCGRRRRRRDRGR 364

RESULT 23
US-10-425-114A-63205
; Sequence 63205, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63205
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73008E02_FLI.pep
US-10-425-114A-63205

Query Match      52.7%; Score 59.5; DB 6; Length 261;
Best Local Similarity 70.6%; Pred. No. 45;
Matches 12; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 RRRRRGRRRRRRPPKK 17
Db 36 RRRRRW-RRRTAPRR 51

RESULT 24
US-10-425-114A-67908
; Sequence 67908, Application US/10425114A
```

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 67908
LENGTH: 323
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLMO17069D08_FLI.pep
US-10-425-114A-67908

Query Match 52.7%; Score 59.5; DB 6; Length 323;
Best Local Similarity 68.4%; Pred. No. 49;
Matches 13; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY 1 RRRRRW-----GRRRRR 14
|||||
DB 292 RRRRRWPVAGRRRRR 310
|||||

RESULT 25

US-10-425-114A-42033
Sequence 42033, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 42033
LENGTH: 175
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700341946_FLI.pep
US-10-425-114A-42033

Query Match 52.2%; Score 59; DB 6; Length 175;
Best Local Similarity 52.2%; Pred. No. 41;
Matches 12; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

QY 1 RRRRRW--GRRRRRPKKRKV 21
|||||
DB 98 RRRRRWQRRRRQAPPQEL 120
|||||

RESULT 26

US-10-425-114A-48319
Sequence 48319, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 48319
LENGTH: 176
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3912-046-G9_FLI.pep
US-10-425-114A-48319

Query Match 52.2%; Score 59; DB 6; Length 176;
Best Local Similarity 78.6%; Pred. No. 41;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRR 14
|||||
DB 77 RRRRQWGRRRSWR 90
|||||

RESULT 27

PCT-US03-30720-2504
Sequence 2504, Application PC/TUS0330720
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Zhiwei
APPLICANT: Zhou, Ping
APPLICANT: Zhang, Jie
APPLICANT: Ghosh, Malabika
APPLICANT: Ren, Feiyan
APPLICANT: Asundi, Vinod
APPLICANT: Zhao, Qing A.
APPLICANT: Xue, Aidong J.
APPLICANT: Chen, Rui-hong
APPLICANT: Wehrman, Tom
APPLICANT: Ma, Yungqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Gezhi
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 819CIP/PCI
CURRENT APPLICATION NUMBER: PCT/US03/30720
CURRENT FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: 60/416,186
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: PCT/US01/04927
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: PCT/US01/04941
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/US01/08656
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 10/084,643
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 2564
SOFTWARE: pt_FL_genes Version 6.0
SEQ ID NO 2504
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature

; LOCATION: (1)...(255)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set for
PCT-US03-30720-2504

Query Match 52.2%; Score 59; DB 1; Length 255;
Best Local Similarity 84.6%; Pred. No. 49;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRWGRRRR 13
DB 235 RARRRWGRRRR 247

RESULT 28

US-10-425-114A-69249
; Sequence 69249, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69249
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-103-H11_FLI.pep
US-10-425-114A-69249

Query Match 52.2%; Score 59; DB 6; Length 259;
Best Local Similarity 70.6%; Pred. No. 49;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPKK 17
DB 147 RRGRRRQRRRRRRR 163

RESULT 29

US-10-425-114A-63686
; Sequence 63686, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63686
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-075-B3_FLI.pep
US-10-425-114A-63686

Query Match 52.2%; Score 59; DB 6; Length 316;
Best Local Similarity 51.1%; Pred. No. 54;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 RRRRWGRRRRRPKKRK 20
DB 226 RRRRGARRRRRRRRR 243

RESULT 30

US-10-425-114A-68862
; Sequence 68862, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68862
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3066-040-C10_FLI.pep
US-10-425-114A-68862

Query Match 51.8%; Score 58.5; DB 6; Length 144;
Best Local Similarity 43.8%; Pred. No. 42;
Matches 14; Conservative 2; Mismatches 3; Indels 13; Gaps 1;

QY 1 RRRRR-----RWGRRRRRRPKKR 19
DB 51 RRRRPSRLRVGVRRSPRRRRRRRRRRR 82

RESULT 31

US-09-910-432-7
; Sequence 7, Application US/09910432
; GENERAL INFORMATION:
; APPLICANT: Waugh, Jacob
; APPLICANT: Dake, Michael
; APPLICANT: Essentia Biosystems, Inc.
; TITLE OF INVENTION: Multi-Component Biological Transport Systems
; FILE REFERENCE: 020154-000110US
; CURRENT APPLICATION NUMBER: US/09/910,432
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/220,244
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: positively
; OTHER INFORMATION: charged branching group (efficiency group)
; OTHER INFORMATION: attached to solid backbone
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)...(3)
; OTHER INFORMATION: Gly at positions 1-3 may be present or absent
US-09-910-432-7

Query Match 51.3%; Score 58; DB 5; Length 22;
Best Local Similarity 68.4%; Pred. No. 19;
Matches 13; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 1 RRRRRWGRRRRRRPKKR 19

```

US-09-910-432-14
DB 6 RRRRRR-RRRRRRRR 22
||||| ||||| ::|
Query Match 51.3%; Score 58; DB 5; Length 37;
Best Local Similarity 68.4%; Pred. No. 25;
Matches 13; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

RESULT 32
US-10-471-074-2
; Sequence 2, Application US/10471074
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; TITLE OF INVENTION: MODIFIED PROTAMINE WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-122
; CURRENT APPLICATION NUMBER: US/10/471,074
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: EP 01105778.3
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/EP02/02241
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified salmon protamine
; NAME/KEY: VARIANT
; LOCATION: 12, 20, 28
; OTHER INFORMATION: Xaa = Val, Ala, Cys, Asp, Glu, His, Lys, Asn, Pro,
; OTHER INFORMATION: Glu, Arg, Ser or Thr
; OTHER INFORMATION: Xaa = Val, Ala, Cys, Asp, Glu, His, Lys, Asn, Pro,
; OTHER INFORMATION: Glu, Arg, Ser or Thr
; OTHER INFORMATION: Xaa - Gly, Ile or Thr
US-10-471-074-2
Query Match 51.3%; Score 58; DB 6; Length 33;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 RRRRRGRRRRRPPKKK 20
DB 14 RRRPRXSRRRRRGR 33
||||| ||||| ::|

RESULT 33
US-09-910-432-14
; Sequence 14, Application US/09910432
; GENERAL INFORMATION:
; APPLICANT: Waugh, Jacob
; APPLICANT: Duke, Michael
; APPLICANT: Essentia Biosystems, Inc.
; TITLE OF INVENTION: Multi-Component Biological Transport Systems
; FILE REFERENCE: 020154-000110US
; CURRENT APPLICATION NUMBER: US/09/910,432
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/220,244
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: positively
; OTHER INFORMATION: charged branching group (efficiency group)
; OTHER INFORMATION: attached to solid backbone
; NAME/KEY: MOD RES
; LOCATION: (1)-(20)
; OTHER INFORMATION: Gly at positions 1-20 may be present or absent

US-09-910-432-14
Query Match 51.3%; Score 58; DB 5; Length 37;
Best Local Similarity 68.4%; Pred. No. 25;
Matches 13; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

OY 1 RRRRRGRRRRRPPKKK 19
DB 21 RRRRRR-RRRRRRRR 37
||||| ||||| ::|

RESULT 34
PCT-US03-33947-952
; Sequence 952, Application PC/TUS0333947
; GENERAL INFORMATION:
; APPLICANT: FIVEPRIME THERAPEUTICS, INC.
; TITLE OF INVENTION: HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES AND METHODS
; TITLE OF INVENTION: OF THEIR USE
; FILE REFERENCE: 08940.0017-00304
; CURRENT APPLICATION NUMBER: PCT/US03/33947
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US 60/421,080
; PRIOR FILING DATE: 2002-12-25
; PRIOR APPLICATION NUMBER: US 60/421,061
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/421,614
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/421,552
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/422,178
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: US 60/422,177
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: US 60/426,384
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/426,394
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/426,355
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/426,430
; PRIOR FILING DATE: 2002-11-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2352
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 952
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-33947-952

US-10-425-114A-47461
Query Match 51.3%; Score 58; DB 1; Length 75;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 10; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY 1 RRRRRGRRRRRPPKKK 20
DB 33 RRRRRRKKKKKKKKKK 52
||||| ::|||

RESULT 35
US-10-425-114A-47461
; Sequence 47461, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
```

```

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47461
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700106742_FLI.pep
US-10-425-114A-47461

Query Match      51.3%; Score 58; DB 6; Length 162;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRP 15
   ||||| ||||| ||
Db 88 RRRRRWGRRRRRP 102
   ||||| ||||| ||

RESULT 36
US-10-425-114A-60931
; Sequence 60931, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60931
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3355-008-G7_FLI.pep
US-10-425-114A-60931

Query Match      51.3%; Score 58; DB 6; Length 163;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRP 15
   ||||| ||||| ||
Db 88 RRRRRWGRRRRRP 102
   ||||| ||||| ||

RESULT 37
US-10-425-114A-49344
; Sequence 49344, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49344
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700264501_FLI.pep
US-10-425-114A-49344

Query Match      51.3%; Score 58; DB 6; Length 183;
Best Local Similarity 62.5%; Pred. No. 51;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RRRRWGRRRRPKKK 18
   ||||| ||||| ||
Db 27 RRRRWGRRRRPKKK 42
   ||||| ||||| ||

RESULT 38
US-10-425-114A-61244
; Sequence 61244, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 61244
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4309-013-D9_FLI.pep
US-10-425-114A-61244

Query Match      51.3%; Score 58; DB 6; Length 441;
Best Local Similarity 68.4%; Pred. No. 77;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKK 19
   ||||| ||||| ||
Db 174 RRRRRWGRRRRRPKKK 192
   ||||| ||||| ||

RESULT 39
US-10-425-114A-59210
; Sequence 59210, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59210
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700264501_FLI.pep
US-10-425-114A-59210

Query Match      51.3%; Score 58; DB 6; Length 507;
Best Local Similarity 63.2%; Pred. No. 82;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```

QY 3 RRRRWGRRRRRPPKKRKV 21
 ||| ||||| |::
 Db 43 RRGKGRRRRRRANKWREI 61

RESULT 40
 US-10-322-281-358
 ; Sequence 358, Application US/10322281
 ; GENERAL INFORMATION:
 ; APPLICANT: David W. Morris
 ; APPLICANT: Marc S. Malandro
 ; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
 ; FILE REFERENCE: 529452001000
 ; CURRENT APPLICATION NUMBER: US/10/322,281
 ; CURRENT FILING DATE: 2002-12-17
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 358
 ; LENGTH: 870
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-322-281-358

Query Match 51.3%; Score 58; DB 6; Length 870;
 Best Local Similarity 55.0%; Pred. No. 1e+02;
 Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPPKKRK 20
 ||| ||||| |::
 Db 80 RRRRRAPRRRRRRRR 99

Search completed: January 23, 2004, 11:20:38
 Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2004, 11:15:55 ; Search time 22 Seconds
(without alignments)
40.388 Million cell updates/sec

Title: US-10-002-884A-2

Perfect score: 113
Sequence: 1 RRRRRWRRRRRRPKKRVK 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	59.3	657	3	US-07-705-490-14
2	67	59.3	657	3	US-07-751-891B-14
3	66	58.4	20	4	US-09-083-259-10
4	66	58.4	20	4	US-09-039-780A-5
5	66	58.4	20	4	US-09-396-193-10
6	66	58.4	25	4	US-09-083-259-11
7	66	58.4	25	4	US-09-396-195-11
8	66	58.4	84	4	US-09-420-592A-9
9	66	58.4	84	4	US-09-420-592A-11
10	65.5	58.0	770	4	US-09-245-248B-31
11	61	54.0	531	4	US-09-252-991A-24404
12	61	54.0	714	4	US-09-252-991A-29806
13	60.5	53.5	154	4	US-09-252-991A-29293
14	60	53.1	22	5	PCT-US95-06077-29
15	60	53.1	34	4	US-08-857-636-73
16	60	53.1	301	2	US-08-656-906-25
17	60	53.1	301	3	US-09-217-847-25
18	59	52.2	310	4	US-09-252-991A-23221
19	58	51.3	284	4	US-09-252-991A-20377
20	58	51.3	280	4	US-09-252-991A-22385
21	58	51.3	327	4	US-09-252-991A-29443
22	58	51.3	1213	3	US-09-413-814-79
23	57	50.4	23	2	US-08-847-176-19
24	57	50.4	28	1	US-08-281-702A-8
25	57	50.4	28	2	US-08-618-917-8
26	57	50.4	32	1	US-08-152-488-9
27	57	50.4	32	1	US-08-303-025-9

28	57	50.4	32	1	US-08-677-304-9	Sequence 9, Appli
29	57	50.4	32	2	US-08-436-703B-14	Sequence 14, Appli
30	57	50.4	40	4	US-09-039-780A-6	Sequence 6, Appli
31	57	50.4	83	4	US-09-420-592A-10	Sequence 10, Appli
32	57	50.4	309	4	US-09-252-991A-17744	Sequence 17744, A
33	56.5	50.0	147	4	US-09-252-991A-29687	Sequence 29687, A
34	56.5	50.0	270	4	US-09-252-991A-27118	Sequence 27118, A
35	56	49.6	23	2	US-08-847-176-2	Sequence 2, Appli
36	55.5	49.1	726	4	US-09-252-991A-18271	Sequence 18271, A
37	55	48.7	15	4	US-09-083-259-9	Sequence 9, Appli
38	55	48.7	15	4	US-09-396-193-9	Sequence 9, Appli
39	55	48.7	79	4	US-09-252-991A-27207	Sequence 27207, A
40	55	48.7	143	4	US-09-252-991A-29749	Sequence 29749, A
41	55	48.7	229	4	US-09-252-991A-29511	Sequence 29511, A
42	55	48.7	346	4	US-09-252-991A-21487	Sequence 21487, A
43	54.5	48.2	426	4	US-09-252-991A-32191	Sequence 32191, A
44	54	47.8	209	4	US-09-252-991A-31640	Sequence 31640, A
45	54	47.8	377	4	US-09-252-991A-27247	Sequence 27247, A

ALIGNMENTS

RESULT 1
US-07-705-490-14
; Sequence 14, Application US/07705490
; Patent No. 6107025
; GENERAL INFORMATION:
; APPLICANT: Caskey, C. T.
; APPLICANT: Nelson, David L.
; APPLICANT: Pieretti, Maura
; APPLICANT: Warren, Stephen T.
; APPLICANT: Oostera, Ben A.
; TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas D. Paul
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07705490
; FILING DATE: 19910708
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5350
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 657 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHEICAL: YES
; FRAGMENT TYPE: C-terminal
US-07-705-490-14

Query Match 59.3%; Score 67; DB 3; Length 657;
Best Local Similarity 61.9%; Pred. No. 0.19;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRKV 21
 ||||| ||||| : : : :
 Db 23 RRRRRRRRRRRRRRRRL 43

RESULT 2

US-07-751-891B-14
 ; Sequence 14, Application US/07751891B
 ; Patent No. 6180337

GENERAL INFORMATION:

APPLICANT: Caskey, C. T.
 Nelson, David L.
 Pieretti, Maura
 Warren, Stephen T.
 Oostra, Ben A.
 Fu, Ying-hui

TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Thomas D. Paul
 STREET: 1301 McKinney, Suite 5100
 CITY: Houston
 STATE: Texas
 COUNTRY: U.S.A.
 ZIP: 77010-3095

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07751.891B
 FILING DATE: 29-Aug-1991
 CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Paul, Thomas D.
 REGISTRATION NUMBER: 32,714
 REFERENCE/DOCKET NUMBER: D-5350
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713/651-5325
 TELEFAX: 713/651-5246
 TELEX: 762829

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
 LENGTH: 657 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: YES
 FRAGMENT TYPE: C-terminal
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Query Match 59.3%; Score 67; DB 3; Length 657;
 Best Local Similarity 61.9%; Pred. No. 0.19;
 Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRKV 21
 ||||| ||||| : : : :
 Db 23 RRRRRRRRRRRRRRRRL 43

RESULT 3

US-09-083-259-10
 ; Sequence 10, Application US/09083259
 ; Patent No. 6306993

GENERAL INFORMATION:

APPLICANT: Rothbard, Jonathan B.
 Wender, Paul A.

TITLE OF INVENTION: METHOD AND COMPOSITION FOR

ENHANCING TRANSPORT ACROSS BIOLOGICAL MEMBRANES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Ave., Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/083,259
 FILING DATE: 21-MAY-1998
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/047,345
 FILING DATE: 21-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Powers, Vincent M.
 REGISTRATION NUMBER: 36,246
 REFERENCE/DOCKET NUMBER: 8600-0182.30
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-324-0880
 TELEFAX: 650-324-0960
 TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-083-259-10

Query Match 58.4%; Score 66; DB 4; Length 20;
 Best Local Similarity 65.0%; Pred. No. 0.0099;
 Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRKV 20

||||| ||||| : : : :
 Db 1 RRRRRRRRRRRRRRRRRR 20

RESULT 4

US-09-039-780A-5
 ; Sequence 5, Application US/09039780A
 ; Patent No. 6376248

GENERAL INFORMATION:

APPLICANT: HAWLEY-NELSON, PAMELA
 LAN, JIANQING
 SHIH, POJEN
 JESSE, JOEL A.
 SCHIFFERLI, KEVIN P.
 GEBEYERU, GULIAT

TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS

NUMBER OF SEQUENCES: 120

CORRESPONDENCE ADDRESS:

ADDRESSEE: GREENLEE, WINNER & SULLIVAN
 STREET: 5370 MANHATTAN CIRCLE, SUITE 201
 CITY: BOULDER
 STATE: CO
 COUNTRY: US
 ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/039,780A
 FILING DATE: 16-Mar-1998
 CLASSIFICATION: <Unknown>

Sequence 11, Application US/09396195
Patent No. 6495663
GENERAL INFORMATION:
APPLICANT: Rothbard, Jonathan B.
APPLICANT: Wender, Paul A.
TITLE OF INVENTION: METHOD AND COMPOSITION FOR
TITLE OF INVENTION: ENHANCING TRANSPORT ACROSS BIOLOGICAL MEMBRANES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09396,195
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/083,259
FILING DATE: 21-MAY-1998
APPLICATION NUMBER: 60/047,345
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Powers, Vincent M.
REGISTRATION NUMBER: 36,246
REFERENCE/DOCKET NUMBER: 8600-0182.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-396-195-11
Query Match 58.4%; Score 66; DB 4; Length 25;
Best Local Similarity 65.0%; Pred. No. 0.012;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RRRRRWGRRRRRPKKKRK 20
Db 1 RRRRRRRRRRRRRRRRRR 20
RESULT 8
US-09-420-592A-9
Sequence 9, Application US/09420592A
Patent No. 6333396
GENERAL INFORMATION:
APPLICANT: Filpula, David R.
APPLICANT: Wang, Maoliang
TITLE OF INVENTION: No. 6333396a1 Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.2300001
CURRENT APPLICATION NUMBER: US/09/420,592A
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 84
Query Match 58.4%; Score 66; DB 4; Length 25;
Best Local Similarity 65.0%; Pred. No. 0.012;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RRRRRWGRRRRRPKKKRK 20
Db 1 RRRRRRRRRRRRRRRRRR 20
RESULT 8
US-09-420-592A-9
Sequence 9, Application US/09420592A
Patent No. 6333396
GENERAL INFORMATION:
APPLICANT: Filpula, David R.
APPLICANT: Wang, Maoliang
TITLE OF INVENTION: No. 6333396a1 Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.2300001
CURRENT APPLICATION NUMBER: US/09/420,592A
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 84

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
OTHER INFORMATION: binding region
OTHER INFORMATION: Amino acids in positions 1-56 may be absent or
OTHER INFORMATION: present.
NAME/KEY: UNSURE
LOCATION: (57)..(76)
OTHER INFORMATION: May be any amino acid.
OTHER INFORMATION: Amino acids in positions 57-76 may be absent or
OTHER INFORMATION: present.
US-09-420-592A-9
Query Match 58.4%; Score 66; DB 4; Length 84;
Best Local Similarity 65.0%; Pred. No. 0.038;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RRRRRWGRRRRRPKKKRK 20
Db 1 RRRRRRRRRRRRRRRRRR 20
RESULT 9
US-09-420-592A-11
Sequence 11, Application US/09420592A
Patent No. 6333396
GENERAL INFORMATION:
APPLICANT: Filpula, David R.
APPLICANT: Wang, Maoliang
APPLICANT: Whitlow, Marc D.
TITLE OF INVENTION: No. 6333396e1 Method for Targeted Delivery of Nucleic Acids
FILE REFERENCE: 0977.2300001
CURRENT APPLICATION NUMBER: US/09/420,592A
CURRENT FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/104,949
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 84
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
OTHER INFORMATION: binding region
OTHER INFORMATION: Amino acids in positions 1-56 may be absent or
OTHER INFORMATION: present.
NAME/KEY: UNSURE
LOCATION: (57)..(76)
OTHER INFORMATION: May be any amino acid.
OTHER INFORMATION: Amino acids in positions 57-76 may be absent or
OTHER INFORMATION: present.
US-09-420-592A-11
Query Match 58.4%; Score 66; DB 4; Length 84;
Best Local Similarity 65.0%; Pred. No. 0.038;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 1 RRRRRWGRRRRRPKKKRK 20
Db 1 RRRRRRRRRRRRRRRRRR 20
RESULT 10
US-09-245-248B-31
Sequence 31, Application US/09245248B
Patent No. 6395472
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Leary, Thomas
APPLICANT: Erker, James
APPLICANT: Chalmers, Michelle


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/247,991
; FILING DATE: 23-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: IRI44PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-06077-29

Query Match 53.1%; Score 60; DB 5; Length 22;
Best Local Similarity 52.6%; Pred. No. 0.066;
Matches 10; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 RRRRWGRRRRPPKKRK 20
Db 3 RKRRQGRKKRRQGRKKR 21

```

```

RESULT 15
US-08-857-636-73
; Sequence 73, Application US/08857636
; Patent No. 6552181
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael Carlton
; APPLICANT: Hahn, Heidi Eve
; APPLICANT: Wicking, Carol
; APPLICANT: Christiansen, Jeffrey
; APPLICANT: Zaphiropoulos, Peter G.
; APPLICANT: Gailani, Mae R.
; APPLICANT: Shanley, Susan Mary
; APPLICANT: Chidambaram, Abirami
; APPLICANT: Vorechovsky, Igor
; APPLICANT: Holmberg-Lindstrom, Erika
; APPLICANT: Udden, Anne Birgitte
; APPLICANT: Gillies, Susan Alana
; APPLICANT: Negus, Kylie
; APPLICANT: Smyth, Ian McLeod
; APPLICANT: Pressman, Carol Leah
; APPLICANT: Leffell, David J.
; APPLICANT: Gerrard, Bernard
; APPLICANT: Goldstein, Alisa Miriam
; APPLICANT: Wainwright, Brandon
; APPLICANT: Toftgard, Rune Carl-Magnus
; APPLICANT: Chenevix-Trench, Georgia
; APPLICANT: Bale, Allen E.
; TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/857,636
; FILING DATE: 16-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: US 60/017,906
; FILING DATE: 17-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P00011
; FILING DATE: 21-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P00363
; FILING DATE: 07-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,765
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-278200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-857-636-73

```

```

Query Match 53.1%; Score 60; DB 4; Length 34;
Best Local Similarity 65.0%; Pred. No. 0.099;
Matches 13; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

```

```

QY 1 RRRRWGRRRRPPKKRK 20
Db 1 RRRRR--RRRRRRRRR 18

```

```

RESULT 16
US-08-656-906-25
; Sequence 25, Application US/08656906
; Patent No. 5972901
; GENERAL INFORMATION:
; APPLICANT: Ferkol Jr., Thomas W.
; APPLICANT: Davis, Pamela B.
; APPLICANT: Ziady, Assem-Galal
; TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
; TITLE OF INVENTION: Mediated Gene Transfer
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,906
; FILING DATE: 03-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/
; FILING DATE: 03-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 95/25809
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/216,534
; FILING DATE: 23-MAR-1994
; ATTORNEY/AGENT INFORMATION:

```

```
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: CASE-02280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-656-906-25

Query Match      53.1%; Score 60; DB 2; Length 301;
Best Local Similarity 65.0%; Pred. No. 0.76;
Matches 13; Conservative 3; Mismatches 4; Indels 4; Gaps 0;

QY      1 RRRRRWGRRRRRPKKKRK 20
        ||||| ||||| :||
Db      273 RRRRRCCRRRRCCRRRR 292
        ||||| ||||| :||

RESULT 18
US-09-252-991A-23221
; Sequence 23221, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23221
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-23221

Query Match      52.2%; Score 59; DB 4; Length 310;
Best Local Similarity 55.0%; Pred. No. 1.1;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 RRRRRWGRRRRRPKKKRK 20
        ||||| ||||| :||
Db      137 RHSSRRAGSHRRRRPRPQR 156
        ||||| ||||| :||

RESULT 19
US-09-252-991A-20377
; Sequence 20377, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20377
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-20377

Query Match      51.3%; Score 58; DB 4; Length 224;
Best Local Similarity 52.0%; Pred. No. 1.1;
Matches 13; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY      1 RRRRRWGRRRRR-----RPKKRK 19
        ||||| ||||| ||||| :||
Db      171 RRRRSWHRRRRRAAGRRDRPGRRR 195
        ||||| ||||| ||||| :||

RESULT 20
US-09-217-847-25
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: CASE-02280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-656-906-25

Query Match      53.1%; Score 60; DB 2; Length 301;
Best Local Similarity 65.0%; Pred. No. 0.76;
Matches 13; Conservative 3; Mismatches 4; Indels 4; Gaps 0;

QY      1 RRRRRWGRRRRRPKKKRK 20
        ||||| ||||| :||
Db      273 RRRRRCCRRRRCCRRRR 292
        ||||| ||||| :||

RESULT 17
US-09-217-847-25
; Sequence 25, Application US/09217847
; Patent No. 6200801
; GENERAL INFORMATION:
; APPLICANT: Ferkol Jr., Thomas W.
; APPLICANT: Davis, Pamela B.
; APPLICANT: Ziady, Assen-Galal
; TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
; TITLE OF INVENTION: Mediated Gene Transfer
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,847
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/656,906
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 95/25809
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/216,534
; FILING DATE: 23-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: CASE-02280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-217-847-25
```

Thu Jan 29 10:08:38 2004

```
US-09-252-991A-22385
; Sequence 22385, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22385
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22385
Query Match 51.3%; Score 58; DB 4; Length 280;
Best Local Similarity 50.0%; Pred. No. 1.3;
Matches 13; Conservative 2; Mismatches 5; Indels 5; Gaps 1;

QY 1 RRRR-----RWGRRRRRPPKXK 20
   ||||| ||||| ||||| |||||
Db 153 RRRRWIGGPRWRRRRRRHFGNRR 178

RESULT 21
US-09-252-991A-29443
; Sequence 29443, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29443
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29443
Query Match 51.3%; Score 58; DB 4; Length 327;
Best Local Similarity 70.6%; Pred. No. 1.5;
Matches 12; Conservative 1; Mismatches 4; Indels 4; Gaps 0;

QY 4 RRRWRRRRRPPKXK 20
   ||||| ||||| |||||
Db 253 RRAAGRRRRRPPDQPRK 269

RESULT 22
US-09-413-814-79
; Sequence 79, Application US/09413814
; Patent No. 6225064
; GENERAL INFORMATION:
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
; APPLICANT: Bristol-Myers Squibb, Co.
; APPLICANT: Beyer, Stefan
; APPLICANT: Bloecker, Helmut
; APPLICANT: Brandt, Petra
; APPLICANT: Cino, Paul M
; APPLICANT: Dougherty, Brian A
```

```
; APPLICANT: Goldberg, Steven L
; APPLICANT: Hofle, Gerhard
; APPLICANT: Mueller, Joachim
; APPLICANT: Reichenbach, Hans
; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
; FILE REFERENCE: PCT/US 99/23535
; CURRENT APPLICATION NUMBER: US/09/413,814
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: DE 198 46 493.2
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 1213
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-79
Query Match 51.3%; Score 58; DB 3; Length 1213;
Best Local Similarity 64.7%; Pred. No. 5.1;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPPK 17
   ||||| ||||| |||||
Db 432 RRRRRWRAPLRPEE 448

RESULT 23
US-08-847-176-19
; Sequence 19, Application US/08847176
; Patent No. 5989814
; GENERAL INFORMATION:
; APPLICANT: Frankel, Alan
; APPLICANT: Tat, Ruoying
; TITLE OF INVENTION: Screening Methods in Eucaryotic Cells
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,176
; FILING DATE: 01-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 2307AA-079100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-847-176-19
Query Match 50.4%; Score 57; DB 2; Length 23;
Best Local Similarity 68.4%; Pred. No. 0.17;
Matches 13; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

QY 1 RRRRRWRRRRRPPKKK 19
Db 5 RRRRRRRRRRRRAAAR 23

RESULT 24
US-08-281-702A-8
; Sequence 8, Application US/08281702A
; Patent No. 5534424
; GENERAL INFORMATION:
; APPLICANT: Golubev, Daniel B
; APPLICANT: Chaihorsky, Alexander
; TITLE OF INVENTION: PEPTIDE-CONTAINING VACCINE AGAINST
; TITLE OF INVENTION: ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Karl F. Ross, PC
; STREET: 5676 Riverdale Ave.
; CITY: Bronx
; STATE: NY
; COUNTRY: USA
; ZIP: 10471

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,702A
FILING DATE: 27-JUL-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan E
REGISTRATION NUMBER: 26,963
REFERENCE/DOCKET NUMBER: 19236
TELECOMMUNICATION INFORMATION:
TELEPHONE: (718) 884-6600
TELEFAX: (718) 601-1099
TELEX: 620428

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-281-702A-8

Query Match 50.4%; Score 57; DB 1; Length 28;
Best Local Similarity 60.0%; Pred. No. 0.2;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWRRRRRPPKKK 20
Db 8 RRRRRRRRRRRRAAAR 27

RESULT 25
US-08-618-917-8
; Sequence 8, Application US/08618917
; Patent No. 5837262
; GENERAL INFORMATION:
; APPLICANT: Golubev, Daniel B
; APPLICANT: Chaihorsky, Alexander
; TITLE OF INVENTION: PEPTIDE VACCINE TO PREVENT DEVELOPMENT OF SEVERAL
; TITLE OF INVENTION: HERPES INFECTIONS AND/OR ATHEROSCLEROTIC PLAQUE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Karl F. Ross, PC
; STREET: 5676 Riverdale Ave.
; CITY: Bronx
; STATE: NY
; COUNTRY: USA
; ZIP: 10471

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,917
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281,702
FILING DATE: 27-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan E
REGISTRATION NUMBER: 26,963
REFERENCE/DOCKET NUMBER: 19236
TELECOMMUNICATION INFORMATION:
TELEPHONE: (718) 884-6600
TELEFAX: (718) 601-1099
TELEX: 620428

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-618-917-8

Query Match 50.4%; Score 57; DB 2; Length 28;
Best Local Similarity 60.0%; Pred. No. 0.2;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWRRRRRPPKKK 20
Db 8 RRRRRRRRRRRRAAAR 27

RESULT 26
US-08-152-488-9
; Sequence 9, Application US/08152488
; Patent No. 5534619
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 512 Springfield Avenue
; CITY: Cranford
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07016-1811

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:

; TELEPHONE: 908-276-3344
; TELEFAX: 908-276-5543
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-9

Query Match 50.4%; Score 57; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.23;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPPKKRK 20
Db 13 RRRRPVSRRRRRGGRRR 32

RESULT 27

US-08-303-025-9
; Sequence 9, Application US/08303025
; Patent No. 5614494

; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 150 West Jefferson, Suite 2500
; CITY: Detroit
; STATE: Michigan
; COUNTRY: United States of America
; ZIP: 48226-4415

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS v.6.22
; SOFTWARE: WordPerfect 6.1; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,025
; FILING DATE: 08-SEPT-1994

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06829
; FILING DATE: 14-AUG-1992
; APPLICATION NUMBER: US 08/152,488
; FILING DATE: 12-NOV-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REFERENCE/DOCKET NUMBER: 7WH-060548-00231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313-496-7622
; TELEFAX: 313-496-8454
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A

; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-9

Query Match 50.4%; Score 57; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.23;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPPKKRK 20
Db 13 RRRRPVSRRRRRGGRRR 32

RESULT 28

US-08-677-304-9
; Sequence 9, Application US/08677304
; Patent No. 5721212

; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Andrews, Philip C.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
; TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
; TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Benita J. Rohm, Esq.
; STREET: 512 Springfield Avenue
; CITY: Cranford
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07016-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6; ASCII (DOS)Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/677,304
; FILING DATE:

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,488
; FILING DATE: 12-NOV-1993
; APPLICATION NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Rohm, Benita J.
; REFERENCE/DOCKET NUMBER: 28,664
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-276-3344
; TELEFAX: 908-276-5543
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid

; STRANDEDNESS: No. 5721212 Relevant
; TOPOLOGY: No. 5721212 Relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: N/A
; PUBLICATION INFORMATION:
; AUTHORS: N/A
; TITLE: N/A
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: PCT/US92/08069

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30


```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Powers, Vincent M.
; REGISTRATION NUMBER: 36,246
; REFERENCE/DOCKET NUMBER: 8600-0182.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0860
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-396-195-9

Query Match          48.7%; Score 55; DB 4; Length 15;
Best Local Similarity 85.7%; Pred. No. 0.21;
Matches 12; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 1 RRRRRWGRRRRR 14
   ||||| |||||
Db 1 RRRRRRRRRRR 14

RESULT 39
US-09-252-991A-27207
; Sequence 27207, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27207
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-27207

Query Match          48.7%; Score 55; DB 4; Length 79;
Best Local Similarity 57.9%; Pred. No. 0.98;
Matches 11; Conservative 3; Mismatches 5; Indels 5; Gaps 0;

QY 1 RRRRRWGRRRRRPKKR 19
   ||||| ||||| :|||:
Db 37 RRRRTCGSRRRRPRRR 55

RESULT 40
US-09-252-991A-23749
; Sequence 23749, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
```

```
; SEQ ID NO 23749
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-23749

Query Match          48.7%; Score 55; DB 4; Length 143;
Best Local Similarity 64.7%; Pred. No. 1.7;
Matches 11; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

QY 1 RRRRRWGRRRRRPKK 17
   ||||| ||||| :|||:
Db 37 RRRRLGSGRRRRPRR 53

Search completed: January 23, 2004, 11:19:28
Job time : 23 secs
```


Thu Jan 29 10:08:38 2004

us-10-002-884a-2.rapb

```

; APPLICANT: Benimetskaya, Lyuba
; APPLICANT: Guzzo-Pernell, Nancy
; TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DOWNR
; TITLE OF INVENTION: PKC-PROTEIN EXPRESSION IN CELLS
; FILE REFERENCE: 0575/63293
; CURRENT APPLICATION NUMBER: US/10/002,884A
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: CONTROL PEPTIDE
;
US-10-002-884A-3

Query Match          93.8%; Score 106; DB 15; Length 21;
Best Local Similarity 95.2%; Pred. No. 5e-06;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRRRRGRRRRRPPKKKKV 21
   |||||
Db 1 RRRRRGRRRRRPPKKKKV 21

RESULT 3
US-10-002-884A-1
; Sequence 1, Application US/10002884A
; Publication No. US20030087810A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Cy A
; APPLICANT: Benimetskaya, Lyuba
; APPLICANT: Guzzo-Pernell, Nancy
; TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DOWNR
; TITLE OF INVENTION: PKC-PROTEIN EXPRESSION IN CELLS
; FILE REFERENCE: 0575/63293
; CURRENT APPLICATION NUMBER: US/10/002,884A
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 32
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: NOVEL PEPTIDE - SV40/PROTAMINE SOURCE
;
US-10-002-884A-1

Query Match          79.6%; Score 90; DB 15; Length 32;
Best Local Similarity 74.1%; Pred. No. 0.0005;
Matches 20; Conservative 1; Mismatches 0; Indels 6; Gaps 1;

QY 1 RRRRRWGRR-----RRRRPKKKKV 21
   |||||
Db 6 RRRRRFGRRRRRVRRRRPKKKKKV 32

RESULT 4
US-10-002-884A-4
; Sequence 4, Application US/10002884A
; Publication No. US20030087810A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Cy A
; APPLICANT: Benimetskaya, Lyuba
; APPLICANT: Guzzo-Pernell, Nancy
; TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DOWNR
; TITLE OF INVENTION: PKC-PROTEIN EXPRESSION IN CELLS
; FILE REFERENCE: 0575/63293
; CURRENT APPLICATION NUMBER: US/10/002,884A
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
;

```

```

; SEQ ID NO 4
; LENGTH: 31
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: CONTROL PEPTIDE
;
US-10-002-884A-4

Query Match          67.3%; Score 76; DB 15; Length 31;
Best Local Similarity 75.0%; Pred. No. 0.02;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPPKKKKK 20
   |||||
Db 6 RRRRRFGRRRRRVRRRRK 25

RESULT 5
US-09-864-761-33832
; Sequence 33832, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00671
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33832
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
;

```

```

;
; FEATURE:
; OTHER INFORMATION: MAP TO AC007857.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.1
US-09-864-761-33832

Query Match          66.4%; Score 75; DB 9; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.061;
Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKK 20
Db 7 KRRRRGRRRRRKKKKR 26

RESULT 6
US-10-029-386-31410
; Sequence 31410, Application US/10C29386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2003-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31410
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC016943.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.86
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.52
US-10-029-386-31410

Query Match          64.6%; Score 73; DB 12; Length 71;
Best Local Similarity 71.4%; Pred. No. 0.089;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKKV 21
Db 50 RRRRRRRRRRRRRKKKV 70

RESULT 7
US-09-864-761-35536
; Sequence 35536, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23

```

```

;
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35536
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006391.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.1
US-09-864-761-35536

Query Match          64.6%; Score 73; DB 9; Length 130;
Best Local Similarity 75.0%; Pred. No. 0.14;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKK 20
Db 54 RRRRRKKRRRRKKKKK 73

RESULT 8
US-09-864-761-42011
; Sequence 42011, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng

```

```

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42011
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007340.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.5
; OTHER INFORMATION: EST_HUMAN HIT: AV718492.1, EVALUATE 3.90e+00
US-09-864-761-42011

```

```

Query Match      63.78; Score 72; DB 9; Length 80;
Best Local Similarity 88.24; Pred. No. 0.13;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 RRRRRRGGRRRRRPPKK 17
    ||||| ||||| ||
Db 62 RRRRRRGGRRRRRKKX 78

```

```

RESULT 9
US-10-029-386-27844
; Sequence 27844, Application US/10029386
; Publication No. US20030194704A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27844
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC017013.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.2
US-10-029-386-27844

```

Query Match 62.8%; Score 71; DB 12; Length 93;
Best Local Similarity 70.0%; Pred. No. 0.19;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 RRRRRRGGRRRRRPPKKKK 20
    ||||| ||||| |||
Db 23 RRRRRRGGRRRRRKKR 42

```

RESULT 10
US-09-864-761-41286
; Sequence 41286, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41286
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL57381.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; US-09-864-761-41286
Query Match 61.9%; Score 70; DB 9; Length 57;
Best Local Similarity 70.0%; Pred. No. 0.17;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRRGGRRRRRPPKPKK 20
Db 38 RRRRRRGGRRRRRPPKPKK 57

RESULT 11
US-10-029-386-30088
; Sequence 30088, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOmica-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30088
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL135920.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8
; US-10-029-386-30088
Query Match 61.1%; Score 69; DB 12; Length 29;
Best Local Similarity 68.4%; Pred. No. 0.13;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRRGGRRRRRPPKPKK 19
Db 11 RRRRRRGGRRRRRPPKPKK 29

```

```

RESULT 12
US-09-864-761-36486
; Sequence 36486, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36486
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010819.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.6
; US-09-864-761-36486
Query Match 61.1%; Score 69; DB 9; Length 41;

```

Best Local Similarity 73.7%; Pred. No. 0.17;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRRWGRRRRRPKKK 20
||||| :|||
Db 1 RRRRSRRRRRRRK 19
||||| :|||

RESULT 13
US-10-029-386-30080
; Sequence 30080, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: ACOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30080
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR22 144.0
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.31
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
US-10-029-386-30080

Query Match 61.1%; Score 69; DB 12; Length 73;
Best Local Similarity 70.0%; Pred. No. 0.26;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPKKK 20
||||| :|||
Db 36 RRRRRRRRRRRKKRR 55
||||| :|||

RESULT 14
US-10-029-386-33054
; Sequence 33054, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: ACOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33054
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011553.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96
US-10-029-386-33054

Query Match 60.2%; Score 68; DB 12; Length 26;
Best Local Similarity 65.0%; Pred. No. 0.15;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPKKK 20
||||| :|||
Db 6 RRRRRRRRRRRKKRR 25
||||| :|||

RESULT 15
US-09-864-761-34889
; Sequence 34889, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: ACOMICA-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34889
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010133.1
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6


```
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.2
US-09-864-761-34889

Query Match
Best Local Similarity 60.2%; Score 68; DB 9; Length 83;
Matches 10; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKPKK 20
   ||||| ||||| |||||
Db 15 RKKRRRRRRKKKKRRRR 34

RESULT 16
US-09-864-761-34765
; Sequence 34765, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34765
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006371.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.4
```

```
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EST_HUMAN HIT: BE958003.1, EVALUE 4.60e+00
US-09-864-761-34765

Query Match
Best Local Similarity 59.3%; Score 67; DB 9; Length 167;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKPKK 20
   ||||| ||||| |||||
Db 34 RRRRRKKKKRRKKRRRR 53

RESULT 17
US-09-911-569-5
; Sequence 5, Application US/09911569
; Publication No. US20030069173A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY-NELSON, PAMELA
; LAN, JIANQING
; SHIH, FOJEN
; JESSE, JOEL A.
; SCHIFFERLI, KEVIN P.
; GEBEYEHU, GULILAT
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREENLEE, WINNER & SULLIVAN
; STREET: 5370 MANHATTAN CIRCLE, SUITE 201
; CITY: BOULDER
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/911,569
; FILING DATE: 23-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/039,780
; FILING DATE: 16-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: SULLIVAN, SALLY A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 32-95D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8080
; TELEFAX: (303)499-8089
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2..20
; OTHER INFORMATION: /product="OTHER"
; /note="ANY OR ALL OF THE AMINO ACIDS 2-20 CAN BE PRESENT OR
; ABSENT"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-911-569-5
```

Thu Jan 29 10:08:38 2004

```

Query Match      58.4%; Score 66; DB 11; Length 20;
Best Local Similarity 65.0%; Pred. No. 0.21; Indels 0; Gaps 0;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPPKKRK 20
   ||||| ||||| :||:
Db 1 RRRRRRRRRRRRRRRR 20

RESULT 19
US-10-338-348-10
; Sequence 10, Application US/10338348
; Publication No. US20030162719A1
; GENERAL INFORMATION:
; APPLICANT: ROTHBARD, JONATHAN B.
; APPLICANT: WENDER, PAUL A.
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR ENHANCING TRANSPORT ACROSS
; TITLE OF INVENTION: BIOLOGICAL MEMBRANES
; FILE REFERENCE: 8400-0005.02
; CURRENT APPLICATION NUMBER: US/10/338,348
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 09/396,194
; PRIOR FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 09/083,259
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 60/047,345
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-338-348-10

Query Match      58.4%; Score 66; DB 12; Length 20;
Best Local Similarity 65.0%; Pred. No. 0.21; Indels 0; Gaps 0;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPPKKRK 20
   ||||| ||||| :||:
Db 1 RRRRRRRRRRRRRRRR 20

RESULT 20
US-10-136-738-44
; Sequence 44, Application US/10136738
; Publication No. US20030108886A1
; GENERAL INFORMATION:
; APPLICANT: Finn, John
; APPLICANT: MacLachlan, Ian
; APPLICANT: Protiva Biotherapeutics Inc.
; TITLE OF INVENTION: Autogene Nucleic Acids Encoding a
; TITLE OF INVENTION: Secretable RNA Polymerase
; FILE REFERENCE: 020801-0003100S
; CURRENT APPLICATION NUMBER: US/10/136,738
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/287,974
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial secretion domain
US-10-136-738-44

Query Match      58.4%; Score 66; DB 15; Length 22;

```

```

Query Match      58.4%; Score 66; DB 11; Length 20;
Best Local Similarity 65.0%; Pred. No. 0.21; Indels 0; Gaps 0;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPPKKRK 20
   ||||| ||||| :||:
Db 1 RRRRRRRRRRRRRRRR 20

RESULT 18
US-10-200-879-5
; Sequence 5, Application US/10200879
; Publication No. US20030144230A1
; GENERAL INFORMATION:
; APPLICANT: HAWLEY-NELSON, PAMELA
; APPLICANT: LAN, JIANQING
; APPLICANT: SHIH, POJEN
; APPLICANT: JESSE, JOEL A.
; APPLICANT: SCHIFFERLI, KEVIN P.
; APPLICANT: GEBEYERU, GULILAT
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GREENLEE, WINNER & SULLIVAN
; STREET: 5370 MANHATTAN CIRCLE, SUITE 201
; CITY: BOULDER
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/200,879
; FILING DATE: 23-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/911,569
; FILING DATE: 23-JUL-2001
; APPLICATION NUMBER: US 09/039,780
; FILING DATE: 16-MAR-1998
; APPLICATION NUMBER: US 08/818,200
; FILING DATE: 14-MAR-1997
; APPLICATION NUMBER: US 08/658,130
; FILING DATE: 04-JUN-1996
; APPLICATION NUMBER: US 08/477,354
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: SULLIVAN, SALLY A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 32-952
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8080
; TELEFAX: (303)499-8089
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2..20
; OTHER INFORMATION: /product= "OTHER"
; /note= "ANY OR ALL OF THE AMINO ACIDS 2-20 CAN BE PRESENT OR
; ABSENT"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-200-879-5

```

```
; OTHER INFORMATION: Description of Artificial Sequence:delivery-enhancing
; OTHER INFORMATION: transporter polymer of poly-arginine molecules between
; OTHER INFORMATION: 6 and 25 residues in length
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (7)-(25)
; OTHER INFORMATION: Arg at positions 7-25 may be present or absent
US-10-209-421-50

Query Match      58.4%; Score 66; DB 15; Length 25;
Best Local Similarity 65.0%; Pred. No. 0.25;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPKKKRK 20
    ||||| ||||| :|:|:
Db 1 RRRRRRRRRRRRRRRRRR 20

RESULT 21
US-10-338-348-11
; Sequence 11, Application US/10338348
; Publication No. US20030162719A1
; GENERAL INFORMATION:
; APPLICANT: ROTHBARD, JONATHAN B.
; APPLICANT: WENDER, PAUL A.
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR ENHANCING TRANSPORT ACROSS
; TITLE OF INVENTION: BIOLOGICAL MEMBRANES
; FILE REFERENCE: 8400-0005.02
; CURRENT APPLICATION NUMBER: US/10/338,348
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 09/396,194
; PRIOR FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 09/083,259
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 60/047,345
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-338-348-11

Query Match      58.4%; Score 66; DB 12; Length 25;
Best Local Similarity 65.0%; Pred. No. 0.25;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPKKKRK 20
    ||||| ||||| :|:|:
Db 1 RRRRRRRRRRRRRRRRRR 20

RESULT 22
US-10-209-421-50
; Sequence 50, Application US/10209421
; Publication No. US20030083256A1
; GENERAL INFORMATION:
; APPLICANT: Rothbard, Jonathan B.
; APPLICANT: Wender, Paul A.
; APPLICANT: McGrane, P. Leo
; APPLICANT: Sista, Lalitha V.S.
; APPLICANT: Kirschberg, Thorsten A.
; APPLICANT: CellGate, Inc.
; TITLE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery
; TITLE OF INVENTION: Across and Into Epithelial Tissues
; FILE REFERENCE: 019801-000211US
; CURRENT APPLICATION NUMBER: US/10/209,421
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 60/150,510
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: US 09/648,400
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:delivery-enhancing
; OTHER INFORMATION: transporter of 5-25 arginine residues
US-10-209-421-51

Query Match      58.4%; Score 66; DB 15; Length 25;
Best Local Similarity 65.0%; Pred. No. 0.25;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPKKKRK 20
    ||||| ||||| :|:|:
Db 1 RRRRRRRRRRRRRRRRRR 20

RESULT 24
US-10-338-348-22
; Sequence 22, Application US/10338348
; Publication No. US20030162719A1
; GENERAL INFORMATION:
; APPLICANT: ROTHBARD, JONATHAN B.
; APPLICANT: WENDER, PAUL A.
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR ENHANCING TRANSPORT ACROSS
; TITLE OF INVENTION: BIOLOGICAL MEMBRANES
; FILE REFERENCE: 8400-0005.02
; CURRENT APPLICATION NUMBER: US/10/338,348
```

; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 09/396,194
; PRIOR FILING DATE: 1999-09-14
; PRIOR APPLICATION NUMBER: 09/083,259
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 60/047,345
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-338-348-22

Query Match 58.4%; Score 66; DB 12; Length 30;
Best Local Similarity 65.0%; Pred. No. 0.29;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPKKKK 20
||||| ||||| :|||
Db 1 RRRRRRRRRRRRRRRR 20

RESULT 25

US-09-910-432-16
; Sequence 16, Application US/09910432
; Publication No. US20030229034A1
; GENERAL INFORMATION:
; APPLICANT: Waugh, Jacob
; APPLICANT: Duke, Michael
; APPLICANT: Essentia Biosystems, Inc.
; TITLE OF INVENTION: Multi-Component Biological Transport Systems
; FILE REFERENCE: 020154-000110US
; CURRENT APPLICATION NUMBER: US/09/910,432
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,244
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: positively
; OTHER INFORMATION: charged branching group (efficiency group)
; OTHER INFORMATION: attached to solid backbone
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(20)
; OTHER INFORMATION: Gly at positions 1-20 may be present or absent
US-09-910-432-16

Query Match 58.4%; Score 66; DB 12; Length 41;
Best Local Similarity 65.0%; Pred. No. 0.37;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPKKKK 20
||||| ||||| :|||
Db 21 RRRRRRRRRRRRRRRR 40

RESULT 26

US-09-910-432-17
; Sequence 17, Application US/09910432
; Publication No. US20030229034A1
; GENERAL INFORMATION:
; APPLICANT: Waugh, Jacob
; APPLICANT: Duke, Michael

; APPLICANT: Essentia Biosystems, Inc.
; TITLE OF INVENTION: Multi-Component Biological Transport Systems
; FILE REFERENCE: 020154-000110US
; CURRENT APPLICATION NUMBER: US/09/910,432
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,244
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: positively
; OTHER INFORMATION: charged branching group (efficiency group)
; OTHER INFORMATION: attached to solid backbone
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(20)
; OTHER INFORMATION: Gly at positions 1-20 may be present or absent
US-09-910-432-17

Query Match 58.4%; Score 66; DB 12; Length 43;
Best Local Similarity 65.0%; Pred. No. 0.38;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPKKKK 20
||||| ||||| :|||
Db 21 RRRRRRRRRRRRRRRR 40

RESULT 27

US-09-910-432-18
; Sequence 18, Application US/09910432
; Publication No. US20030229034A1
; GENERAL INFORMATION:
; APPLICANT: Waugh, Jacob
; APPLICANT: Duke, Michael
; APPLICANT: Essentia Biosystems, Inc.
; TITLE OF INVENTION: Multi-Component Biological Transport Systems
; FILE REFERENCE: 020154-000110US
; CURRENT APPLICATION NUMBER: US/09/910,432
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,244
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: positively
; OTHER INFORMATION: charged branching group (efficiency group)
; OTHER INFORMATION: attached to solid backbone
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(20)
; OTHER INFORMATION: Gly at positions 1-20 may be present or absent
US-09-910-432-18

Query Match 58.4%; Score 66; DB 12; Length 45;
Best Local Similarity 65.0%; Pred. No. 0.4;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPKKKK 20
||||| ||||| :|||
Db 21 RRRRRRRRRRRRRRRR 40

RESULT 28

US-10-029-386-30905

```
; Sequence 30905, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30905
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011400.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.8
US-10-029-386-30905

Query Match          58.4%; Score 66; DB 12; Length 49;
Best Local Similarity 65.0%; Pred. No. 0.43;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGGGRRRRRPPKKKK 20
   ||||| ||||| ::|:
Db 26 RRRRRRRRRRRRRRRR 45

RESULT 29
US-10-029-386-27409
; Sequence 27409, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27409
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR22 212.0
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
US-10-029-386-27409

Query Match          58.4%; Score 66; DB 12; Length 50;
Best Local Similarity 65.0%; Pred. No. 0.43;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGGGRRRRRPPKKKK 20
   ||||| ||||| ::|:
Db 13 RRRRRRRRRRRRRRRR 32

RESULT 30
US-10-002-344A-229
; Sequence 229, Application US/10002344A
; Publication No. US20020172959A1
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Pr
; FILE REFERENCE: DEX-0241
; CURRENT APPLICATION NUMBER: US/10/002,344A
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/242,998
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 229
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-002-344A-229

Query Match          58.4%; Score 66; DB 14; Length 76;
Best Local Similarity 55.0%; Pred. No. 0.61;
Matches 11; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRRRRGGGRRRRRPPKKKK 20
   ::|: ||||| ::|:
Db 28 KKKKKGGGRRRRRPPKKKK 47

RESULT 31
US-09-983-580-9
; Sequence 9, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Maoliang
; APPLICANT: Filpula, David R.
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: NO. US20020151061A1 Method for Targeted Delivery of Nucleic Ac
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: binding region
; OTHER INFORMATION: Amino acids in positions 1-56 may be absent or
; OTHER INFORMATION: present.
; NAME/KEY: UNSURE
; LOCATION: (57)..(76)
; OTHER INFORMATION: May be any amino acid.
; OTHER INFORMATION: Amino acids in positions 57-76 may be absent or
; OTHER INFORMATION: present.
US-09-983-580-9

Query Match          58.4%; Score 66; DB 10; Length 84;
Best Local Similarity 65.0%; Pred. No. 0.66;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGGGRRRRRPPKKKK 20
   ||||| ||||| ::|:
Db 1 RRRRRRRRRRRRRRRR 20
```

```
RESULT 32
US-09-983-580-11
; Sequence 11, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020151061A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: binding region
; OTHER INFORMATION: Amino acids in positions 1-56 may be absent or
; OTHER INFORMATION: present.
; NAME/KEY: UNSURE
; LOCATION: (57)--(76)
; OTHER INFORMATION: May be any amino acid.
; OTHER INFORMATION: Amino acids in positions 57-76 may be absent or
; OTHER INFORMATION: present.
US-09-983-580-11

Query Match          58.4%; Score 66; DB 10; Length 84;
Best Local Similarity 65.0%; Pred. No. 0.66;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGWRRRRRPKKKRK 20
    ||||| ||||| ::::
Db 1 RRRRRRRRRRRRRRRRRR 20

RESULT 33
US-09-985-442-9
; Sequence 9, Application US/09985442
; Patent No. US20020156248A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: binding region
; OTHER INFORMATION: Amino acids in positions 1-56 may be absent or
; OTHER INFORMATION: present.
; NAME/KEY: UNSURE
; LOCATION: (57)--(76)
; OTHER INFORMATION: May be any amino acid.
; OTHER INFORMATION: Amino acids in positions 57-76 may be absent or
; OTHER INFORMATION: present.
US-09-985-442-9

Query Match          58.4%; Score 66; DB 10; Length 84;
Best Local Similarity 65.0%; Pred. No. 0.66;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGWRRRRRPKKKRK 20
    ||||| ||||| ::::
Db 1 RRRRRRRRRRRRRRRRRR 20

RESULT 34
US-09-985-442-11
; Sequence 11, Application US/09985442
; Patent No. US20020156248A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: binding region
; OTHER INFORMATION: Amino acids in positions 1-56 may be absent or
; OTHER INFORMATION: present.
; NAME/KEY: UNSURE
; LOCATION: (57)--(76)
; OTHER INFORMATION: May be any amino acid.
; OTHER INFORMATION: Amino acids in positions 57-76 may be absent or
; OTHER INFORMATION: present.
US-09-985-442-11

Query Match          58.4%; Score 66; DB 10; Length 84;
Best Local Similarity 65.0%; Pred. No. 0.66;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGWRRRRRPKKKRK 20
    ||||| ||||| ::::
Db 1 RRRRRRRRRRRRRRRRRR 20

RESULT 35
US-09-864-761-38160
; Sequence 38160, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
```

```
; LOCATION: (57)--(76)
; OTHER INFORMATION: May be any amino acid.
; OTHER INFORMATION: Amino acids in positions 57-76 may be absent or
; OTHER INFORMATION: present.
US-09-985-442-9

Query Match          58.4%; Score 66; DB 10; Length 84;
Best Local Similarity 65.0%; Pred. No. 0.66;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGWRRRRRPKKKRK 20
    ||||| ||||| ::::
Db 1 RRRRRRRRRRRRRRRRRR 20

RESULT 34
US-09-985-442-11
; Sequence 11, Application US/09985442
; Patent No. US20020156248A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Acid
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: binding region
; OTHER INFORMATION: Amino acids in positions 1-56 may be absent or
; OTHER INFORMATION: present.
; NAME/KEY: UNSURE
; LOCATION: (57)--(76)
; OTHER INFORMATION: May be any amino acid.
; OTHER INFORMATION: Amino acids in positions 57-76 may be absent or
; OTHER INFORMATION: present.
US-09-985-442-11

Query Match          58.4%; Score 66; DB 10; Length 84;
Best Local Similarity 65.0%; Pred. No. 0.66;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRGWRRRRRPKKKRK 20
    ||||| ||||| ::::
Db 1 RRRRRRRRRRRRRRRRRR 20

RESULT 35
US-09-864-761-38160
; Sequence 38160, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
```

```

; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38160
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL033533.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
; US-09-864-761-38160

```

```

Query Match          58.4%; Score 66; DB 9; Length 88;
Best Local Similarity 65.0%; Pred. No. 0.68;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 RRRRRRGGRRRRRRPKKKKK 20
    ||||| ||||| ||||| |||||
Db 43 RRRRRRRRRRRRRRRRRRR 62

```

```

RESULT 36
US-09-864-761-39633
; Sequence 39633, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng

```

```

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; CURRENT APPLICATION NUMBER: US 09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39633
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002465.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.42
; US-09-864-761-39633

```

```

Query Match          58.4%; Score 66; DB 9; Length 95;
Best Local Similarity 65.0%; Pred. No. 0.73;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1 RRRRRRGGRRRRRRPKKKKK 20
    ||||| ||||| ||||| |||||
Db 64 KKKRRRRRRRRRRRRKKKK 83

```

```

RESULT 37
US-09-815-656-31
; Sequence 31, Application US/09815656
; Patent No. US20010041331A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Leary, Thomas
; APPLICANT: Erker, James
; APPLICANT: Chalmers, Michelle
; APPLICANT: Simons, John

```

Thu Jan 29 10:08:38 2004

```

; APPLICANT: Birkenmeyer, Larry
; APPLICANT: Muerthoff, Scott
; APPLICANT: Pilot-Matias, Tami
; APPLICANT: Desai, Suresh
; APPLICANT: Mushahwar, Isa
; TITLE OF INVENTION: METHODS OF UTILIZING THE TT VIRUS
; FILE REFERENCE: 6461 US 01
; CURRENT APPLICATION NUMBER: US/09/815,656
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 09/245,248
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-815-656-31

Query Match      58.0%; Score 65.5; DB 9; Length 770;
Best Local Similarity 73.7%; Pred. No. 4.5;
Matches 14; Conservative 2; Mismatches 1; Gaps 1;

QY 1 RRRRRWGRRRRRPKKRR 19
Db 7 RRRRRW-RRRRRPWRRR 24

RESULT 38
US-09-992-896-9
; Sequence 9, Application US/09992896
; Publication No. US20030022158A1
; GENERAL INFORMATION:
; APPLICANT: Matti Salberg
; TITLE OF INVENTION: PEPTIDES FROM THE TT VIRUS SEQUENCE AND
; TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES BINDING TO THE TT VIRUS
; FILE REFERENCE: TRIPEP.033CP1
; CURRENT APPLICATION NUMBER: US/09/992,896
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/BP00/03958
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: SE 19990001601
; PRIOR FILING DATE: 1999-05-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Immunogen
US-09-992-896-9

Query Match      58.0%; Score 65.5; DB 11; Length 770;
Best Local Similarity 73.7%; Pred. No. 4.5;
Matches 14; Conservative 2; Mismatches 1; Gaps 1;

QY 1 RRRRRWGRRRRRPKKRR 19
Db 7 RRRRRW-RRRRRPWRRR 24

RESULT 39
US-09-864-761-37366
; Sequence 37366, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weisheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

```

```

; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37366
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007335.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.9
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.6
US-09-864-761-37366

Query Match      57.5%; Score 65; DB 9; Length 38;
Best Local Similarity 50.0%; Pred. No. 0.45;
Matches 13; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 RRRRR-----WGRRRRRPKKRRK 20
Db 1 RRRRRRWMTWRRRRRRKTRRRK 26

RESULT 40
US-10-029-386-33742
; Sequence 33742, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:

```



```

; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33742
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002504.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
US-10-029-386-33742

```

```

Query Match          57.5%; Score 65; DB 12; Length 96;
Best Local Similarity 61.9%; Pred. No. 0.96;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```

```
Qy      1 RRRRRRWGRRRRRRPKKRV 21
         |:|:|:| | | | | : |
Db     30 RRRRRRRRRRRRRRRPRRV 50
```

Search completed: January 23, 2004, 11:24:35
Job time : 34 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2004, 11:16:50 ; Search time 21 Seconds
(without alignments)
96.169 Million cell updates/sec

Title: US-10-002-884A-2
Perfect score: 113
Sequence: 1 RRRRRWGRRRRRPKKRV 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	63.7	111	2	TL4306
2	69	61.1	126	2	S58321
3	67	59.3	50	1	HSSH
4	67	59.3	51	1	HSBOS
5	66	58.4	294	2	E87538
6	65	57.5	49	2	S00228
7	65	57.5	58	2	S10755
8	65	57.5	62	2	S10754
9	63	55.8	57	2	A34356
10	63	55.8	234	2	T26560
11	62	54.9	33	2	C21211
12	62	54.9	79	2	S66116
13	61	54.0	33	2	D21211
14	61	54.0	33	2	T01070
15	61	54.0	37	2	S29829
16	61	54.0	41	2	G88208
17	61	54.0	48	2	S29973
18	60	53.1	51	1	HMS81
19	60	53.1	51	2	S03997
20	60	53.1	118	2	S56117
21	60	53.1	604	2	D84235
22	58.5	51.8	45	2	B58208
23	58.5	51.8	45	2	C58208
24	58.5	51.8	45	2	D58208
25	58.5	51.8	47	2	E58208
26	58.5	51.8	47	2	F58208
27	58	51.3	32	1	Y2PK1
28	58	51.3	32	1	IRTR2
29	58	51.3	33	2	E21211

30 58 51.3 78 2 A40973
31 58 51.3 132 2 S10305
32 58 51.3 168 2 A03864
33 57.5 50.9 58 2 A58208
34 57 50.4 27 1 SRAFC
35 57 50.4 32 1 S10NA1
36 57 50.4 32 2 B02669
37 57 50.4 33 1 IRTR1A
38 57 50.4 33 1 IRTR59
39 57 50.4 33 1 IRTR42
40 57 50.4 33 2 A21211
41 57 50.4 33 2 S00710
42 57 50.4 41 2 H58208
43 57 50.4 49 2 S02007
44 57 50.4 58 2 S34045
45 57 50.4 77 2 B40973

ALIGNMENTS

RESULT 1

TL4306
glycine-rich protein - carrot (fragment)
C:Species: Daucus carota (carrot)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: TL4306
R;Lin, X.; Hwang, G.J.; Zimmerman, J.L.
submitted to the EMBL Data Library, January 1996
A:Description: Isolation and characterization of a diverse set of genes from carrot som
A:Reference number: Z17968
A:Accession: TL4306
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 1-111 <LIN>
A:Cross-references: EMBL:U47097; NID:gl276970; PID:gl276971
A:Experimental source: strain Danver Half-long

Query Match 63.7%; Score 72; DB 2; Length 111;
Best Local Similarity 72.2%; Pred. No. 0.047; 3; Indels 0;
Matches 13; Conservative 2; Mismatches 3; Gaps 0;

Qy 1 RRRRRWGRRRRRPKKK 18
Db 67 RRRRRWGRRRRRSSRR 84

RESULT 2

S58321
probable membrane protein YOR309c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein 06105
C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002
C:Accession: S58321; S67215; S71989
R;Pearson, B.M.; Hernandez, Y.; Wolf, S.S.; Kalogeropoulos, A.; Schweizer, M.
submitted to the EMBL Data Library, August 1995
A:Reference number: S58318
A:Accession: S58321
A:Molecule type: DNA
A:Residues: 1-126 <PEA>
A:Cross-references: EMBL:X90565; NID:gl420680; PID:e252431; PID:gl420681; MIPS:YOR309c
R;Pearson, B.M.; Hernandez, Y.; Kalogeropoulos, A.; Schweizer, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67213
A:Accession: S67215
A:Molecule type: DNA
A:Residues: 1-126 <PEW>
A:Cross-references: EMBL:Z75217; NID:gl420680; PID:e252431; PID:gl420681; MIPS:YOR309c
A:Experimental source: strain S288C
R;Pearson, B.M.; Hernandez, Y.; Payne, J.; Wolf, S.S.; Kalogeropoulos, A.; Schweizer, M.
Yeast 12, 1021-1031, 1996
A:Title: Sequencing of a 35.71 kb DNA segment on the right arm of yeast chromosome XV r
A:Reference number: S71986; MUID:97051589; PMID:8896266

A:Accession: S71989
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-126 <PEP>
 A:Cross-references: EMBL:X90565; NID:G940836; PIDN:CAA62164.1; PID:G940840
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
 C:Genetics:
 A:Accession: SGD:S0005836
 A:Map position: 15R
 C:Keywords: transmembrane protein
 F:3-19/Domain: transmembrane #status predicted <TM1>
 F:107-123/Domain: transmembrane #status predicted <TM2>

Query Match 61.1%; Score 69; DB 2; Length 126;
 Best Local Similarity 65.0%; Pred. No. 0.12;
 Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 RRRRRRGGRRRRRRKKKK 20
 |||||:| ||||:| ||||:| ||||:| ||||:|
 Db 62 RRRRRRKKRRRRKRRK 81

RESULT 3
 HSSH
 sperm histone - sheep
 N:Alternate names: cysteine-rich protamine; protamine
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 05-Sep-1997
 C:Accession: A02658
 R:Sautiere, P.; Belaiche, D.; Martinage, A.; Loir, M.
 Eur. J. Biochem. 144, 121-125, 1984
 A:Title: Primary structure of the ram (Ovis aries) protamine.
 A:Reference number: A02658; MUID:85003651; PMID:6479168
 A:Accession: A02658
 A:Molecule type: protein
 A:Residues: 1-50 <SAU>
 C:Superfamily: sperm histone
 C:Keywords: chromosomal protein; DNA binding; nucleosome core; spermatogenesis
 F:5/Disulfide bonds: interchain (to 22) #status predicted
 F:6-14, 39-47/Disulfide bonds: #status predicted
 F:22/Disulfide bonds: interchain (to 5) #status predicted
 F:38/Disulfide bonds: interchain #status predicted

Query Match 59.3%; Score 67; DB 1; Length 50;
 Best Local Similarity 92.9%; Pred. No. 0.1;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRRRRGGRRRRR 14
 |||||:| ||||:| ||||:| ||||:| ||||:|
 Db 23 RRRRRRGGRRRRR 36

RESULT 4
 HSOS
 sperm histone P1 - bovine
 N:Alternate names: arginine-rich protamine; cysteine-rich protamine; protamine P1; sperm
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Apr-1984 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999
 C:Accession: A29911; A26450; A26041; A24375; A61342
 R:Krawetz, S.A.; Connor, W.; Dixon, G.H.
 J. Biol. Chem. 263, 321-326, 1988
 A:Title: Bovine protamine genes contain a single intron. The structures of the two alleles
 A:Reference number: A29911; MUID:88087109; PMID:3335501
 A:Accession: A29911
 A:Molecule type: DNA
 A:Residues: 1-51 <KRA>
 A:Cross-references: GB:W18396; NID:G163619; PIDN:AAA30735.1; PID:G163620
 R:Krawetz, S.A.; Connor, W.; Dixon, G.H.
 DNA 6, 47-57, 1987
 A:Title: Cloning of bovine P1 protamine cDNA and the evolution of vertebrate P1 protamin
 A:Reference number: A26450; MUID:87161234; PMID:3829889
 A:Accession: A26450
 A:Molecule type: mRNA

A:Residues: 1-51 <KR2>
 A:Cross-references: GB:W14559; NID:G163632; PIDN:AAA30741.1; PID:G163633
 R:Lee, C.H.; Mansouri, A.; Hecht, W.; Hecht, N.B.; Engel, W.
 Biol. Chem. Hoppe-Seyler 368, 131-135, 1987
 A:Title: Nucleotide sequence of a bovine protamine cDNA.
 A:Reference number: A26041; MUID:87184911; PMID:2436637
 A:Accession: A26041
 A:Molecule type: mRNA
 A:Residues: 2-51 <LEE>
 A:Cross-references: GB:M18625
 A:Note: the codon for residue 30-Phe is shown as TCT
 R:Mazrimas, J.A.; Corzett, M.; Campos, C.; Balhorn, R.
 Biochim. Biophys. Acta 872, 11-15, 1986
 A:Title: A corrected primary sequence for bull protamine.
 A:Reference number: A24375; MUID:86269988; PMID:3730390
 A:Accession: A24375
 A:Molecule type: protein
 A:Residues: 2-51 <MAZ>
 R:Coalingh, J.P.; Monfoort, C.H.; Roziijn, T.H.; Leuven, J.A.G.; Schiphof, R.; Steyn-Pa
 Biochim. Biophys. Acta 285, 1-14, 1972
 A:Title: The complete amino acid sequence of the basic nuclear protein of bull spermato
 A:Reference number: A61342; MUID:73124384; PMID:4675900
 A:Accession: A61342
 A:Molecule type: protein
 A:Residues: 2-39; 43-51 <COE>
 R:Balhorn, R.; Corzett, M.; Mazrimas, J.; Watkins, B.
 Biochemistry 30, 175-181, 1991
 A:Title: Identification of bull protamine disulfides.
 A:Reference number: A37137; MUID:91105078; PMID:1988019
 A:Contents: annotation: disulfide bonds
 C:Genetics:
 A:Introns: 38/1
 C:Function:
 C:Description: binds to and packages sperm DNA in a condensed form of chromatin that i
 C:Superfamily: sperm histone
 C:Keywords: chromosomal protein; DNA binding; nucleosome core; spermatogenesis
 F:2-51/Product: protamine P1 #status experimental <MAT>
 F:6/Disulfide bonds: interchain (to 23) #status experimental
 F:7-15, 40-48/Disulfide bonds: #status experimental
 F:23/Disulfide bonds: interchain (to 6) #status experimental
 F:39/Disulfide bonds: interchain #status experimental

Query Match 59.3%; Score 67; DB 1; Length 51;
 Best Local Similarity 92.9%; Pred. No. 0.1;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRRRRRGGRRRRR 14
 |||||:| ||||:| ||||:| ||||:| ||||:|
 Db 24 RRRRRRGGRRRRR 37

RESULT 5
 E87538
 hypothetical protein CC2334 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: E87538
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kol
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: E87538
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-294 <STO>
 A:Cross-references: GB:AE005673; NID:G13423859; PIDN:AAK24305.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC2334

Query Match 59.4%; Score 66; DB 2; Length 294;
 Best Local Similarity 65.0%; Pred. No. 0.5;

Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGGRRRRPCKKRV 20
 ||||| ||||| :|||
 Db 175 RRRRFGRRRRRRRRRR 194

RESULT 6
 S00228
 protamine - horse
 N:Alternate names: sperm histone
 C:Species: Equus caballus (domestic horse)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Feb-1997
 C:Accession: S00228
 R:Ammer, H.; Henschen, A.
 A:Title: The major protamine from stallion sperm. Isolation and amino-acid sequence.
 A:Reference number: S00228; MUID:88163084; PMID:3442606
 A:Accession: S00228
 A:Molecule type: protein
 A:Residues: 1-49 <AMM>
 A:Note: the sequence from Fig. 6 is inconsistent with that from Fig.3 in lacking Arg-49
 C:Superfamily: sperm histone
 C:Keywords: DNA binding; nucleus

Query Match 57.5%; Score 65; DB 2; Length 49;
 Best Local Similarity 66.7%; Pred. No. 0.17;
 Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRWGGRRRRPCKKRV 21
 ||||| ||||| :|||
 Db 15 RRRRRRCRRRRRVQRVV 35

RESULT 7
 S10755
 protamine St2a - horse
 C:Species: Equus caballus (domestic horse)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Oct-1999
 C:Accession: S10755; S02787
 R:Pirhonen, A.; Valtanen, P.; Linnala-Kankkunen, A.; Heiskanen, M.L.; Maeenpaae, P.H.
 Biochim. Biophys. Acta 1039, 177-180, 1990
 A:Title: Primary structures of two protamine 2 variants (St2a and St2b) from stallion sperm
 A:Reference number: S10754; MUID:90304188; PMID:2364093
 A:Accession: S10755
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-58 <PIR>
 R:Pirhonen, A.; Linnala-Kankkunen, A.; Maeenpaae, P.H.
 FEBS Lett. 244, 199-202, 1989
 A:Title: Comparison of partial amino acid sequences of two protamine 2 variants from stallion sperm
 A:Reference number: S02786; MUID:89171259; PMID:2924903
 A:Accession: S02787
 A:Molecule type: protein
 A:Residues: 1-25 <PI2>
 C:Superfamily: sperm histone
 C:Keywords: DNA binding; nucleus

Query Match 57.5%; Score 65; DB 2; Length 58;
 Best Local Similarity 65.0%; Pred. No. 0.19;
 Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRWGGRRRRPCKKRV 20
 ||||| ||||| :|||
 Db 21 RRRRRSSRRRRRRCRRR 40

RESULT 8
 S10754
 protamine St2a - horse
 C:Species: Equus caballus (domestic horse)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Oct-1999
 C:Accession: S10754; S02786

Query Match 57.5%; Score 65; DB 2; Length 58;
 Best Local Similarity 65.0%; Pred. No. 0.19;
 Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRWGGRRRRPCKKRV 20
 ||||| ||||| :|||
 Db 21 RRRRRSSRRRRRRCRRR 40

RESULT 8
 S10754
 protamine St2a - horse
 C:Species: Equus caballus (domestic horse)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Oct-1999
 C:Accession: S10754; S02786

R:Pirhonen, A.; Valtanen, P.; Linnala-Kankkunen, A.; Heiskanen, M.L.; Maeenpaae, P.H.
 Biochim. Biophys. Acta 1039, 177-180, 1990
 A:Title: Primary structures of two protamine 2 variants (St2a and St2b) from stallion sperm
 A:Reference number: S10754; MUID:90304188; PMID:2364093
 A:Accession: S10754
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-62 <PIR>
 R:Pirhonen, A.; Linnala-Kankkunen, A.; Maeenpaae, P.H.
 FEBS Lett. 244, 199-202, 1989
 A:Title: Comparison of partial amino acid sequences of two protamine 2 variants from stallion sperm
 A:Reference number: S02786; MUID:89171259; PMID:2924903
 A:Accession: S02786
 A:Molecule type: protein
 A:Residues: 1-25 <PI2>
 C:Superfamily: sperm histone
 C:Keywords: DNA binding; nucleus

Query Match 57.5%; Score 65; DB 2; Length 62;
 Best Local Similarity 65.0%; Pred. No. 0.2;
 Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRWGGRRRRPCKKRV 20
 ||||| ||||| :|||
 Db 25 RRRRRSSRRRRRRCRRR 44

RESULT 9
 A34356
 protamine - Japanese quail
 C:Species: Coturnix coturnix japonica (Japanese quail)
 C>Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 23-Jul-1999
 C:Accession: A34356
 R:Oliva, R.; Goren, R.; Dixon, G.H.
 J. Biol. Chem. 264, 17627-17630, 1989
 A:Title: Quail (Coturnix japonica) protamine, full-length cDNA sequence, and the function
 A:Reference number: A34356; MUID:90036816; PMID:2808336
 A:Accession: A34356
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-57 <OLI>
 A:Cross-references: GB:M30275; NID:g213612; PIDN:AAA49498.1; PID:g213613
 C:Superfamily: sperm histone
 C:Keywords: DNA binding; nucleus; phosphoprotein

Query Match 55.8%; Score 63; DB 2; Length 57;
 Best Local Similarity 92.3%; Pred. No. 0.33;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRRWGRRRRR 14
 ||||| :|||
 Db 42 RRRRRGRRRRR 54

RESULT 10
 T26560
 hypothetical protein Y24F12A.c - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
 C:Accession: T26560
 R:Lennard, N.
 submitted to the EMBL Data Library, September 1999
 A:Reference number: Z20233
 A:Accession: T26560
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-234 <WIL>
 A:Cross-references: EMBL:AL110480; NID:e1542182; PIDN:CAB54379.1; CESP:Y24F12A.c
 A:Experimental source: clone Y24F12A
 C:Genetics:

Query Match 55.8%; Score 63; DB 2; Length 57;
 Best Local Similarity 92.3%; Pred. No. 0.33;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRRRWGRRRRR 14
 ||||| :|||
 Db 42 RRRRRGRRRRR 54

RESULT 10
 T26560
 hypothetical protein Y24F12A.c - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
 C:Accession: T26560
 R:Lennard, N.
 submitted to the EMBL Data Library, September 1999
 A:Reference number: Z20233
 A:Accession: T26560
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-234 <WIL>
 A:Cross-references: EMBL:AL110480; NID:e1542182; PIDN:CAB54379.1; CESP:Y24F12A.c
 A:Experimental source: clone Y24F12A
 C:Genetics:

A:Introns: 12/2; 55/1; 200/1
 C:Superfamily: Caenorhabditis elegans hypothetical protein Y9D1A.2

Query Match 55.8%; Score 63; DB 2; Length 234;
Best Local Similarity 92.9%; Pred. No. 0.95;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRRRRWRRRRR 14
115 RRRRRWRRRRR 128

Db

RESULT 11
C21211
protamine TP16 - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: C21211
R;Aiken, J.M.; McKenzie, D.; Zhao, H.Z.; States, J.C.; Dixon, G.H.
Nucleic Acids Res. 11, 4907-4922, 1983
A;Title: Sequence homologues in the protamine gene family of rainbow trout.
A;Reference number: A21211; MUID:83272939; PMID:6308564
A;Accession: C21211
A;Molecule type: DNA
A;Residues: 1-33 <Aik>
A;Cross-references: EMBL:X01597; NID:G64338; PIDN:CAA25750.1; PID:G64339
A;Note: the authors translated the codon CGC for residue 29 as Gly
C;Superfamily: protamine Y2
C;Keywords: DNA binding; nucleus

Query Match 54.9%; Score 62; DB 2; Length 33;
Best Local Similarity 60.0%; Pred. No. 0.28;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRWRRRRRPPKKRK 20
14 RRRRVSRRRRRRRRRR 33

Db

RESULT 12
S56116
spermatid-specific protein T1 - longfin squid
C;Species: Loligo pealeii (longfin squid)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
R;Wouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andula, N.; Kouach, M.; Jaquinod, M.; S
Biochem. J. 309, 529-534, 1995
A;Title: Squid spermiogenesis: molecular characterization of testis-specific pro-protami
A;Reference number: S56116; MUID:95351983; PMID:7626016
A;Accession: S56116
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-79 <WOU>
C;Superfamily: sperm histone

Query Match 54.9%; Score 62; DB 2; Length 79;
Best Local Similarity 66.7%; Pred. No. 0.55;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRRRWRRRRRPPKKRK 19
22 RRRRRSRRRRRRRRRR 39

Db

RESULT 13
D21211
protamine TP17 - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Feb-1997
C;Accession: D21211
R;Aiken, J.M.; McKenzie, D.; Zhao, H.Z.; States, J.C.; Dixon, G.H.
Nucleic Acids Res. 11, 4907-4922, 1983
A;Title: Sequence homologues in the protamine gene family of rainbow trout.
A;Reference number: A21211; MUID:83272939; PMID:6308564
A;Accession: D21211

A;Molecule type: DNA
A;Residues: 1-33 <Aik>
A;Cross-references: EMBL:X01598
A;Note: the authors translated the codon CGC for residue 29 as Gly
C;Superfamily: protamine Y2
C;Keywords: DNA binding; nucleus

Query Match 54.0%; Score 61; DB 2; Length 33;
Best Local Similarity 60.0%; Pred. No. 0.37;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRWRRRRRPPKKRK 20
14 RRRRVSRRRRRRRRRR 33

RESULT 14

T01070
protamine - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Jul-1999
C;Accession: T01070
R;Aiken, J.M.; McKenzie, D.; Zhao, H.Z.; States, J.C.; Dixon, G.H.
Nucleic Acids Res. 11, 4907-4922, 1983
A;Title: Sequence homologues in the protamine gene family of rainbow trout.
A;Reference number: A21211; MUID:83272939; PMID:6308564
A;Accession: T01070
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-33 <Aik>
A;Cross-references: EMBL:X01598; NID:G64340; PIDN:CAA25751.1; PID:G64341
C;Superfamily: protamine Y2

Query Match 54.0%; Score 61; DB 2; Length 33;
Best Local Similarity 60.0%; Pred. No. 0.37;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRWRRRRRPPKKRK 20
14 RRRRVSRRRRRRRRRR 33

RESULT 15

S29829
protamine Z3 - smaller spotted catshark
N;Alternate names: Scyllorhynchus Z3
C;Species: Scyllorhynchus canicula (smaller spotted catshark, smaller spotted dogfish)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Oct-1999
C;Accession: S29829; A41269; S12284
R;Kouach, M.; Jaquinod, M.; Bellaiche, D.; Sautiere, P.; van Dorsselaer, A.; Chevaillie
Biochim. Biophys. Acta 1162, 99-104, 1993
A;Title: A corrected primary structure for dog-fish Scyllorhynchus caniculus protamine
A;Reference number: S29829; MUID:93192312; PMID:8448201
A;Accession: S29829
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-37 <KOU>
R;Sautiere, P.; Briand, G.; Gusse, M.; Chevaillier, P.
Eur. J. Biochem. 119, 251-255, 1981
A;Title: Primary structure of a protamine isolated from the sperm nuclei of the dog-fi
A;Reference number: A41269; MUID:82072694; PMID:7198042
A;Accession: A41269
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-31 <SAU>
R;Gusse, M.; Sautiere, P.; Chauviere, M.; Chevaillier, P.
Biochim. Biophys. Acta 748, 93-98, 1983
A;Title: Extraction, purification and characterization of the sperm protamines of the
A;Reference number: S01463; MUID:84000513; PMID:6615852
A;Accession: S12284
A;Molecule type: protein
A;Residues: 1-5 <GUS>
C;Superfamily: protamine Y2

A:Molecule type: protein
A:Residues: 2-51 <AMW>
C:Superfamily: sperm histone
C:Keywords: DNA binding; nucleus
F;2-51/Product: protamine 1 #status experimental <MAT>

Query Match 53.1%; Score 60; DB 2; Length 51;
Best Local Similarity 65.0%; Pred. No. 0.66;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRREWGRRRRRPPKKRK 20
||||| ||||| : : :
Db 23 RRRRRCRRRRRRCCRRR 42

RESULT 20

S56117
spermatid-specific protein T2 precursor - longfin squid
N;Alternate names: sperm protamin SP
C;Species: Loligo pealeii (longfin squid)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S56117
R;Wouters-Tyrou, D.; Martin-Ponthieu, A.; Ledoux-Andulia, N.; Kouach, M.; Jaquinod, M.; S
Biochem. J. 309, 529-534, 1995
A;Title: Squid spermiogenesis: molecular characterization of testis-specific pro-protami
A;Reference number: S56116; MUID:95351983; PMID:7626016
A;Accession: S56117
A;Status: preliminary
A:Molecule type: protein
A;Residues: 1-118 <WOU>

Query Match 53.1%; Score 60; DB 2; Length 118;
Best Local Similarity 60.0%; Pred. No. 1.3;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRREWGRRRRRPPKKRK 20
||||| ||||| : : :
Db 22 RRRRRCRRRRRRCCRRR 41

RESULT 21

D84235
hypothetical protein Vng0779c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 21-Jun-2002
C;Accession: D84235
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithausner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabil
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, F.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: D84235
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-604 <STO>
A;Cross-references: GB:AE004437; NID:gl0580354; PIDN:AAG19248.1; GSPDB:GN00138
C;Gene: VNG0779C
C;Superfamily: conserved hypothetical protein Mj1198

Query Match 53.1%; Score 60; DB 2; Length 604;
Best Local Similarity 61.9%; Pred. No. 4.4;
Matches 13; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 1 RRRRR--WGRRRRRPPKKR 19
||| :||| ||||| : : :
Db 575 RTORRTFWGRRLRRRPGR 595

RESULT 22

B58208

protamine II-1 - painted turtle
C;Species: Chrysemys picta (painted turtle)
C;Date: 08-Nov-1996 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Accession: B58208
R;Hunt, J.G.; Kasinsky, H.E.; Elsey, R.M.; Wright, C.L.; Rice, P.; Bell, J.E.; Sharp, I
J. Biol. Chem. 271, 23547-23557, 1996
A;Title: Protamines of reptiles.
A;Reference number: A58208; MUID:96394458; PMID:8798564
A;Accession: B58208
A;Status: preliminary
A:Molecule type: protein
A;Residues: 1-45 <HUN>
C;Superfamily: sperm histone

Query Match 51.8%; Score 58.5; DB 2; Length 45;
Best Local Similarity 56.0%; Pred. No. 0.93;
Matches 14; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 1 RRRRREWGR----RRRRPPKKRK 20
||||| ||||| : : :
Db 2 RRRRRCGRGRRRRRRHGRRR 26

RESULT 23

C58208
protamine II-2 - painted turtle
C;Species: Chrysemys picta (painted turtle)
C;Date: 08-Nov-1996 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Accession: C58208
R;Hunt, J.G.; Kasinsky, H.E.; Elsey, R.M.; Wright, C.L.; Rice, P.; Bell, J.E.; Sharp, I
J. Biol. Chem. 271, 23547-23557, 1996
A;Title: Protamines of reptiles.
A;Reference number: A58208; MUID:96394458; PMID:8798564
A;Accession: C58208
A;Status: preliminary
A:Molecule type: protein
A;Residues: 1-45 <HUN>
C;Superfamily: sperm histone

Query Match 51.8%; Score 58.5; DB 2; Length 45;
Best Local Similarity 56.0%; Pred. No. 0.93;
Matches 14; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 1 RRRRREWGR----RRRRPPKKRK 20
||||| ||||| : : :
Db 2 RRRRRCGRGRRRRRRHGRRR 26

RESULT 24

D58208
protamine II-3 - painted turtle
C;Species: Chrysemys picta (painted turtle)
C;Date: 08-Nov-1996 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Accession: D58208
R;Hunt, J.G.; Kasinsky, H.E.; Elsey, R.M.; Wright, C.L.; Rice, P.; Bell, J.E.; Sharp, I
J. Biol. Chem. 271, 23547-23557, 1996
A;Title: Protamines of reptiles.
A;Reference number: A58208; MUID:96394458; PMID:8798564
A;Accession: D58208
A;Status: preliminary
A:Molecule type: protein
A;Residues: 1-45 <HUN>
C;Superfamily: sperm histone

Query Match 51.8%; Score 58.5; DB 2; Length 45;
Best Local Similarity 56.0%; Pred. No. 0.93;
Matches 14; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 1 RRRRREWGR----RRRRPPKKRK 20
||||| ||||| : : :
Db 2 RRRRRCGRGRRRRRRHGRRR 26

RESULT 25
E58208
protamine II-4 - painted turtle
C;Species: Chrysemys picta (painted turtle)
C;Date: 08-Nov-1996 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Accession: E58208
R;Hunt, J.G.; Kasinsky, H.E.; Elsev, R.M.; Wright, C.L.; Rice, P.; Bell, J.E.; Sharp, D.
J. Biol. Chem. 271, 23547-23557, 1996
A;Title: Protamines of reptiles.
A;Reference number: A58208; MUID:96394458; PMID:8798564
A;Accession: E58208
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-47 <HUN>
C;Superfamily: sperm histone

Query Match 51.8%; Score 58.5; DB 2; Length 47;
Best Local Similarity 56.0%; Pred. No. 0.96;
Matches 14; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 1 RRRRRWGR-----RRRRPKKKRK 20
||||| ||| ||||| :||
Db 2 RRRRRGGGCGSGRRRRRHGRRR 26
||||| ||| ||||| :||

RESULT 26
F58208
protamine II-5 - painted turtle
C;Species: Chrysemys picta (painted turtle)
C;Date: 08-Nov-1996 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Accession: F58208
R;Hunt, J.G.; Kasinsky, H.E.; Elsev, R.M.; Wright, C.L.; Rice, P.; Bell, J.E.; Sharp, D.
J. Biol. Chem. 271, 23547-23557, 1996
A;Title: Protamines of reptiles.
A;Reference number: A58208; MUID:96394458; PMID:8798564
A;Accession: F58208
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-47 <HUN>
C;Superfamily: sperm histone

Query Match 51.8%; Score 58.5; DB 2; Length 47;
Best Local Similarity 56.0%; Pred. No. 0.96;
Matches 14; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 1 RRRRRWGR-----RRRRPKKKRK 20
||||| ||| ||||| :||
Db 2 RRRRRGGGCGSGRRRRRHGRRR 26
||||| ||| ||||| :||

RESULT 27
Y2PK1
protamine I - northern pike
C;Species: Esox lucius (northern pike)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 16-Feb-1997
C;Accession: A02667
R;Speckert, W.; Kennedy, B.; Daisley, S.L.; Davies, P.
Eur. J. Biochem. 136, 283-289, 1983
A;Title: Primary structure of protamine from the northern pike Esox lucius.
A;Reference number: A02667; MUID:84028647; PMID:6628381
A;Accession: A02667
A;Molecule type: protein
A;Residues: 1-32 <SPE>
A;Note: 9-Ser was found in 50% of the molecules; this heterogeneity
C;Superfamily: protamine Y2
C;Keywords: chromosomal protein; DNA binding; spermatogenesis

Query Match 51.3%; Score 58; DB 1; Length 32;
Best Local Similarity 63.6%; Pred. No. 0.83;
Matches 14; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 RRRRRWGR-----RRRRPKKKRK 20
||||| ||| ||||| :||

Db 2 RRRRASSGRRRRRRPKMSRR 23

RESULT 28
I1R2R
protamine II - rainbow trout
N;Alternate names: iridine
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 12-Aug-1981 #sequence_revision 12-Aug-1981 #text_change 16-Feb-1997
C;Accession: A02672
R;Ando, T.; Watanabe, S.
Int. J. Protein Res. 1, 221-224, 1969
A;Title: A new method for fractionation of protamines and the amino acid sequences of E
A;Reference number: A91774; MUID:72030546; PMID:4953052
A;Accession: A02672
A;Molecule type: protein
A;Residues: 1-32 <AND>
C;Superfamily: protamine Y2
C;Keywords: chromosomal protein; DNA binding

Query Match 51.3%; Score 58; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.83;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
||||| ||| ||||| :||
Db 13 RRRRRVSRRRRRRGRRR 32
||||| ||| ||||| :||

RESULT 29
E21211
protamine TP21 - rainbow trout
N;Alternate names: protamine 2a
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Aug-1997
C;Accession: E21211; C24970
R;Aiken, J.M.; McKenzie, D.; Zhao, H.Z.; States, J.C.; Dixon, G.H.
Nucleic Acids Res. 11, 4907-4922, 1983
A;Title: Sequence homologies in the protamine gene family of rainbow trout.
A;Reference number: A21211; MUID:83272939; PMID:6308564
A;Accession: E21211
A;Molecule type: DNA
A;Residues: 1-33 <AIK>
A;Cross-references: EMBL:X01599
R;McKay, D.J.; Renaux, B.S.; Dixon, G.H.
Eur. J. Biochem. 158, 361-366, 1986
A;Title: Rainbow trout protamines. Amino acid sequences of six distinct proteins from a
A;Reference number: A91170; MUID:86274711; PMID:3755398
A;Accession: C24970
A;Molecule type: protein
A;Residues: 2-33 <MCK>
C;Superfamily: protamine Y2
C;Keywords: DNA binding; nucleus
F;2-33/Product: Protamine TP21 #status experimental <MAT>

Query Match 51.3%; Score 58; DB 2; Length 33;
Best Local Similarity 60.0%; Pred. No. 0.85;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
||||| ||| ||||| :||
Db 14 RRRRRVSRRRRRRGRRR 33
||||| ||| ||||| :||

RESULT 30
A40973
spermatid-specific protein T1 precursor - common cuttlefish
N;Alternate names: arginine-rich protamine; testis-specific protein T1
C;Species: Sepia officinalis (common cuttlefish)
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Sep-1998
C;Accession: A40973; S14085
R;Mouters-Tyrrou, D.; Chartier-Harlin, M.C.; Martin-Ponthieu, A.; Boutillon, C.; Van Dor
J. Biol. Chem. 266, 17388-17395, 1991

A;Title: Cuttlefish spermatid-specific protein T. Molecular characterization of two vari
A;Reference number: A40973; MUID:91373359; PMID:1894625
A;Accession: A40973
A;Molecule type: protein
A;Residues: 1-78 <WOU>
R;Martin-Ponchieu, A.; Wouters-Tyrou, D.; Belaiche, D.; Sautiere, P.; Schindler, P.; van
Eur. J. Biochem. 195, 611-619, 1991
A;Title: Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct variants.
A;Reference number: S14085; MUID:91153298; PMID:1999185
A;Accession: S14085
A;Molecule type: protein
A;Residues: 22-78 <WAB>
C;Superfamily: sperm histone
C;Keywords: DNA binding; nucleus; phosphoprotein; spermatogenesis
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-78/Product: protamine variant Spt #status experimental <MAT>
Query Match 51.3%; Score 58; DB 2; Length 78;
Best Local Similarity 57.9%; Pred. No. 1.6;
Matches 11; Conservative 4; Mismatches 4; Indels 4; Gaps 0;
QY 2 RRRRRWGRRRRRPKKKRK 20
Db 22 RRRRRSRRRRSRRSR 40
RESULT 31
S10305
protamine - boll weevil
C;Species: Anthonomus grandis (boll weevil)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
R;Trewitt, P.M.; Hellmann, L.J.; Kumaran, A.K.
Nucleic Acids Res. 18, 3646, 1990
A;Title: Boll weevil testis-specific cDNA.
A;Reference number: S10305; MUID:90301495; PMID:2362819
A;Accession: S10305
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <TRE>
A;Cross-references: EMBL:X52058; NID:g5597; PIDN:CAA36282.1; PID:g5598
C;Keywords: DNA binding; nucleus
Query Match 51.3%; Score 58; DB 2; Length 132;
Best Local Similarity 60.8%; Pred. No. 2.4;
Matches 12; Conservative 4; Mismatches 4; Indels 4; Gaps 0;
QY 1 RRRRRWGRRRRRPKKKRK 20
Db 103 RRRRRSRRRRSRRSR 122
RESULT 32
A03964
hypothetical 17.7K protein - human adenovirus 2
C;Species: Mastadenovirus h2 (human adenovirus 2)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Sep-1999
C;Accession: F92351; F92352; A03864
R;Gingaras, T.R.; Sclaky, D.; Gelinias, R.E.; Bing-Dong, J.; Yen, C.E.; Kelly, M.M.; Bull
J. Biol. Chem. 257, 13475-13491, 1982
A;Title: Nucleotide sequences from the adenovirus-2 genome.
A;Reference number: A92351; MUID:83056843; PMID:7142161
A;Accession: F92351
A;Molecule type: DNA
A;Residues: 1-168 <GIN>
R;Alestrom, P.; Akusjarvi, G.; Pettersson, M.; Pettersson, U.
J. Biol. Chem. 257, 13492-13498, 1982
A;Title: DNA sequence analysis of the region encoding the terminal protein and the hypot
A;Reference number: A92352; MUID:83056844; PMID:7142162
A;Accession: F92352
A;Molecule type: DNA
A;Residues: 1-168 <ALE>
C;Superfamily: human adenovirus 2 hypothetical 17.7K protein

Query Match 51.3%; Score 58; DB 2; Length 168;
Best Local Similarity 52.0%; Pred. No. 2.9;
Matches 13; Conservative 4; Mismatches 4; Indels 4; Gaps 1;
QY 1 RRRRRWGRRRRRPKKKRK 21
Db 44 RRRRRTGRRSTKRSIISPRRRRV 68
RESULT 33
A58208
protamine I-1 - painted turtle
C;Species: Chrysemys picta (painted turtle)
C;Date: 08-Nov-1996 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
C;Accession: A58208
R;Hunt, J.G.; Kasinsky, H.E.; Elsey, R.M.; Wright, C.L.; Rice, P.; Bell, J.E.; Sharp, J
J. Biol. Chem. 271, 23547-23557, 1996
A;Title: Protamines of reptiles.
A;Reference number: A58208; MUID:96394458; PMID:8798564
A;Accession: A58208
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-58 <HUN>
C;Superfamily: sperm histone

Query Match 50.9%; Score 57.5; DB 2; Length 58;
Best Local Similarity 56.0%; Pred. No. 1.5;
Matches 14; Conservative 3; Mismatches 3; Indels 5; Gaps 1;
QY 1 RRRRRWGR-----RRRRPKKKRK 20
Db 14 RRRRRGGGRRRRRRRHGGRR 38

RESULT 34

SRAPC
protamine B - Russian sturgeon
N;Alternate names: sturine
C;Species: Acipenser gueldenstaedti (Russian sturgeon)
C;Date: 12-Aug-1981 #sequence_revision 12-Aug-1981 #text_change 16-Feb-1997
C;Accession: A02665
R;Yulikova, E.P.; Evseenko, L.K.; Baratova, L.A.; Belyanova, L.P.; Rybin, V.K.; Silaev
Bioorg. Khim. 2, 1613-1617, 1976
A;Reference number: A02665
A;Accession: A02665
A;Molecule type: protein
A;Residues: 1-27 <YUL>
C;Superfamily: protamine Y2
C;Keywords: chromosomal protein; DNA binding; spermatogenesis

Query Match 50.4%; Score 57; DB 1; Length 27;
Best Local Similarity 85.7%; Pred. No. 0.95;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 RRRRRWGRRRRR 14
Db 13 RRRRRHRRRRR 26

RESULT 35

SLONAI
protamine AI - chum salmon
N;Alternate names: salmine AI
C;Species: Oncorhynchus keta (chum salmon)
C;Date: 12-Aug-1981 #sequence_revision 12-Aug-1981 #text_change 16-Feb-1997
C;Accession: A02669
R;Ando, T.; Watanabe, S.
Int. J. Protein Res. 1, 221-224, 1969
A;Title: A new method for fractionation of protamines and the amino acid sequences of
A;Reference number: A91774; MUID:72030546; PMID:4953052
A;Accession: A02669
A;Molecule type: protein

A;Residues: 1-32 <AND>
C;Superfamily: protamine Y2
C;Keywords: chromosomal protein; DNA binding; spermatogenesis; testis

Query Match 50.4%; Score 57; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 1.1;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKXK 20
||||| ||||| :|:
Db 13 RRRPRVSRRRRRGRRRR 32

RESULT 36
protamine (salmine) AII - chum salmon
B02669
N;Alternate names: salmine AI
C;Species: Oncorhynchus keta (chum salmon)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 17-Mar-1994
C;Accession: B02669; A02669
R;Ando, T.; Watanabe, S.
Int. J. Protein Res. 1, 221-224, 1969
A;Title: A new method for fractionation of protamines and the amino acid sequences of salmon
A;Reference number: A91774; MUID:72030546; PMID:4953052
A;Accession: B02669
A;Molecule type: protein
A;Residues: 1-32 <AND>
A;Note: an additional Arg may be present (possibly after Arg-15); residues at positions
C;Superfamily: protamine Y2
C;Keywords: chromosomal protein; spermatogenesis; testis

Query Match 50.4%; Score 57; DB 2; Length 32;
Best Local Similarity 60.0%; Pred. No. 1.1;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKXK 20
||||| ||||| :|:
Db 13 RRRPRVSRRRRRGRRRR 32

RESULT 37
INTRIA
protamine IA - rainbow trout
N;Alternate names: iridine
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 12-Aug-1981 #sequence_revision 12-Aug-1981 #text_change 16-Feb-1997
C;Accession: A02670
R;Ando, T.; Watanabe, S.
Int. J. Protein Res. 1, 221-224, 1969
A;Title: A new method for fractionation of protamines and the amino acid sequences of salmon
A;Reference number: A91774; MUID:72030546; PMID:4953052
A;Accession: A02670
A;Molecule type: protein
A;Residues: 1-33 <AND>
C;Superfamily: protamine Y2
C;Keywords: chromosomal protein; DNA binding; spermatogenesis

Query Match 50.4%; Score 57; DB 1; Length 33;
Best Local Similarity 60.0%; Pred. No. 1.1;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKXK 20
||||| ||||| :|:
Db 14 RRRPRVSRRRRRGRRRR 33

RESULT 38
INTR59
protamine CII - rainbow trout
N;Alternate names: protamine 2b
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 18-Aug-1982 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: A27776; A93210; D24970; B93723; C93723; A02671

R;States, J.C.; Connor, W.; Wosnick, M.A.; Aiken, J.M.; Gedamu, L.; Dixon, G.H.
Nucleic Acids Res. 10, 4551-4563, 1982
A;Title: Nucleotide sequence of a protamine component CII gene of Salmo gairdnerii.
A;Reference number: A93435; MUID:83038616; PMID:6290986
A;Accession: A27776
A;Molecule type: DNA
A;Residues: 1-33 <STA>
R;Jenkins, J.R.

Nature 279, 809-811, 1979
A;Title: Sequence divergence of rainbow trout protamine mRNAs; comparison of coding and
A;Reference number: A93210; MUID:79199790; PMID:450133
A;Accession: A93210
A;Molecule type: mRNA
A;Residues: 7-33 <JEN>
A;Cross-references: GB:M10718; NID:g213841; PIDN:AAA49608.1; PID:g213842
A;Experimental source: clone pTF11
R;McKay, D.J.; Renaux, B.S.; Dixon, G.H.
Eur. J. Biochem. 158, 361-366, 1986
A;Title: Rainbow trout protamines. Amino acid sequences of six distinct proteins from
A;Reference number: A91170; MUID:86274711; PMID:3755398
A;Accession: D24970
A;Molecule type: protein
A;Residues: 2-33 <MCK>
R;Gedamu, L.; Wosnick, M.A.; Connor, W.; Watson, D.C.; Dixon, G.H.; Iatrou, K.
Nucleic Acids Res. 9, 1463-1482, 1981
A;Title: Molecular analysis of the protamine multi-gene family in rainbow trout testis.
A;Reference number: A93723; MUID:81198983; PMID:6262730
A;Accession: B93723
A;Molecule type: protein
A;Residues: 2-33 <GED>
A;Experimental source: clone pRTP59
A;Accession: C93723
A;Molecule type: mRNA
A;Residues: 7-33 <GE2>
C;Comment: The partial protein sequences translated from mRNA clones pRTP59 and pTF11 a
g regions but not in the 3' noncoding regions.
C;Genetics:
C;Introns: #status absent
C;Superfamily: protamine Y2
C;Keywords: chromosomal protein; DNA binding; spermatogenesis
F:2-33/Product: protamine CII #status experimental <MAI>

Query Match 50.4%; Score 57; DB 1; Length 33;
Best Local Similarity 60.0%; Pred. No. 1.1;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKXK 20
||||| ||||| :|:
Db 14 RRRPRVSRRRRRGRRRR 33

RESULT 39
INTR42
protamine 2c - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 18-Aug-1982 #sequence_revision 12-Apr-1996 #text_change 24-Sep-1999
C;Accession: B21211; D93723; B93210; E24970; A02676
R;Aiken, J.M.; McKenzie, D.; Zhao, H.Z.; States, J.C.; Dixon, G.H.
Nucleic Acids Res. 11, 4907-4922, 1983
A;Title: Sequence homologies in the protamine gene family of rainbow trout.
A;Reference number: A21211; MUID:83272939; PMID:6308564
A;Accession: B21211
A;Molecule type: DNA
A;Residues: 1-33 <AIK>
A;Cross-references: EMBL:X01596; NID:964336; PIDN:CAA25749.1; PID:g64337
A;Experimental source: clone TP15
R;Gedamu, L.; Wosnick, M.A.; Connor, W.; Watson, D.C.; Dixon, G.H.; Iatrou, K.
Nucleic Acids Res. 9, 1463-1482, 1981
A;Title: Molecular analysis of the protamine multi-gene family in rainbow trout testis.
A;Reference number: A93723; MUID:81198983; PMID:6262730
A;Accession: D93723
A;Molecule type: mRNA
A;Residues: 7-33 <GED>

A;Experimental source: clone pRTP242
 R;Jenkins, J.R.
 Nature 279, 809-811, 1979
 A;Title: Sequence divergence of rainbow trout protamine mRNAs; comparison of coding and
 A;Reference number: A93210; MUID:79199790; PMID:450133
 A;Accession: B93210
 A;Molecule type: mRNA
 A;Residues: 7-33 <JEN>
 A;Cross-references: GB:X02924; GB:M10717; NID:964344; PIDN:CAA25680.1; PID:964345
 A;Experimental source: clone pTP8
 R;McKay, D.J.; Renaux, B.S.; Dixon, G.H.
 Eur. J. Biochem. 158, 361-366, 1986
 A;Title: Rainbow trout protamines. Amino acid sequences of six distinct proteins from a
 A;Reference number: A91170; MUID:86274711; PMID:3755398
 A;Accession: E24970
 A;Molecule type: protein
 A;Residues: 2-33 <MCK>
 C;Superfamily: protamine Y2
 C;Keywords: chromosomal protein; DNA binding; spermatogenesis
 F;2-33/Product: protamine 2c #status experimental <MAT>

Query Match 50.4%; Score 57; DB 1; Length 33;
 Best Local Similarity 60.0%; Pred. No. 1.1;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RRRRRRWGRRRRRPKKKK 20
 ||||| ||||| : :
 Db 14 RRRPRVSRRRRRGGRRR 33

RESULT 40
 A21211
 protamine TP14 - rainbow trout
 C;Species: Oncorhynchus mykiss (rainbow trout)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
 C;Accession: A21211
 R;Aiken, J.M.; McKenzie, D.; Zhao, H.Z.; States, J.C.; Dixon, G.H.
 Nucleic Acids Res. 11, 4907-4922, 1983
 A;Title: Sequence homologies in the protamine gene family of rainbow trout.
 A;Reference number: A21211; MUID:83272939; PMID:6308564
 A;Accession: A21211
 A;Molecule type: DNA
 A;Residues: 1-33 <AIK>
 A;Cross-references: EMBL:X01595; NID:964334; PIDN:CAA25748.1; PID:964335
 C;Superfamily: protamine Y2
 C;Keywords: DNA binding; nucleus

Query Match 50.4%; Score 57; DB 2; Length 33;
 Best Local Similarity 60.0%; Pred. No. 1.1;
 Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RRRRRRWGRRRRRPKKKK 20
 ||||| ||||| : :
 Db 14 RRRPRVSRRRRRGGRRR 33

Search completed: January 23, 2004, 11:20:02
 Job time : 22 secs

CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -!- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
 CC DNA-HELIX.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Testis.
 CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M14559; AAA30741.1; -;
 CC EMBL; M18396; AAA30735.1; -;
 CC EMBL; M18395; AAA30736.1; -;
 CC EMBL; M18625; AAA30742.1; -;
 CC PIR; A23911; HSBOS.
 CC InterPro: IPR000221; Protamine P1.
 CC Pfam: PF00260; protamine P1; 1.
 CC PROSITE: PS00048; PROTAMINE P1; 1.
 CC Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 CC Testis; DNA condensation; Nuclear protein.
 CC INIT MET 0 0 INTERCHAIN (WITH C-22).
 CC FT DISULFID 5 5
 CC FT DISULFID 6 14
 CC FT DISULFID 22 22 INTERCHAIN (WITH C-5).
 CC FT DISULFID 38 38 INTERCHAIN (WITH C-38).
 CC FT DISULFID 39 47
 CC FT DISULFID 29 29 F -> S (IN REF. 3).
 CC FT CONFLICT 39 41 MISSING (IN REF. 5).
 CC FT CONFLICT 39 41
 CC SQ SEQUENCE 50 AA; 6627 MW; 9B2A69D98D30D2C7 CRC64;
 CC
 CC Query Match 59.3%; Score 67; DB 1; Length 50;
 CC Best Local Similarity 92.9%; Pred. No. 0.009;
 CC Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 RRRRRWGRRRRR 14
 CC DB 23 RRRRRFGRRRRR 36
 CC
 CC RESULT 2
 CC HSPI SHEEP
 CC ID HSPI SHEEP STANDARD; PRT; 50 AA.
 CC AC P04102;
 CC DT 01-NOV-1986 (Rel. 03, Created)
 CC DT 01-NOV-1986 (Rel. 03, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Sperm protamine P1 (Cysteine-rich protamine).
 CC GN PRM1 OR PRM-1.
 CC OS Ovis aries (Sheep), and
 CC Capra hircus (Goat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Caprinae; Ovis.
 CC OX NCBI_TaxID=9940, 9925;
 CC RN [1]
 CC RP SEQUENCE
 CC RC SPECIES=Sheep;
 CC RX MEDLINE=85003651; PubMed=6479168;
 CC RA Sautiere P., Belaiche D., Martinge A., Loir M.;
 CC RT "Primary structure of the ram (Ovis aries) protamine.";
 CC RL Eur. J. Biochem. 144:121-125(1984).
 CC RN [2]
 CC RP SEQUENCE
 CC RC SPECIES=C.hircus;
 CC RX MEDLINE=89078594; PubMed=3060372;
 CC RA Ammer H., Henschen A.;
 CC RT "Primary structure of rabbit sperm protamine, the first protamine of
 CC its type with an aberrant N-terminal.";

RL FEBS Lett. 242:111-116(1988).
 CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
 CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
 CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -!- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
 CC DNA-HELIX (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Testis.
 CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
 CC PIR; A02658; HSSH.
 CC InterPro: IPR000221; Protamine P1.
 CC Pfam: PF00260; protamine P1; 1.
 CC PROSITE: PS00048; PROTAMINE P1; 1.
 CC Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 CC Testis; DNA condensation; Nuclear protein.
 CC FT DISULFID 5 5 INTERCHAIN (WITH C-22) (BY SIMILARITY).
 CC FT DISULFID 6 14 BY SIMILARITY.
 CC FT DISULFID 22 22 INTERCHAIN (WITH C-5) (BY SIMILARITY).
 CC FT DISULFID 38 38 INTERCHAIN (WITH C-38) (BY SIMILARITY).
 CC FT DISULFID 39 47 BY SIMILARITY.
 CC SQ SEQUENCE 50 AA; 6712 MW; 6B2A78D98D2242DA CRC64;
 CC
 CC Query Match 59.3%; Score 67; DB 1; Length 50;
 CC Best Local Similarity 92.9%; Pred. No. 0.009;
 CC Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 RRRRRWGRRRRR 14
 CC DB 23 RRRRRFGRRRRR 36
 CC
 CC RESULT 3
 CC HSPI HORSE
 CC ID HSPI HORSE STANDARD; PRT; 49 AA.
 CC AC P15341;
 CC DT 01-APR-1990 (Rel. 14, Created)
 CC DT 01-APR-1990 (Rel. 14, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Sperm protamine P1 (Cysteine-rich protamine) (Protamine St1).
 CC GN PRM1 OR PRM-1.
 CC OS Equus caballus (Horse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 CC OX NCBI_TaxID=9796;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RA Skow L.C., Massey V.K.;
 CC RL Submitted (XXX-1993) to the EMBL/GenBank/DBJ databases.
 CC RN [2]
 CC RP SEQUENCE
 CC RX MEDLINE=87242490; PubMed=3593735;
 CC RA Belaiche D., Loir M., Kruggie W., Sautiere P.;
 CC RT "Isolation and characterization of two protamines St1 and St2 from
 CC stallion spermatozoa, and amino-acid sequence of the major protamine
 CC St1.";
 CC RL Biochim. Biophys. Acta 913:145-149(1987).
 CC RN [3]
 CC RP SEQUENCE OF 1-48.
 CC RX MEDLINE=88163084; PubMed=3442606;
 CC RA Ammer H., Henschen A.;
 CC RT "The major protamine from stallion sperm. Isolation and amino-acid
 CC sequence.";
 CC RL Biol. Chem. Hoppe-Seyler 368:1619-1626(1987).
 CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
 CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
 CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -!- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
 CC DNA-HELIX.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Testis.
 CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; L10654; AAA30957.1; --
 DR PIR; S00228; S00228.
 DR InterPro; IPR000221; Protamine P1.
 DR Pfam; PF00260; protamine P1; 1.
 DR PROSITE; PS00048; PROTAMINE P1; 1.
 KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 KW Testis; DNA condensation; Nuclear protein.
 FT INIT-MET 0 0 INTERCHAIN (WITH C-22) (BY SIMILARITY).
 FT DISULFID 5 5 BY SIMILARITY.
 FT DISULFID 6 14 INTERCHAIN (WITH C-5) (BY SIMILARITY).
 FT DISULFID 22 22 INTERCHAIN (WITH C-36) (BY SIMILARITY).
 FT DISULFID 36 36 BY SIMILARITY.
 FT DISULFID 37 45 BY SIMILARITY.
 SQ SEQUENCE 49 AA; 6599 MW; BF16BEFEC0D7AE74 CRC64;

Query Match 57.5%; Score 65; DB 1; Length 49;
 Best Local Similarity 66.7%; Pred. No. 0.016;
 Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRKV 21
 DQ 15 RRRRRRRRRRRRSVRQRRV 35

RESULT 4

HSP3_HORSE
 ID_HSP3_HORSE STANDARD; PRT; 58 AA.
 AC P15343;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sperm histone P2B (ST2B).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=90304188; PubMed=2364093;
 RA Pirhonen A., Valtanen P., Linnala-Kankkunen A., Heiskanen M.-L.,
 RA Maenpaa P.K.;
 RT "Primary structures of two protamine 2 variants (St2a and St2b) from
 RT stallion spermatozoa.";
 RL Biochim. Biophys. Acta 1039:177-180 (1990).
 RN [2]

Query Match 57.5%; Score 65; DB 1; Length 58;
 Best Local Similarity 65.0%; Pred. No. 0.019;
 Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
 DQ 25 RRRRRSSRRRRRRCRRR 44

RESULT 6

HSP2_HORSE
 ID_HSP2_HORSE STANDARD; PRT; 62 AA.
 AC P15342;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sperm histone P2A (ST2A).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=90304188; PubMed=2364093;
 RA Pirhonen A., Valtanen P., Linnala-Kankkunen A., Heiskanen M.-L.,
 RA Maenpaa P.K.;
 RT "Primary structures of two protamine 2 variants (St2a and St2b) from
 RT stallion spermatozoa.";
 RL Biochim. Biophys. Acta 1039:177-180 (1990).
 RN [2]

Query Match 57.5%; Score 65; DB 1; Length 58;
 Best Local Similarity 65.0%; Pred. No. 0.019;
 Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
 DQ 25 RRRRRSSRRRRRRCRRR 44

```

RT the function and evolution of vertebrate protamines."
RL J. Biol. Chem. 264:17627-17630(1989).
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M30275; AAA49498.1; --
DR PIR; A34356; A34356.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE P1; 1.
DR Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein; Phosphorylation.
FT INIT MET 0 0
FT MOD RES 8 8 PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE 56 AA; 7697 MW; 1894402E5FA44FAB CRC64;

Query Match 55.8%; Score 63; DB 1; Length 56;
Best Local Similarity 92.3%; Pred. No. 0.033; Indels 0; Gaps 0;
Matches 12; Conservative 1; Mismatches 0;

QY 2 RRRRRGGRRRRR 14
DB 41 RRRRRGGRRRRR 53

RESULT 7
PRT7 ONCMY STANDARD; PRT; 32 AA.
AC P08146; 1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Protamine Tpl16.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83272939; PubMed=6308564;
RA Aiken J.M., McKenzie D., Zhao H.-Z., States J.C., Dixon G.H.;
RT "Sequence homologies in the protamine gene family of rainbow trout."
RL Nucleic Acids Res. 11:4907-4922(1983).
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01597; CAA25750.1; --
DR PIR; C21211; C21211.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;

```

```

KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0
SQ SEQUENCE 32 AA; 4323 MW; B07A9C9D8CC796FF CRC64;

Query Match 54.9%; Score 62; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.026; Indels 0;
Matches 12; Conservative 4; Mismatches 4; Gaps 0;

QY 1 RRRRRGGRRRRRPPKKRK 20
DB 13 RRRRRGGRRRRRGGRRRR 32

RESULT 8
PRT9 ONCMY STANDARD; PRT; 32 AA.
AC P08147;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Protamine Tpl17.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83272939; PubMed=6308564;
RA Aiken J.M., McKenzie D., Zhao H.-Z., States J.C., Dixon G.H.;
RT "Sequence homologies in the protamine gene family of rainbow trout."
RL Nucleic Acids Res. 11:4907-4922(1983).
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01598; CAA25751.1; --
DR PIR; T01070; T01070.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0
SQ SEQUENCE 32 AA; 4349 MW; AC0A9C9D8CC796EA CRC64;

Query Match 54.0%; Score 61; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.034; Indels 0;
Matches 12; Conservative 4; Mismatches 4; Gaps 0;

QY 1 RRRRRGGRRRRRPPKKRK 20
DB 13 RRRRRGGRRRRRGGRRRR 32

RESULT 9
PRT3 SCYCA STANDARD; PRT; 37 AA.
AC P30258;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Protamine Z3 (Scylliorhine Z3).
OS Scylliorhine canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoida; Carchariniiformes;

```

```
OC Scyllorhinidae: Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC MEDLINE=82072694; PubMed=7198042;
RX Sautiere P., Briand G., Gusse M., Chevaillier P.;
RA "Primary structure of the protamine isolated from the sperm nuclei of
RT the dog-fish Scyllorhinus caniculus.";
RL Eur. J. Biochem. 119:251-255(1981).
RN [2]
RN REVISIONS.
RP MEDLINE=93192312; PubMed=8448201;
RX Kouach N., Jaquinod M., Belaiche D., Sautiere P., van Dorselaer A.,
RA Chevaillier P., Briand G.;
RT "A corrected primary structure for dog-fish Scyllorhinus caniculus
RL protamine Z3.";
RN Biochim. Biophys. Acta 1162:99-104(1993).
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- TISSUE SPECIFICITY: Testis.
DR PIR; S29829; S29829.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
SQ SEQUENCE 37 AA; 4748 MW; EC236D6C38D5091 CRC64;

Query Match 54.0%; Score 61; DB 1; Length 37;
Best Local Similarity 66.7%; Pred. No. 0.04;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRRWGRRRRRPPKXK 19
DB 11 RGRRGGRRRRRRRRR 28

RESULT 10
HSP1_CAVPO
ID HSP1_CAVPO STANDARD; PRT; 47 AA.
AC P35304;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P1 (Cysteine-rich protamine).
GN PRM1 OR PRM-1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=JM109;
RC Queralto R., Adroer R., Oliva R.;
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
CC DNA-HELIX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M83896; AAA58349.1; -.

DR EMBL; Z11544; CAA77643.1; -.
DR EMBL; Z11545; CAA77644.1; -.
DR PIR; S29973; S29973.
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE P1; 1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0 BY SIMILARITY.
SQ SEQUENCE 47 AA; 6553 MW; D937107E37DE704D CRC64;

Query Match 54.0%; Score 61; DB 1; Length 47;
Best Local Similarity 60.0%; Pred. No. 0.05;
Matches 12; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPPKXK 20
DB 15 RRRRRFVRRRRCHRRRR 34

RESULT 11
HSP1_MOUSE
ID HSP1_MOUSE STANDARD; PRT; 50 AA.
AC P02319;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P1 (Cysteine-rich protamine).
GN PRM1 OR PRM-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=85199803; PubMed=2986684;
RX Kleene K.C., Distel R.J., Hecht N.B.;
RT "Nucleotide sequence of a cDNA clone encoding mouse protamine 1.";
RL Biochemistry 24:719-722(1985).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=87260978; PubMed=3037541;
RX Johnson P.A., Pschon J.J., Velick P.C., Palmiter R.D., Hecht N.B.;
RA "Sequence homologies in the mouse protamine 1 and 2 genes.";
RT "Spermatid-specific expression of protamine 1 in transgenic mice.";
RL Biochim. Biophys. Acta 950:45-53(1988).
RN [3]
RN SEQUENCE FROM N.A.
RP MEDLINE=87260978; PubMed=3037541;
RX Pschon J.J., Behringer R.R., Brinster R.L., Palmiter R.D.;
RA "Spermatid-specific expression of protamine 1 in transgenic mice.";
RT "Gene expression during spermatogenesis.";
RL Ann. N.Y. Acad. Sci. 513:90-101(1987).
RN [5]
RN SEQUENCE FROM N.A.
RP MEDLINE=88181903; PubMed=3445973;
RX Hecht N.B.;
RA "Gene expression during spermatogenesis.";
RL Ann. N.Y. Acad. Sci. 513:90-101(1987).
RN [5]
RN SEQUENCE FROM N.A.
RP STRAIN=C129;
RC Schlueter G., Engel W.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
CC DNA-HELIX (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M83896; AAA58349.1; -.

```


Partial structural analysis of the basic chromosomal protein of rat spermatocoea.";
Biochim. Biophys. Acta 427:752-757(1976).
-!- FUNCTION: PROTAMININS SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-!- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE DNA-HELIX (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: Testis.
-!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; Z46939; CAA87061.1; -;
PIR; S03997; S03997. Protamine_P1.
InterPro; IPR000221; Protamine_P1; 1.
Pfam; PF00260; Protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
INIT MET 0 0 INTERCHAIN (WITH C-21) (BY SIMILARITY).
FT DISULFID 5 5 BY SIMILARITY.
FT DISULFID 6 14 INTERCHAIN (WITH C-5) (BY SIMILARITY).
FT DISULFID 21 21 INTERCHAIN (WITH C-36) (BY SIMILARITY).
FT DISULFID 36 36 BY SIMILARITY.
FT DISULFID 37 47
SQ SEQUENCE 50 AA; 6889 MW; B60B9F3D1BB6D978 CRC64;

Query Match 53.1%; Score 60; DB 1; Length 50;
Best Local Similarity 65.0%; Pred. No. 0.071;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRRGGRRRRRPPKKRK 20
Db 22 RRRRRRCCRRRRRCCRRRR 41

RESULT 13
HSPI_OCTVU STANDARD; PRT; 56 AA.
ID HSPI_OCTVU AC P83214;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P1 (Pol.) [Contains: Sperm protamine P2 (Po2) (Main protamine)].
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=6645;
RN [1]
RP SEQUENCE, FUNCTION, PHOSPHORYLATION, AND MASS SPECTROMETRY.
RC Tissue=Sperm;
RA Gimenez-Bonafé P., Ribes E., Buesa C., Sautiere P., Kouach M., Ausio J., Kasinsky H.E., Chiva M.;
RT "Chromatin remodelling and protamines during spermiogenesis of Octopus vulgaris (Cephalopoda)".
RT J. Exp. Zool. 0:0-0(2001).
RL -!- FUNCTION: Protamines substitute for histones in the chromatin of sperm during the haploid phase of spermatogenesis. They compact sperm DNA into a highly condensed, stable and inactive complex.
CC -!- FUNCTION: Octopus spermiogenesis is characterized by a double nuclear protein transition: Histones are first replaced by P1, which allows the chromatin to adopt a shape that is not as relaxed as with histones. The majority of P1 is later replaced by P2,
CC

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; K02926; AAA39980.1; -;
DR EMBL; X07625; CAA30472.1; -;
DR EMBL; X14003; CAA32169.1; -;
DR EMBL; M27500; AAA39985.1; -;
DR EMBL; Z47352; CAA87410.1; -;
DR PIR; I51954; HSMSS1.
DR MGD; MGI:97765; Pmt1.
DR InterPro; IPR000221; Protamine_P1.
DR Pfam; PF00260; Protamine_P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
INIT MET 0 0 INTERCHAIN (WITH C-21) (BY SIMILARITY).
FT DISULFID 5 5 BY SIMILARITY.
FT DISULFID 6 14 INTERCHAIN (WITH C-5) (BY SIMILARITY).
FT DISULFID 21 21 INTERCHAIN (WITH C-36) (BY SIMILARITY).
FT DISULFID 36 36 BY SIMILARITY.
FT DISULFID 37 47
SQ SEQUENCE 50 AA; 6827 MW; B61CAF3D1BBF4978 CRC64;

Query Match 53.1%; Score 60; DB 1; Length 50;
Best Local Similarity 65.0%; Pred. No. 0.071;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RRRRRRGGRRRRRPPKKRK 20
Db 22 RRRRRRCCRRRRRCCRRRR 41

RESULT 12
HSPI_RAT STANDARD; PRT; 50 AA.
ID HSPI_RAT AC P10118;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P1 (Cysteine-rich protamine).
GN PM1 OR PM-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89335257; PubMed=2757789;
RA Klemm U., Lee C.H., Burfeind P., Hake S., Engel W.;
RT "Nucleotide sequence of a cDNA encoding rat protamine and the haploid expression of the gene during rat spermatogenesis".
RL Biol. Chem. Hoppe-Seyler 370:293-301(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=96341725; PubMed=8720108;
RA Schluter G., Celik A., Obata R., Schlicker M., Hofferbert S., Schlung A., Adam I.M., Engel W.;
RT "Sequence analysis of the conserved protamine gene cluster shows that it contains a fourth expressed gene".
RL Mol. Reprod. Dev. 43:1-6(1996).
RN [3]
RP SEQUENCE.
RC MEDLINE=89207111; PubMed=3072011;
RA Ammer H., Henschel A.;
RT "Rat sperm protamine. Isolation and sequence analysis".
RL Biol. Chem. Hoppe-Seyler 369:1301-1306(1988).
RN [4]
RP SEQUENCE OF 1-15 AND 44-50.
RC MEDLINE=76184789; PubMed=1268226;
RA Kistler W.S., Keim P.S., Heinrikson R.L.;

forming a compact chromatin. P2 is the main protamine of sperm.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- TISSUE SPECIFICITY: Testis.

CC -1- PTM: P2 is phosphorylated in immature sperm. It is dephosphorylated in mature sperm allowing a stronger interaction with DNA.

CC -1- MASS SPECTROMETRY: MW=7428; METHOD=Electrospray; RANGE=1-56.

CC -1- MASS SPECTROMETRY: MW=6028; METHOD=Electrospray; RANGE=15-56.

CC DR GO:0005718; C:nucleosome; NAS.

CC DR GO:0005634; C:nucleus; NAS.

CC DR GO:0003677; F:DNA binding activity; NAS.

CC DR GO:0007001; P:chromosome organization and biogenesis (sen. .); NAS.

CC DR GO:0007076; P:mitotic chromosome condensation; NAS.

CC DR GO:0006334; P:nucleosome assembly; NAS.

CC DR GO:0007283; P:spermatogenesis; NAS.

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; DNA condensation; Nuclear protein; Phosphorylation.

FT CHAIN 1 56 SPERM PROTAMINE P1.

FT PROPEP 1 14

FT CHAIN 15 56 SPERM PROTAMINE P2.

FT DOMAIN 13 25 POLY-ARG.

FT DOMAIN 35 49 POLY-ARG.

FT DOMAIN 52 56 POLY-ARG.

SQ SEQUENCE 56 AA; 7430 MW; 41EFA8E024A93D6 CRC64;

Query Match 52.2%; Score 59; DB 1; Length 56;

Best Local Similarity 92.3%; Pred. No. 0.11;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRR 13

Db 44 RRRRRGGRRRR 56

RESULT 14

HSPI1 TRIVU STANDARD; PRT; 61 AA.

AC P42152;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sperm protamine P1.

GN PRM1.

OS Trichosurus vulpecula (Brush-tailed possum).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.

OX NCBI_TaxID=9337;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spem;

RX MEDLINE=95215351; PubMed=7700877;

RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;

RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";

RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995)

CC -1- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- TISSUE SPECIFICITY: Testis.

CC -1- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; L32744; AAA99479.1; -

DR InterPro; IPR000221; Protamine P1.

DR Pfam; PF00260; protamine_P1.

DR PROSITE; PS00048; PROTAMINE_P1; 1.

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.

FT INIT MET 0 BY SIMILARITY.

SQ SEQUENCE 61 AA; 8571 MW; 802287B627EE816C CRC64;

Query Match 52.2%; Score 59; DB 1; Length 61;

Best Local Similarity 63.2%; Pred. No. 0.12;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRR 19

Db 28 RRRRRRGRRRR 46

RESULT 15

YBFH APLCA STANDARD; PRT; 253 AA.

AC P41824;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Y-box factor homolog (APY1).

OS Aplysia californica (California sea hare).

CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

CC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspiidea;

CC Aplysioidea; Aplysiidae; Aplysia.

CC NCBI_TaxID=6500;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94333813; PubMed=7520012;

RA Skehel P.A., Bartsch D.;

RT "Characterization of a Y-Box factor from Aplysia californica.";

RL Gene 145:231-235(1994).

CC -1- FUNCTION: BINDS RNA IN VITRO.

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- PTM: PHOSPHORYLATION ACTIVATES IN VITRO RNA-BINDING (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; U02684; AAA60373.1; -

DR HSP; P41016; 1C90.

DR InterPro; IPR002059; Cold_shock.

DR Pfam; PF00313; CSD; 1.

DR PRINTS; PD00050; COLDSHOCK.

DR ProDom; PD000621; Cold_shock; 1.

DR SMART; SM00357; CSP; 1.

DR PROSITE; PS00352; COLD_SHOCK; 1.

KW Transcription regulation; RNA-binding; Nuclear protein; Phosphorylation.

FT DOMAIN 35 99 CSD.

FT MOD RES 226 226 ARG-RICH REGION (BASIC).

FT DOMAIN 116 138 ARG-RICH REGION (BASIC).

FT DOMAIN 152 173 ARG-RICH REGION (BASIC).

FT DOMAIN 186 204 ARG-RICH REGION (BASIC).

FT DOMAIN 234 253 ARG-RICH REGION (BASIC).

SQ SEQUENCE 253 AA; 29439 MW; AA3400013E4EE3 CRC64;

Query Match 52.2%; Score 59; DB 1; Length 253;

Best Local Similarity 50.0%; Pred. No. 0.46;

Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRR 20

Db 234 RRRRWGLPQRQRPQR 253

CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.

DR PIR; A02672; ITR2.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
SQ SEQUENCE 32 AA; 4224 MW; 65300C9D90B796E8 CRC64;

Query Match 51.3%; Score 58; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.083; Indels 0; Gaps 0;
Matches 12; Conservative 3; Mismatches 5;

QY 1 RRRRRRGGRRRRRPPKKRK 20
||| ||| ||| ||| ||| : : :
DB 13 RRRRRVSRRRRRRGGRRR 32

RESULT 18

PTL ESOLU STANDARD; PRT; 32 AA.

AC P02325; (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Protamine I.
OS Esx lucius (Northern pike).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Esociformes;
OC Esocidae; Esoc.
OX NCBI_TaxID=8010;
RN [1]
RP SEQUENCE
RX MEDLINE=84028647; PubMed=6628381;
RA Speckert W., Kennedy B., Daisley S.L., Davies P.;
RT "Primary structure of protamine from the Northern pike Esx lucius.";
RL Eur. J. Biochem. 136:283-289(1983).
CC -1- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- MISCELLANEOUS: THE HETEROGENEITY INDICATES THE EXISTENCE OF OTHER
CC PROTAMINES.
DR PIR; A02667; YZPK1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT VARIANT 9 28 G -> S (IN 50% OF THE MOLECULES).
FT VARIANT 28 28 G -> S (IN 50% OF THE MOLECULES).
SQ SEQUENCE 32 AA; 4139 MW; F9AF8FDF922A5EF CRC64;

Query Match 51.3%; Score 58; DB 1; Length 32;
Best Local Similarity 63.6%; Pred. No. 0.083; Indels 2; Gaps 1;
Matches 14; Conservative 1; Mismatches 5;

QY 1 RRRRRRGGRRRRRPPKKRK 20
||| ||| ||| ||| ||| : : :
DB 2 RRRRRSGRPVRRRRRPPKMSR 23

RESULT 19

PTB ONCMY STANDARD; PRT; 32 AA.

ID PRTB ONCMY
AC P12817; (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Protamine 2A.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]

RESULT 16

HSP5 OCTVU STANDARD; PRT; 30 AA.

AC P83217; (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P5 (PoS).
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=6645;
RN [1]

SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RP TISSUE=Sperm;
RC Gimenez-Bonafe P., Ribes E., Buesa C., Sautiere P., Kouach M.,
RA Ausio J., Kasinsky H.E., Chiva M.;
RT "Chromatin remodelling and protamines during spermiogenesis of Octopus
vulgaris (Cephalopoda)."
RL J. Exp. Zool. 0:0-0(2001).
CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive
CC complex.

CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- MASS SPECTROMETRY: MW=3941; METHOD=Electrospray.
DR GO; GO:0005718; C:nucleosome; NAS.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003677; F:DNA binding activity; NAS.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. .; NAS.
DR GO; GO:0007076; P:mitotic chromosome condensation; NAS.
DR GO; GO:0006334; P:nucleosome assembly; NAS.
DR GO; GO:0007283; P:spermatogenesis; NAS.
KW Chromosomal protein; Nucleosome core; Spermatogenesis;
KW DNA-binding; DNA condensation; Nuclear protein.
FT DOMAIN 2 15 POLY-ARG.
FT DOMAIN 17 26 POLY-ARG.
SQ SEQUENCE 30 AA; 3943 MW; 14F1BC7E4D277049 CRC64;

Query Match 51.3%; Score 58; DB 1; Length 30;
Best Local Similarity 63.2%; Pred. No. 0.078; Indels 0; Gaps 0;
Matches 12; Conservative 3; Mismatches 4;

QY 1 RRRRRRGGRRRRRPPKKRK 19
||| ||| ||| ||| ||| : : :
DB 2 RRRRRRGGRRRRRGGRRR 20

RESULT 17

PR13 ONCMY STANDARD; PRT; 32 AA.

AC P02330; (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Protamine II (Iridine II).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]

SEQUENCE.

RP MEDLINE=72030546; PubMed=4953052;
RA Ando T., Watanabe S.;
RT "A new method for fractionation of protamines and the amino acid
sequences of salmine and three components of iridine."
RL Int. J. Protein Res. 1:221-224(1969).
CC -1- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

```
RP SEQUENCE.
RX MEDLINE=96274711; PubMed=3755398;
RA McKay D.J., Renaux B.S., Dixon G.H.;
RT "Rainbow trout protamines. Amino acid sequences of six distinct
  proteins from a single testis.";
RL Eur. J. Biochem. 158:361-366(1986).
CC -!- FUNCTION: PROTEIN: SUBSTITUTION FOR HISTONES IN THE CHROMATIN OF
  SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
  SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC PIR; E21211;
DR Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
SQ SEQUENCE 32 AA; 4224 MW; B07A9C9D90B796FF CRC64;

Query Match 51.3%; Score 58; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.083;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRRGGRRRRRPPKKKK 20
Db 13 RRRRRVRRRRRRGGRRR 32

RESULT 20
PRT1 SEPOF
ID PRT1 SEPOF STANDARD; PRT; 78 AA.
AC P80001;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Spermatid-specific protein T1 [contains: Sperm protamine SP1].
OS Sepia officinalis (Common cuttlefish).
CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
CC Decapodiformes; Sepioidea; Sepiidae; Sepia.
CC NCBI_TaxID=6610;
RN [1]
RP SEQUENCE.
RX MEDLINE=91373359; PubMed=1894625;
RA Wouters-Tyrou D., Chartier-Harlin M.-C., Martin-Ponthieu A.,
RA Boutillon C., van Dorsselaer A., Sautiere P.;
RT "Cuttlefish spermatid-specific protein T1. Molecular characterization
  of two variants T1 and T2, putative precursors of sperm protamine
  variants Sp1 and Sp2.";
RL J. Biol. Chem. 266:17388-17395(1991).
RN [2]
RP SEQUENCE OF 22-78.
RX MEDLINE=91153298; PubMed=1999185;
RA Martin-Ponthieu A., Wouters-Tyrou D., Belaiche D., Sautiere P.,
RA Schindler P., van Dorsselaer A.;
RT "Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct
  variants.";
RL Eur. J. Biochem. 195:611-619(1991).
CC -!- FUNCTION: CUTTLEFISH SPERMIOGENESIS IS CHARACTERIZED BY A DOUBLE
  NUCLEAR PROTEIN TRANSITION: HISTONES -> SPERMATID-SPECIFIC
  PROTEINS (T1/T2) -> PROTEIN: SPERMATID-SPECIFIC. THE PROTEIN: SPERMATID-SPECIFIC
  SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- DEVELOPMENTAL STAGE: SPERMIOGENESIS.
CC -!- PTM: PHOSPHORYLATION OCCURS AT DIFFERENT DEGREES. THE
  TRIPHOSPHORYLATED FORM MAY BE PREDOMINANT IN T1. SP1 APPEARS TO BE
  PHOSPHORYLATED IN ELONGATED SPERMATIDS, BUT DEPHOSPHORYLATED IN
  MATURE SPERM CELLS.
CC -!- SIMILARITY: HIGH, TO S.OFFICINALIS SPERMATID-SPECIFIC PROTEIN T2.
DR PIR; A40973; A40973.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein; Phosphorylation;
KW Multigene family.
FT CHAIN 1 78 SPERMATID-SPECIFIC PROTEIN T1.
FT CHAIN 22 78 SPERM PROTEIN SP1.
FT DOMAIN 1 21 HYDROPHOBIC.
```

RN SEQUENCE FROM N.A.
 RP MEDLINE=83056843; PubMed=7142161;
 RX Geringas T.R., Sclay D., Gellinas R.E., Bing-Dong J., Yen C.E.,
 RA Kelly M.M., Bullock P.A., Parsons B.L., O'Neill K.E., Roberts R.J.;
 RT "Nucleotide sequences from the adenovirus-2 genome."
 RL J. Biol. Chem. 257:13475-13491(1982).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=83056844; PubMed=7142162;
 RX Alstrom P., Akusjaervi G., Pettersson M., Pettersson U.;
 RA "DNA sequence analysis of the region encoding the terminal protein
 RT and the hypothetical N-gene product of adenovirus type 2."
 RL J. Biol. Chem. 257:13492-13498(1982).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----NOT ANNOTATED_CDS-----
 CC EMBL; J01917; -; NOT ANNOTATED_CDS.
 CC PIR; F92351; A03864.
 CC Hypothetical protein.
 KW SEQUENCE 168 AA; 17703 MW; F29A2BDCBE95F80E CRC64;
 SQ
 Query Match 51.3%; Score 58; DB 1; Length 168;
 Best Local Similarity 52.0%; Pred. No. 0.42; 4; Indels 4; Gaps 1;
 Matches 13; Conservative 4; Mismatches 4;
 QY 1 RRRRRWGRRRRR---PKKKRV 21
 DB 44 RRRRTGRRSTKRSIIIPRRMV 68
 RESULT 23
 HSP1_AEP RU STANDARD; PRT; 60 AA.
 AC Q9GLP9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sperm protamine P1.
 GN PRM1.
 OS Aepyrymnus rufescens (Rufous rat-kangaroo) (Rufous bettong).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Potoroidae; Aepyrymnus.
 OX NCBI_TaxID=38598;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP Burk A., Springer M.S.;
 RA "Intergenic relationships among Macropodidae (Metatheria:
 RT Diprotodontia) and the chronicle of kangaroo evolution."
 RL J. Mammal. Evol. 7:213-237(2000).
 CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
 CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
 CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Testis.
 CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF187547; AA027964.1; -;
 DR InterPro; IPR000221; Protamine_P1.
 DR

DR Pfam; PF00260; protamine P1; 2.
 DR PROSITE; PS00048; PROTAMINE_P1; 1.
 KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 KW Testis; DNA condensation; Nuclear protein.
 FT INIT MET 0 BY SIMILARITY
 SQ SEQUENCE 60 AA; 8445 MW; IDC24691644AI7E0 CRC64;
 Query Match 50.9%; Score 57.5; DB 1; Length 60;
 Best Local Similarity 57.1%; Pred. No. 0.18;
 Matches 12; Conservative 5; Mismatches 3; Indels 1; Gaps 1;
 QY 1 RRRRRW-GRRRRRPKKKRK 20
 DB 25 RRRRRYGRSRRRRRRRR 45
 RESULT 24
 PRTB ACIGU STANDARD; PRT; 27 AA.
 ID PRTB ACIGU STANDARD; PRT; 27 AA.
 AC P02323;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Protamine B (Sturine B) (Stellin B)
 OS Acipenser guldenstadti (Caspian sturgeon) (Russian sturgeon), and
 OS Acipenser stellatus (Sevruga).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
 OC Acipenser.
 OX NCBI_TaxID=7902, 7903;
 RN [1]
 RN SEQUENCE.
 RC SPECIES=A.guldenstadti;
 RA Yulikova E.P., Evseenko L.K., Baratova L.A., Belyanova L.P.,
 RA Rybin V.K., Silaev A.B.;
 RT "The primary structure of sturine B, a protamine from Caspian
 RT sturgeon."
 RL Bioorg. Khim. 2:1613-1617(1976).
 RN [2]
 RN SEQUENCE.
 RC SPECIES=A.stellatus;
 RA Rybin V.K., Yulikova E.P.;
 RL Khim. Prirod. Soedin. 5:700-704(1979).
 CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
 CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
 CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Testis.
 CC PIR; A02665; SRAPC.
 DR Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 KW Testis; DNA condensation; Nuclear protein.
 SQ SEQUENCE 27 AA; 3707 MW; E300B46B1737EC80 CRC64;
 Query Match 50.4%; Score 57; DB 1; Length 27;
 Best Local Similarity 85.7%; Pred. No. 0.095;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RRRRRWGRRRRR 14
 DB 13 RRRRRHGRRRGR 26
 RESULT 25
 PRT1 ONCKE STANDARD; PRT; 32 AA.
 ID PRT1 ONCKE STANDARD; PRT; 32 AA.
 AC P02327;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Protamine (Salmine AI) (Protamine 2B).
 OS Oncorhynchus keta (Chum salmon), and
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8018, 8022;
RN [1]
RN SEQUENCE FROM N.A.
RC SPECIES=O. mykiss;
RC MEDLINE=88259242; PubMed=2838640;
RX Moir R.D., Dixon G.H.;
RA "Characterization of a protamine gene from the chum salmon
RT (Oncorhynchus keta).";
RL J. Mol. Evol. 27:8-16(1988).
RN [2]
RN SEQUENCE.
RP SPECIES=O. mykiss;
RP MEDLINE=72030546; PubMed=4953052;
RX Ando T., Watanabe S.;
RA "A new method for fractionation of protamines and the amino acid
RT sequences of salmon and three components of iridine.";
RL Int. J. Protein Res. 1:221-224(1969).
RN [3]
RN SEQUENCE OF 6-32 FROM N.A. (CLONE PTP59).
RP SPECIES=O. mykiss;
RP MEDLINE=81198983; PubMed=6262730;
RX Gedamu L., Wosnick M.A., Connor W., Watson D.C., Dixon G.H.,
RA Iatrou K.;
RA "Molecular analysis of the protamine multi-gene family in rainbow
RT trout testis.";
RL Nucleic Acids Res. 9:1463-1482(1981).
RN [4]
RN SEQUENCE OF 6-32 FROM N.A. (CLONE PTP11).
RP SPECIES=O. mykiss;
RP MEDLINE=79199790; PubMed=450133;
RX Jenkins J.R.;
RA "Sequence divergence of rainbow trout protamine mRNAs; comparison of
RT coding and non-coding nucleotide sequences in three protamine cDNA
RT plasmids.";
RL Nature 279:809-811(1979).
RN [5]
RN SEQUENCE FROM N.A. (CLONE TP21).
RP SPECIES=O. mykiss;
RP MEDLINE=83272939; PubMed=6308564;
RX Aiken J.M., McKenzie D., Zhao H.-Z., States J.C., Dixon G.H.;
RA "Sequence homologies in the protamine gene family of rainbow trout.";
RL Nucleic Acids Res. 11:4907-4922(1983).
RN [6]
RN SEQUENCE.
RP SPECIES=O. mykiss;
RP MEDLINE=86274711; PubMed=3755398;
RX McKay D.J., Renaux B.S., Dixon G.H.;
RA "rainbow trout protamines. Amino acid sequences of six distinct
RT proteins from a single testis.";
RL Eur. J. Biochem. 158:361-366(1986).
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X07511; CAA30391.1; -
CC EMBL; X01599; CAA25752.1; -
CC EMBL; M10718; AAA49608.1; -
CC PIR; A02669; SLONAL.
CC PIR; A27776; ITRF59.
CC PIR; S00710; S00710.
CC Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0
SQ SEQUENCE 32 AA; 4250 MW; ACOA9C9D90B796EA CRC64;
Query Match 50.4%; Score 57; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.11;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 RRRRRWGRRRRRPKKXK 20
Db 13 RRRRPVSRRRRRGGRRR 32
RESULT 26
PRT5 ONCMY STANDARD; PRT; 32 AA.
AC P02334;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Protamine 2C.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RN SEQUENCE FROM N.A. (CLONE TP15).
RP MEDLINE=83272939; PubMed=6308564;
RX Aiken J.M., McKenzie D., Zhao H.-Z., States J.C., Dixon G.H.;
RA "Sequence homologies in the protamine gene family of rainbow trout.";
RL Nucleic Acids Res. 11:4907-4922(1983).
RN [2]
RN SEQUENCE OF 6-32 FROM N.A. (CLONE PTP242).
RP MEDLINE=81198983; PubMed=6262730;
RX Gedamu L., Wosnick M.A., Connor W., Watson D.C., Dixon G.H.,
RA Iatrou K.;
RA "Molecular analysis of the protamine multi-gene family in rainbow
RT trout testis.";
RL Nucleic Acids Res. 9:1463-1482(1981).
RN [3]
RN SEQUENCE OF 6-32 FROM N.A. (CLONE PTP8).
RP MEDLINE=79199790; PubMed=450133;
RX Jenkins J.R.;
RA "Sequence divergence of rainbow trout protamine mRNAs; comparison of
RT coding and non-coding nucleotide sequences in three protamine cDNA
RT plasmids.";
RL Nature 279:809-811(1979).
RN [4]
RN SEQUENCE (2C).
RP MEDLINE=86274711; PubMed=3755398;
RX McKay D.J., Renaux B.S., Dixon G.H.;
RA "rainbow trout protamines. Amino acid sequences of six distinct
RT proteins from a single testis.";
RL Eur. J. Biochem. 158:361-366(1986).
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X02924; CAA26680.1; -
CC EMBL; X01596; CAA25749.1; -
CC EMBL; M10717; AAA49610.1; -
CC PIR; B21211; ITRF42.

Thu Jan 29 10:08:39 2004

us-10-002-884a-2.rsp

```

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0
SQ SEQUENCE 32 AA; 4319 MW; AD1A8D9D90B796EA CRC64;

Query Match 50.4%; Score 57; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.11;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKK 20
DB 13 RRRPRVSRRRRRGGRRR 32

RESULT 27
PR12_ONCMY STANDARD; PRT; 32 AA.
AC P08145;
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Protamine TP14.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
[1]
SEQUENCE FROM N.A.
MEDLINE=83272939; PubMed=6309564;
AC Aiken J.M., McKenzie D., Zhao H.-Z., States J.C., Dixon G.H.;
RA "Sequence homologies in the protamine gene family of rainbow trout.";
RT Nucleic Acids Res. 11:4907-4922(1983).
RL Nucleic Acids Res. 11:4907-4922(1983).
CC -!- FUNCTION: PROTEIN'S SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X01595; CAA25748.1; --
DR PIR; A21211; A21211.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0
SQ SEQUENCE 32 AA; 4260 MW; 5D388D9D90B796E9 CRC64;

Query Match 50.4%; Score 57; DB 1; Length 32;
Best Local Similarity 60.0%; Pred. No. 0.11;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKK 20
DB 13 RRRPRVSRRRRRGGRRR 32

RESULT 28
PR12_ONCMY STANDARD; PRT; 33 AA.
AC P02328;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Protamine IA (Iridine IA).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
[1]
RP SEQUENCE.
RX MEDLINE=72030546; PubMed=4953052;
RA Ando T., Watanabe S.;
RT "A new method for fractionation of protamines and the amino acid
RT sequences of salmon and three components of iridine.";
RL Int. J. Protein Res. 1:221-224(1969)
CC -!- FUNCTION: PROTEIN'S SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- TISSUE SPECIFICITY: Testis.
DR PIR; A02670; IRIRIA.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
SQ SEQUENCE 33 AA; 4406 MW; F92CA9C80A1FF2 CRC64;

Query Match 50.4%; Score 57; DB 1; Length 33;
Best Local Similarity 60.0%; Pred. No. 0.12;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKK 20
DB 14 RRRPRVSRRRRRGGRRR 33

RESULT 29
HSPL_RABIT STANDARD; PRT; 49 AA.
AC P10119;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P1 (Cysteine-rich protamine).
DE Sperm protamine P1 (Cysteine-rich protamine).
GN PM1 OR PM-1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
[1]
RP SEQUENCE.
RX MEDLINE=89078594; PubMed=3060372;
RA Ammer H., Henschen A.;
RT "Primary structure of rabbit sperm protamine, the first protamine of
RT its type with an aberrant N-terminal.";
RL FEBS Lett. 242:111-116(1988).
CC -!- FUNCTION: PROTEIN'S SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
CC DNA-HELIX (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
DR PIR; S02007; S02007.
DR InterPro; IPR000221; Protamine_P1.
DR Pfam; PF00260; protamine_P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT DISULFID 5 5 INTERCHAIN (WITH C-21) (BY SIMILARITY).
FT DISULFID 6 14 BY SIMILARITY.
FT DISULFID 21 21 INTERCHAIN (WITH C-5) (BY SIMILARITY).
FT DISULFID 37 37 INTERCHAIN (WITH C-37) (BY SIMILARITY).
FT DISULFID 38 46 BY SIMILARITY.
FT SEQUENCE 49 AA; 6656 MW; 488752B63395DA61 CRC64;

Query Match 50.4%; Score 57; DB 1; Length 49;
Best Local Similarity 65.0%; Pred. No. 0.17;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```


OY 2 RRRRWRGRRRRRPPKRRKV 21
DB 15 RRRRRRCRRRRRCRRRV 34

RESULT 30

HSPI_DIDMA
ID HSPI_DIDMA STANDARD; PRT; 57 AA.
AC P35305;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P1.
GN PRM1

OS Didelphis marsupialis virginiana (North American opossum), and
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eucelostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267, 13616;
RN [1]

RP SEQUENCE FROM N.A.
RC SPECIES=D.marsupialis;
RX MEDLINE=93345500; PubMed=8344286;
RA Winkfein R.J., Nishikawa S., Connor W., Dixon G.H.;

RT "Characterization of a marsupial sperm protamine gene and its
RT transcripts from the North American opossum (Didelphis
RT marsupialis).";
RL Eur. J. Biochem. 215:63-72 (1993).
RN [2]

RP SEQUENCE FROM N.A.
RC SPECIES=M.domestica;
RX MEDLINE=92515351; PubMed=7700877;

RA Refief J.D., Krajewski C., Westernman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes.";
RL Proc. R. Soc. Lond. B, Biol. Sci. 259:7-14 (1995).
CC -!- FUNCTION: PROTEIN SUBSTITUTION FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; L17007; AAA02812.1; -;
DR EMBL; X74044; CAA52193.1; -;
DR EMBL; L35448; AAA74612.1; -;
DR PIR; S34045; S34045.

DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine_P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0 BY SIMILARITY.
SQ SEQUENCE 57 AA; 7810 MW; 2837158280214E52 CRC64;

Query March 50.4%; Score 57; DB 1; Length 57;
Best Local Similarity 54.2%; Pred. No. 0.2;
Matches 13; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

OY 1 RRRRRWRGRRRRRRPPKRRK 20

DB 30 RRRRRRRGRGRRGRRRSPHRRR 53

RESULT 31

PRT2_SEPOF
ID PRT2_SEPOF STANDARD; PRT; 77 AA.
AC P80002;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sperm-specific protein T2 [Contains: Sperm protamine SP2].
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE.
RX MEDLINE=91373359; PubMed=1894625;
RA Wouters-Tyrou D., Chartier-Harlin M.-C., Martin-Ponthieu A.,
RA Boutillon C., van Dorselaer A., Sautiere P.;

RT "Cuttlefish sperm-specific protein T2. Molecular characterization
RT of two variants T1 and T2, putative precursors of sperm protamine
RT variants Sp1 and Sp2.";
RL J. Biol. Chem. 266:17388-17395 (1991).
RN [2]

RP SEQUENCE OF 22-77.
RX MEDLINE=91153298; PubMed=1999185;
RA Martin-Ponthieu A., Wouters-Tyrou D., Belaiche D., Sautiere P.,
RA Schindler P., van Dorselaer A.;

RT "Cuttlefish sperm protamines. 1. Amino acid sequences of two distinct
RT variants.";
RL Eur. J. Biochem. 195:611-619 (1991).
CC -!- FUNCTION: CUTTLEFISH SPERMIOGENESIS IS CHARACTERIZED BY A DOUBLE
CC NUCLEAR PROTEIN TRANSITION: HISTONES -> SPERMATID-SPECIFIC
CC PROTEINS (T1/T2) -> PROTAMINES (SP1/SP2). THE PROTAMINES COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.

CC -!- DEVELOPMENTAL STAGE: SPERMIOGENESIS.
CC -!- PM: PHOSPHORYLATION OCCURS AT DIFFERENT DEGREES. THE
CC TRIPHOSPHORYLATED FORM MAY BE PREDOMINANT IN T2. SP2 APPEARS TO BE
CC PHOSPHORYLATED IN ELONGATED SPERMATIDS, BUT DEPHOSPHORYLATED IN
CC MATURE SPERM CELLS.

CC -!- SIMILARITY: HIGH, TO S.OFFICINALIS SPERMATID-SPECIFIC PROTEIN T1.
DR PIR; B40973; B40973.

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein; Phosphorylation;

KW Multigene family.
FT CHAIN 1 77 SPERMATID-SPECIFIC PROTEIN T2.

FT CHAIN 22 77 SPERM PROTAMINE SP2.
FT DOMAIN 1 21 HYDROPHOBIC

FT DOMAIN 22 77 ARG-RICH (HIGHLY BASIC).
FT VARIANT 1 1 MISSING (IN T2B).

SQ SEQUENCE 77 AA; 10485 MW; 0F2C1B215292E0D7 CRC64;

Query Match 50.4%; Score 57; DB 1; Length 77;
Best Local Similarity 63.2%; Pred. No. 0.26;
Matches 12; Conservative 3; Mismatches 4; Indels 4; Gaps 0;

OY 1 RRRRRWRGRRRRRRPPKRRK 19

DB 48 RRRRRRRRRRRRRRRRRR 66

RESULT 32

Y278_MYCTU
ID Y278_MYCTU STANDARD; PRT; 957 AA.
AC P56877;

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical PE-PGRS family protein Rv0278c precursor.

GN Rv0278C OR MT0291 OR MTV035.06C.

OS Mycobacterium tuberculosis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773;


```

RN  SEQUENCE FROM N.A.
RP  STRAIN=H37Rv;
RX  MEDLINE=98295987; PubMed=9634230;
RA  Gordon S.V., Brosch R., Parkhill J., Garnier T., Church C., Harris D.,
RA  Cline S.T., Eigmeier K., Gas S., Barry C.E. III, Tekai F.,
RA  Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA  Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA  Hornsby T., Jagels K., Krogh A., McLean S., Moule S., Murphy L.,
RA  Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA  Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA  Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT  "Deciphering the biology of Mycobacterium tuberculosis from the
RT  complete genome sequence.";
RL  Nature 393:537-544(1998).
RN  SEQUENCE FROM N.A.
RP  STRAIN=CDC 1551 / Oshkosh;
RA  Fleischmann R.D., Alland R., Eisen J.A., Carpenter L., White O.,
RA  Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA  Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA  Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA  Bishai W.;
RT  "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT  laboratory strains.";
RL  Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.
CC  -!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
CC  SUBFAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@sib-sib.ch).
CC  -----
DR  EMBL; AL021930; CAA17353.1; -
DR  EMBL; AE006936; AAX44511.1; ALT_INIT.
DR  PIR; D70835; D70835.
DR  TIGR; MT0291; -
DR  TubercuList; Rv0278c; -.
DR  InterPro; IPR000084; PE_region.
DR  Pfam; PF00934; PE; 1.
KW  Hypothetical protein; Repeat; Signal; Complete proteome.
FT  SIGNAL 1 30 POTENTIAL.
FT  CHAIN 31 957 HYPOTHETICAL PE-PGRS FAMILY PROTEIN
FT  TUBERCULIST; Rv0278c.
FT  CONFLICT 40 40 M -> I (IN REF. 2).
FT  CONFLICT 158 163 MISSING (IN REF. 2).
FT  CONFLICT 807 807 R -> G (IN REF. 2).
SQ  SEQUENCE 957 AA; 81905 MW; 71EBABD417FBA47C CRC64;

Query Match 50.4%; Score 57; DB 1; Length 957;
Best Local Similarity 50.0%; Pred. No. 3;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1-RRRRRWGRRRRRPPKKR 20
DB 886 RYRQWCRQRADQRQ 905

RESULT 33
HSP3 OCTVU
ID HSP3 OCTVU STANDARD; PRT; 24 AA.
AC P33215;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Sperm protamine P3 (Pc3) (Fragmentation)
OS Octopus vulgaris (Octopus)
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.

SEQUENCE FROM N.A.
MEDLINE=92051332; PubMed=1840669;
Quaralt R., Oliva R.;
RT Isolated with PCR using consensus oligonucleotides.";
RL Nucleic Acids Res. 19:5786-5786(1991).
CC -!- FUNCTION: PROTAMINE SUBSTITUTION FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
CC DNA-HELIX (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
-----

```

```

OX NCBI_TaxID=6645;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Sperm;
RA Ginezer-Bonafé P., Ribes E., Buesa C., Sautiere P., Kouach M.,
RA Ausio J., Kasinsky H.E., Chiva M.;
RT "Chromatin remodeling and protamines during spermiogenesis of Octopus
RT vulgaris (Cephalopoda).";
RL J. Exp. Zool. 0:0-0(2001).
CC -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC sperm during the haploid phase of spermatogenesis. They compact
CC sperm DNA into a highly condensed, stable and inactive
CC complex.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- MASS SPECTROMETRY: MW=4389; METHOD=Electrospray.
DR GO; GO:0005718; C:nucleosome; NAS.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003677; F:DNA binding activity; NAS.
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .); NAS.
DR GO; GO:0007076; P:mitotic chromosome condensation; NAS.
DR GO; GO:0006334; P:nucleosome assembly; NAS.
DR GO; GO:0007283; P:spermatogenesis; NAS.
KW Chromosomal protein; Nucleosome core; Spermatogenesis;
KW DNA-binding; DNA condensation; Nuclear protein.
FT DOMAIN 1 16 POLY-ARG.
FT NON TER 24 24
SQ SEQUENCE 24 AA; 3381 MW; 308E90ED9D2C9C9C CRC64;

Query Match 49.5%; Score 56; DB 1; Length 24;
Best Local Similarity 63.2%; Pred. No. 0.11;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1-RRRRRWGRRRRRPPKKR 19
DB 3-RRRRRWGRRRRRGRSR 21

RESULT 34
HSP1 SAGIM
ID HSP1 SAGIM STANDARD; PRT; 49 AA.
AC P24714;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sperm protamine P1 (Cysteine-rich protamine).
GN PRM1.
OS Saginus imperator (Emperor tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=9491;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92051332; PubMed=1840669;
RA Quaralt R., Oliva R.;
RT Isolated with PCR using consensus oligonucleotides.";
RL Nucleic Acids Res. 19:5786-5786(1991).
CC -!- FUNCTION: PROTAMINE SUBSTITUTION FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBUNIT: CROSS-LINKED BY INTERCHAIN DISULFIDE BONDS AROUND THE
CC DNA-HELIX (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
-----

```

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch)

DR EMBL; X61678; CAA43853.1; -
DR PIR; S22582; S22582
DR InterPro; IPR000221; Protamine_P1.
DR Pfam; PF00260; protamine_P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0
SQ SEQUENCE 49 AA; 6545 MW; 8389C403F5B207F6 CRC64;

Query Match 49.6%; Score 56; DB 1; Length 49;
Best Local Similarity 61.1%; Pred. No. 0.23;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 3 RRRRWGRRRRRPPKKRK 20
Db 16 RRRRWGRRRRRPPKKRK 33

RESULT 35
HSP_CHICK
ID HSP CHICK STANDARD; PRT; 61 AA.
AC P15340; P02320;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm histone (Protamine) (Galline).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89308679; PubMed=2745455;
RA Oliva R., Dixon G.H.;
RT "Chicken protamine genes are intronless. The complete genomic
sequence and organization of the two loci";
RL J. Biol. Chem. 264:12472-12481(1989).
[2]
RP SEQUENCE OF 48-61 FROM N.A.
RX MEDLINE=89112514; PubMed=2892748;
RA Oliva R., Mezquita J., Mezquita C., Dixon G.H.;
RT "Haploid expression of the rooster protamine mRNA in the postmeiotic
stages of spermatogenesis";
RL Dev. Biol. 125:332-340(1988).
[3]
RP SEQUENCE.

TISSUE=Sperm;
MEDLINE=77050757; PubMed=992941;
NAKANO M., Tobita T., Ando T.;
RT "Studies on a protamine (galline) from fowl sperm. 3. The total amino
acid sequence of intact galline molecule";
RL Int. J. Pept. Protein Res. 8:565-578(1976).
-1- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- TISSUE SPECIFICITY: Testis.
-1- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
-1- CAUTION: REF.3 SEQUENCE WAS VERY DIFFERENT FROM THAT OBTAINED BY
REF.1 AND REF.2.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch)

CC EMBL; L38713; AAA58721.1; -
DR EMBL; M28100; AAA78951.1; -
DR EMBL; M19078; AAA49049.1; ALT_SEQ.
DR PIR; A34326; A34326.
DR InterPro; IPR000221; Protamine_P1.
DR Pfam; PF00260; protamine_P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein; Phosphorylation.
FT INIT MET 0
FT MOD_RES 8
SQ SEQUENCE 61 AA; 7986 MW; 191E27BD3A73AAA3 CRC64;

Query Match 49.6%; Score 56; DB 1; Length 61;
Best Local Similarity 60.0%; Pred. No. 0.28;
Matches 12; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
Qy 1 RRRRWGRRRRRPPKKRK 20
Db 16 RRRRWGRRRRRPPKKRK 33

RESULT 36
HSP1_DROAU
ID HSP1_DROAU STANDARD; PRT; 63 AA.
AC P42132;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P1.
DE Sperm protamine P1.
GN PRM1.
OS Dromiciops australis (Monito del Monte) (Dromiciops gliroides).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Microbiotheria; Microbiotheriidae; Dromiciops.
OX NCBI_TaxID=33562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95215351; PubMed=7700877;
RA Retief J.D., Krajewski C., Western M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes";
RL Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
-1- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- TISSUE SPECIFICITY: Testis.
-1- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch)

EMBL; L35449; AAA74611.1; -
DR InterPro; IPR000221; Protamine_P1.
DR Pfam; PF00260; protamine_P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0
SQ SEQUENCE 63 AA; 8860 MW; D3C0B6A287139372 CRC64;

Query Match 49.6%; Score 56; DB 1; Length 63;
Best Local Similarity 60.0%; Pred. No. 0.29;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 1 RRRRWGRRRRRPPKKRK 20
Db 16 RRRRWGRRRRRPPKKRK 33

```
Db 16 RRRRRRLRRRRRRRRSRR 35
RESULT 37
VCO7_ADE02 STANDARD; PRT; 198 AA.
AC P03266; F12542;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Major core protein precursor (Protein VII) (pVII).
GN PVII
OS Human adenovirus type 2, and
OS Human adenovirus type 5.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515, 28285;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human adenovirus type 2;
RX MEDLINE=85054835; PubMed=6094534;
RA Alestroem P., Akusjaervi G., Lager M., Yeh-Kai L., Pettersson U.;
RT "Genes encoding the core proteins of adenovirus type 2.";
RL J. Biol. Chem. 259:13980-13985(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human adenovirus type 2;
RX MEDLINE=83221511; PubMed=6574459;
RA Sung M.T., Cao T.M., Coleman R.T., Budelier K.A.;
RT "Gene and protein sequences of adenovirus protein VI-2, a hybrid basic
chromosomal protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2902-2906(1983).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human adenovirus type 2;
RX MEDLINE=92087470; PubMed=1727603;
RA Chroboczek J., Bieber P., Jacrot B.;
RT "The sequence of the genome of adenovirus type 5 and its comparison
with the genome of adenovirus type 2.";
RL Virology 186:280-285(1992).
RN [4]
RP SEQUENCE OF 1-136 FROM N.A.
RC SPECIES=Human adenovirus type 5;
RX MEDLINE=89137988; PubMed=3224820;
RA Neumann R., Chroboczek J., Jacrot B.;
RT "Determination of the nucleotide sequence for the penton-base gene of
human adenovirus type 5.";
RL Gene 69:153-157(1988).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J01917; AAA92212.1; -;
DR EMBL; M73260; AAA96408.1; ALT_SEQ.
DR EMBL; M22141; AAA42520.1; -;
DR PIR; C03837; FOAD72.
DR PIR; PT0067; FOADH5.
DR InterPro; IPR004912; Adeno_VII.
DR Pfam; PF03228; Adeno_VII; 1.
KW Core protein; Late protein.
FT PROPEP 1 24
FT CHAIN 25 198 MAJOR CORE PROTEIN.
FT SITE 24 25 CLEAVAGE (BY ADENOVIRUS PROTEASE).
FT CONFLICT 112 112 MISSING (IN REF. 2).
SQ SEQUENCE 198 AA; 21992 MW; 7D5A8D426F08E952 CRC64;
Query Match 49.6%; Score 56; DB 1; Length 198;
Best Local Similarity 73.3%; Pred. No. 0.88;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
-----
Db 1 RRRRRRWGRRRRRRP 15
:|||||
99 KRRRRVARRRRRP 113
RESULT 38
HSPI_PHACI STANDARD; PRT; 59 AA.
AC P79930;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P1.
GN PRM1.
OS Phascolarctos cinereus (Koala).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phascolarctidae; Phascolarctos.
OX NCBI_TaxID=38626;
RN [1]
RP SEQUENCE FROM N.A.
RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U87789; AAB89911.1; -;
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0 0 BY SIMILARITY.
SQ SEQUENCE 59 AA; 8271 MW; 4E1FB24E21952EA2 CRC64;
Query Match 48.7%; Score 55; DB 1; Length 59;
Best Local Similarity 61.1%; Pred. No. 0.37;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
-----
Oy 1 RRRRRRWGRRRRRRP 18
:|||||
Db 30 RYRRRRGRRRRRRRRRP 47
RESULT 39
HSPI_CAEFU STANDARD; PRT; 60 AA.
AC P42131;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P1.
GN PRM1.
OS Caenolestes fuliginosus (Shrew opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
OX NCBI_TaxID=37696;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spem;
RX MEDLINE=95215351; PubMed=7700877;
EX
```

RA Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
RT "Molecular phylogeny and evolution of marsupial protamine P1 genes."
RL Proc. R. Soc. Lond. B. Biol. Sci. 259:7-14(1995).
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L35332; AAA74598.1; -;
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0 BY SIMILARITY.
SQ SEQUENCE 60 AA; 8514 MW; 7630B63AD33A9B05 CRC64;

Query Match 48.7%; Score 55; DB 1; Length 60;
Best Local Similarity 55.0%; Pred. No. 0.37;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
Db 26 RSRRRYRRRRRRRRGR 45

RESULT 40
HSPI1 DENG0
ID HSPI1 DENG0 STANDARD; PRT; 60 AA.
AC G9GJ01;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sperm protamine P1.
GN PRM1.
OS Dendrolagus goodfellowi (Goodfellow's tree kangaroo),
OS Onychogalea unguifera (Northern nail-tailed wallaby), and
OS Setonix brachyurus (Quokka).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Dendrolagus.
OX NCBI_TaxID=69260, 65626, 30670;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=D.goodfellowi, O.unguifera, and S.brachyurus;
RA Burk A., Springer M.S.;
RT "Intergenic relationships among Macropodoidea (Metatheria:
RT Diprotodontia) and the chronicle of kangaroo evolution."
RL J. Mammal. Evol. 7:213-237(2000).
CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Testis.
CC -!- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC

DR EMBL; AF187537; AAG27954.1; -;
DR EMBL; AF187543; AAG27960.1; -;
DR EMBL; AF187541; AAG27958.1; -;
DR InterPro; IPR000221; Protamine P1.
DR Pfam; PF00260; Protamine P1; 1.
DR PROSITE; PS00048; PROTAMINE_P1; 1.
KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
KW Testis; DNA condensation; Nuclear protein.
FT INIT MET 0 BY SIMILARITY.
SQ SEQUENCE 60 AA; 8415 MW; 96255C81892B4B2F CRC64;

Query Match 48.7%; Score 55; DB 1; Length 60;
Best Local Similarity 55.0%; Pred. No. 0.37;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKKRK 20
Db 25 RSRRRYRRRRRRRRGR 44

Search completed: January 23, 2004, 11:18:04
Job time : 12 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 23, 2004, 11:12:45 ; Search time 36 Seconds
(without alignments)
150.531 Million cell updates/sec

Title: US-10-002-884A-2

Perfect score: 113

Sequence: 1 RRRRRWGRRRRRPKKRV 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	78.5	69.5	772	12	Q99AR3	Q99ar3 tt virus, a
2	72.5	64.2	745	12	Q91PS7	Q91ps7 tt virus. o
3	72	63.7	111	10	Q39682	Q39682 daucus caro
4	72	63.7	720	12	Q9DT76	Q9dt76 tt virus. o
5	72	63.7	750	12	Q91D04	Q91d04 tt virus. o
6	71	62.8	719	12	Q914N0	Q914n0 tt virus. o
7	71	62.8	720	12	Q9DUB7	Q9dub7 tt virus. o
8	71	62.8	740	12	Q98Y63	Q98y63 tt virus. o
9	70	61.9	340	10	Q942H5	Q942h5 ocyza sativ
10	70	61.9	745	12	Q99AOC	Q99aoc tt virus. o
11	69.5	61.5	748	12	Q9DT81	Q9dt81 tt virus. o
12	69	61.1	49	12	Q8V7C2	Q8v7c2 tt virus. o
13	69	61.1	49	12	Q8V7C1	Q8v7c1 tt virus. o
14	69	61.1	115	11	Q8BXG9	Q8bxg9 mus musculu
15	69	61.1	126	3	Q12444	Q12444 saccharomyc
16	69	61.1	154	11	Q8BHV2	Q8bhv2 mus musculu

RESULT 1

Q99AR3
ID Q99AR3 PRELIMINARY; PRT; 772 AA.
AC Q99AR3; (TREMREL. 17, Created)
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
DE Orf1 (Hypothetical 90.9 kDa protein).
OS TT virus, and
OS TTV-like virus DXLI.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887, 167758;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=TT virus; STRAIN=TCN-E;
RA Luo K.-X., He H.-F., Liu D.-X., Liu Z.-H., Xiao H., Jiang X.-J.,
RA Liang W.-F., Zhang L.;
RT "Novel variants related to TT virus wide distribution in China.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=TTV-like virus DXLI;
RA Luo K.X., He H.T., Xiao H., Liang W.F., Liu D.X.;
RT "A novel TTV-like genome detected in both feces and blood from patients in a hepatitis outbreak";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF345522; AAK11698.1; -;
DR EMBL; AF345076; AAL37157.1; -;
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT ORF1; 1.
KW Hypothetical protein.
SQ SEQUENCE 772 AA; 89580F204155FDE3 CRC64;

Query Match 69.5%; Score 78.5; DB 12; Length 772;
Best Local Similarity 78.9%; Pred. No. 0.0093;
Matches 15; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 RRRRRWGRRRRRPKKRV 19
||||| ||||| ||||| ||||| |||||

Q9d5g1 mus musculu
Q91ps3 tt virus. o
Q8v7g3 tt virus. o
Q8v7g0 tt virus. o
Q9wsv7 tt virus. d
Q9jg80 tt virus. o
Q9jnh31 tt virus. o
Q9ifv0 tt virus. p
Q9jgt1 tt virus. p
Q9vvf1 drosophila
Q9atd2 tt virus. o
Q9jg78 tt virus. o
Q9wt88 tt virus. o
Q91cy5 tt virus. o
Q8v7e7 tt virus. o
Q8v7c6 tt virus. o
Q9que4 tt virus. h
Q9qud8 tt virus. h
Q8v7e3 tt virus. o
Q9asw3 caulobacter
Q91cy9 tt virus. o
Q9ykl1 tt virus. o
Q9jg32 tt virus. o
Q91pq4 tt virus. p
Q91rd8 tt virus. l
Q9wax2 tt virus. l
Q70810 tt virus. l
Q70802 tt virus. l
Q9wqh0 tt virus. h

ALIGNMENTS

```
Db 14 RRRRRW-RRRRRRPRRR 31

RESULT 2
Q91PS7 PRELIMINARY; PRT; 745 AA.
AC Q91PS7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE ORF1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kt-08F;
RA Okamoto H.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Kt-08F;
RX MEDLINE=21440417; PubMed=11556704;
RA Muijono D.H., Nishizawa T., Tsuda F., Takahashi M., Okamoto H.;
RT "Molecular epidemiology of TT virus (TTV) and characterization of two novel TTV genotypes in Indonesia.";
RL Arch. Virol. 146:1249-1266(2001).
DR EMBL; AB054647; BAB61607.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
SQ SEQUENCE 745 AA; 85318 MW; B248C4CFCE853900 CRC64;

Query Match 64.2%; Score 72.5; DB 12; Length 745;
Best Local Similarity 65.2%; Pred. No. 0.058;
Matches 15; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 1 RRRRWGRR--RRRPKKRK 20
DB 46 RRRRWGRRRYTTLRLRRRK 68

RESULT 3
Q39682 PRELIMINARY; PRT; 111 AA.
AC Q39682;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Glycine-rich protein (Fragment).
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Panver Half-long; TISSUE=Somatic embryos at the globular stage;
RA Lin X., Hwang G.-J., Zimmerman J.L.;
RT "Isolation and characterization of a diverse set of genes from carrot somatic embryos.";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U47097; AAB01097.1; -.
FT NON_TER 1
SQ SEQUENCE 111 AA; 13829 MW; 082789CCADFA1C2A CRC64;

Query Match 63.7%; Score 72; DB 10; Length 111;
Best Local Similarity 72.2%; Pred. No. 0.013;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRWGRRRRRPKKK 18
DB 67 RRRRWGRRRRRRSSRR 84

Db 14 RRRRRW-RRRRRRPRRR 31

RESULT 4
Q9DT76 PRELIMINARY; PRT; 720 AA.
AC Q9DT76;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE ORF1 (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TYM9;
RX MEDLINE=20568739; PubMed=11118348;
RA Okamoto H., Nishizawa T., Tawara A., Takahashi M., Kishimoto J., Sai T., Sugai Y.;
RT "TT virus mRNAs detected in the bone marrow cells from an infected individual.";
RL Biochem. Biophys. Res. Commun. 279:700-707(2000).
DR EMBL; AB050453; BAB19934.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
FT NON_TER 1
SQ SEQUENCE 720 AA; 84418 MW; BCD2269BF14EDFC CRC64;

Query Match 63.7%; Score 72; DB 12; Length 720;
Best Local Similarity 60.0%; Pred. No. 0.066;
Matches 15; Conservative 3; Mismatches 1; Indels 6; Gaps 1;

QY 2 RRRRWGRR--RRRPKKRK 20
DB 15 RRRRWGRRGRRTYLRRLKKRK 39

RESULT 5
Q9TD04 PRELIMINARY; PRT; 750 AA.
AC Q9TD04;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE ORF1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21488921; PubMed=11601907;
RA Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F., Yoshikawa A.;
RT "Heterogeneous distribution of TT virus of distinct genotypes in multiple tissues from infected humans.";
RL Virology 288:358-368(2001).
DR EMBL; AB060592; BAB69900.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
SQ SEQUENCE 750 AA; 89223 MW; 616EC86DC3469091 CRC64;

Query Match 63.7%; Score 72; DB 12; Length 750;
Best Local Similarity 60.0%; Pred. No. 0.069;
Matches 15; Conservative 3; Mismatches 1; Indels 6; Gaps 1;

QY 2 RRRRWGRR--RRRPKKRK 20
DB 43 RRRRWGRRGRRTYLRRLKKRK 67

RESULT 6
Q914N0 PRELIMINARY; PRT; 719 AA.
AC Q914N0;
```

0.

RA Luo K.-X., He H.-T., Liu D.-X., Liu Z.-H., Xao H., Jiang X.-J.,
RA Liang W.-F., Zhang L.;
RL "Novel variants related to TT virus wide distribution in China."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF345529; AAK11712.1; -;
DR InterPro: IPR004219; TTvirus_Unk.
DR Pfam: PF02956; TT_ORF1; 1.
SQ SEQUENCE 745 AA; 98755 MW; 66E440909BAACC8E CRC64;

Query Match 61.9%; Score 70; DB 12; Length 745;
Best Local Similarity 48.6%; Pred. No. 0.13;
Matches 17; Conservative 0; Mismatches 4; Indels 14; Gaps 1;

QY 1 RRRRWGRRR-----RRPKKKRV 21
DB 45 RTTTRRWGRRRGRWRRRTYVRKGRHKKKRLV 79

RESULT 11

Q9DT81 PRELIMINARY; PRT; 748 AA.
AC Q9DT81;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE ORF1 (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TYM9;
RX MEDLINE=20568739; PubMed=1118348;
RA Okamoto H., Nishizawa T., Tawara A., Takahashi M., Kishimoto J.,
RA Sai T., Sugai Y.;
RT "TT virus MENAS detected in the bone marrow cells from an infected
RT individual."
RL Biochem. Biophys. Res. Commun. 279:700-707(2000).
DR EMBL: AB050448; BAB19928.1; -;
DR InterPro: IPR004219; TTvirus_Unk.
DR Pfam: PF02956; TT_ORF1; 1.
SQ SEQUENCE 748 AA; 98552 MW; D65CCB2CAAC5CE26F CRC64;

Query Match 61.5%; Score 69.5; DB 12; Length 748;
Best Local Similarity 66.7%; Pred. No. 0.15;
Matches 16; Conservative 0; Mismatches 3; Indels 5; Gaps 1;

QY 2 RRRRWGRRRPP-----KKKK 20
DB 43 RRRRWGRRRGRRTYLRGLKKK 66

RESULT 12

Q8V7C2 PRELIMINARY; PRT; 49 AA.
AC Q8V7C2;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE ORF1 (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21844401; PubMed=11855633;
RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
RA Okamoto H.;
RT "Analysis of the complete genomes of thirteen TT virus variants
RT classifiable into the fourth and fifth genetic groups, isolated from
RT viremic infants."
RL Arch. Virol. 147:21-41(2002).
DR EMBL: AB064628; BAB79400.1; -;

FT NON_TER 49 49
SQ SEQUENCE 49 AA; 7107 MW; DF3310365A077B66 CRC64;
Query Match 61.1%; Score 69; DB 12; Length 49;
Best Local Similarity 66.7%; Pred. No. 0.016;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRRWGRRRPPKKR 19
DB 22 RLRRWPRRRRRPRRR 39

RESULT 13

Q8V7C1 PRELIMINARY; PRT; 49 AA.
AC Q8V7C1;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE ORF1 (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21844401; PubMed=11855633;
RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
RA Okamoto H.;
RT "Analysis of the complete genomes of thirteen TT virus variants
RT classifiable into the fourth and fifth genetic groups, isolated from
RT viremic infants."
RL Arch. Virol. 147:21-41(2002).
DR EMBL: AB064629; BAB79402.1; -;
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 7034 MW; C1EA6EBF6A1DCFC CRC64;

Query Match 61.1%; Score 69; DB 12; Length 49;
Best Local Similarity 66.7%; Pred. No. 0.016;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRRWGRRRPPKKR 19
DB 22 RLRRWPRRRRRPRRR 39

RESULT 14

Q8BXG9 PRELIMINARY; PRT; 115 AA.
AC Q8BXG9;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Hypothetical arginine-rich region containing protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Cerebellum;
RC MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL: AK047167; BAC32979.1; -;
KW Hypothetical protein.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 13938 MW; 6C0F7EED8669CF65 CRC64;
Query Match 61.1%; Score 69; DB 11; Length 115;
Best Local Similarity 70.0%; Pred. No. 0.033;

Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKXK 20
||||| :||| :|||
Db 40 RRRRRRRRRRRRRRRK 59

RESULT 15

Q12444 PRELIMINARY; PRT; 126 AA.
AC Q12444;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF YOR309C.
GN YOR309C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1] _
RP SEQUENCE FROM N.A.
RA Pearson B.M., Hernando Y., Kalogeropoulos A., Schweizer M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RA Pearson B.M., Hernando Y., Wolf S.S., Kalogeropoulos A., Schweizer M.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; 275217; CAA9629.1;
DR EMBL; X90565; CAA62164.1;
DR SGD; S0005836; YOR309C.
SQ SEQUENCE 126 AA; 16294 MW; 46BF1F4C664802C8 CRC64;

Query Match 61.1%; Score 69; DB 3; Length 126;

Best Local Similarity 65.0%; Pred. No. 0.036;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKXK 20
||||| :||| :|||
Db 62 RRRRRRRRRRRRRK 81

RESULT 16

Q8BHV2 PRELIMINARY; PRT; 154 AA.
AC Q8BHV2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE weakly similar to hypothetical 10.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK08253; BAC38447.1;
KW Hypothetical protein.
SQ SEQUENCE 154 AA; 19596 MW; AEB8158A4839A216 CRC64;

Query Match 61.1%; Score 69; DB 11; Length 154;

Best Local Similarity 70.0%; Pred. No. 0.043;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPKKXK 20
||||| :||| :|||
Db 52 RRRRRRRRRRRRRK 71

RESULT 17

Q9D5G1 PRELIMINARY; PRT; 169 AA.
AC Q9D5G1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adult male testis cDNA, RIKEN full-length enriched library,
clone:493044p10 product:hypothetical Arginine-rich region containing
protein, full insert sequence (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium,
RA "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44 (1999).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861;

```
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA "RIKEN integrated sequence analysis (RISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
DR EMBL; AK015384; BAB29822.2; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 169 AA; 19305 MW; 91B959380A694CC CRC64;

Query Match 61.1%; Score 69; DB 11; Length 169;
Best Local Similarity 70.0%; Pred. No. 0.047;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGRRRRRPPKKRK 20
Db 120 RRRRRRRRRRRRRRRRR 139

RESULT 18
Q91PS3 PRELIMINARY; PRT; 742 AA.
AC Q91PS3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KC-10F;
RX MEDLINE=2144017; PubMed=11556704;
RA Muljono D.H., Nishizawa T., Tsuda F., Takahashi M., Okamoto H.;
RT "Molecular epidemiology of TT virus (TTV) and characterization of two
RL novel TTV genotypes in Indonesia."
RL Arch. Virol. 146:1249-1266(2001).
DR EMBL; AB054648; BAB61611.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
SQ SEQUENCE 742 AA; 88114 MW; A4E27AB09163DB5A CRC64;

Query Match 61.1%; Score 69; DB 12; Length 742;
Best Local Similarity 56.0%; Pred. No. 0.17;
Matches 14; Conservative 4; Mismatches 3; Indels 4; Gaps 1;

QY 1 RRRRRWGRRR---RRRPPKKRKV 21
Db 47 RRRRRGWARRRYLRARRVRKKKI 71

RESULT 19
Q8V7G3 PRELIMINARY; PRT; 743 AA.
AC Q8V7G3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT39F;
RA Okamoto H.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CT39F;
RX MEDLINE=21844401; PubMed=11855633;
RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
RA Okamoto H.;
RT "Analysis of the complete genomes of thirteen TT virus variants
RT classifiable into the fourth and fifth genetic groups, isolated from
RT viremic infants."
RL Arch. Virol. 147:21-41(2002).
DR EMBL; AB064604; BAB79346.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
SQ SEQUENCE 743 AA; 87446 MW; 547BE571CDAF87C4 CRC64;

Query Match 61.1%; Score 69; DB 12; Length 743;
Best Local Similarity 66.7%; Pred. No. 0.17;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRRWGRRRRRPPKKRK 19
Db 22 RLRRWPFRSRRRRRRR 39

RESULT 20
Q8V7G0 PRELIMINARY; PRT; 744 AA.
ID Q8V7G0;
AC Q8V7G0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT44F;
RA Okamoto H.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CT44F;
RX MEDLINE=21844401; PubMed=11855633;
RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
RA Okamoto H.;
RT "Analysis of the complete genomes of thirteen TT virus variants
RT classifiable into the fourth and fifth genetic groups, isolated from
RT viremic infants."
RL Arch. Virol. 147:21-41(2002).
DR EMBL; AB064605; BAB79350.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
SQ SEQUENCE 744 AA; 87602 MW; 33C2D5349CFEBA69 CRC64;

Query Match 61.1%; Score 69; DB 12; Length 744;
Best Local Similarity 66.7%; Pred. No. 0.17;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRRRWGRRRRRPPKKRK 19
Db 22 RLRRWPFRSRRRRRRR 39

RESULT 21
Q9WSV7 PRELIMINARY; PRT; 745 AA.
ID Q9WSV7;
AC Q9WSV7;
```

```

DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE DNA, complete genome, isolate:TTV SANBAN.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=TTV SANBAN;
RA Hijikata M.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=TTV SANBAN;
RX MEDLINE=9933592; PubMed=10403352;
RA Hijikata M., Takahashi K., Mishihiro S.;
RT "Complete circular DNA genome of a TT virus variant (isolate name of SANBAN) and 44 partial ORF2 sequences implicating a great degree of diversity beyond genotypes.";
RT RT Virology 260:17-22(1999).
RL EMBL; AB025946; BAA82149.2; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
SQ SEQUENCE 745 AA; 88622 MW; 08288DEB94C61324 CRC64;

Query Match 61.1%; Score 69; DB 12; Length 745;
Best Local Similarity 45.7%; Pred. No. 0.17;
Matches 16; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 RRRRRWGRRR-----RRRPKKKKRV 21
DB 45 RTRRRWGRRRYRGWRRRTYVRGRRHKKKKRLI 79

RESULT 22
QY 1 RRRRRWGRRR-----RRRPKKKKRV 21
DB 45 RTRRRWGRRRYRGWRRRTYVRGRRHKKKKRLI 79

ID Q9JG80 PRELIMINARY; PRT; 746 AA.
AC Q9JG80;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE ORF1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=TTVsan-IR1031;
RA Mishihiro S., Hijikata M., Takahashi K.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=TTVsan-IR1031;
RX MEDLINE=20428649; PubMed=10971131;
RA Takahashi K., Hijikata M., Samokhvalov E.I., Mishihiro S.;
RT "Full or near full length nucleotide sequences of TT virus variants (types SANBAN and YONBAN) and the TT virus-like mini virus.";
RT Intervirology 43:119-123(2000).
RL EMBL; AB038619; BAA93579.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
SQ SEQUENCE 746 AA; 88486 MW; B7F7F76E9734886A CRC64;

Query Match 61.1%; Score 69; DB 12; Length 746;
Best Local Similarity 45.7%; Pred. No. 0.17;
Matches 16; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 RRRRRWGRRR-----RRRPKKKKRV 21
DB 45 RTRRRWGRRRYRGWRRRTYVRGRRHKKKKRLI 79
```

```

RESULT 23
QY 1 RRRRRWGRRR-----RRRPKKKKRV 21
DB 45 RTRRRWGRRRYRGWRRRTYVRGRRHKKKKRLI 79

ID Q9JH31 PRELIMINARY; PRT; 746 AA.
AC Q9JH31;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE ORF1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=TUN02;
RA Okamoto H.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=TUN02;
RX MEDLINE=20456801; PubMed=11003468;
RA Ukita M., Okamoto H., Nishizawa T., Tawara A., Takahashi M.,
RA Izuka H., Miyakawa Y., Mayumi M.;
RT "The entire nucleotide sequences of two distinct TT virus (TTV) isolates (TUN01 and TUN02) remotely related to the original TTV isolates.";
RT Arch. Virol. 145:1543-1559(2000).
RL Arch. Virol. 145:1543-1559(2000).
DR EMBL; AB028669; BAA94878.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
SQ SEQUENCE 746 AA; 88561 MW; E0B22953AE764E3E CRC64;

Query Match 61.1%; Score 69; DB 12; Length 746;
Best Local Similarity 45.7%; Pred. No. 0.17;
Matches 16; Conservative 1; Mismatches 4; Indels 14; Gaps 1;

QY 1 RRRRRWGRRR-----RRRPKKKKRV 21
DB 45 RTRRRWGRRRYRGWRRRTYVRGRRHKKKKRLI 79

RESULT 24
QY 1 RRRRRWGRRR-----RRRPKKKKRV 21
DB 45 RTRRRWGRRRYRGWRRRTYVRGRRHKKKKRLI 79

ID Q9IFV0 PRELIMINARY; PRT; 766 AA.
AC Q9IFV0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Putative capsid protein.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=PMV;
RX MEDLINE=20409089; PubMed=10950985;
RA Hallett R.L., Clewley J.P., Bobet F., McKiernan P.J., Teo C.G.;
RT "Characterization of a highly divergent TT virus genome.";
RL J. Gen. Virol. 81:2273-2279(2000).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=PMV;
RA Hallett R.L., Clewley J.P., Teo C.G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF261761; AAF82559.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
SQ SEQUENCE 766 AA; 90844 MW; 22E5A3BBA3CC8187 CRC64;

Query Match 61.1%; Score 69; DB 12; Length 766;
Best Local Similarity 60.9%; Pred. No. 0.18;
Matches 14; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

QY 2 RRRRWGRRR-----RRRPKKKKRV 20
```

```

Db      8 RRRRRRRRRRTTWRPRPRR 30
||||| ||| ||| ||| |||
RESULT 25
ID Q9JGT1 PRELIMINARY; PRT; 764 AA.
AC Q9JGT1;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE PORFI.
OS TT virus.
OS Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20417334; PubMed=10963344;
RA Tanaka Y., Orico E., Ono T., Nakano T., Hayashi K., Kato T.,
RA Mukaiide M., Iida S., Mizokami M.;
RT Identification of a 23kDa protein encoded by putative open reading
RT frame 2 of TT virus (TTV) genotype 1 different from the other
RT genotypes."
RL Arch. Virol. 145:1385-1398 (2000).
DR EMBL; AB030486; BAA90403.1; -.
DR InterPro; IPR000413; Integrin_alpha.
DR Pfam; PF02956; TT_ORF1; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
SQ SEQUENCE 764 AA; 90154 MW; ABFA76D763251AED CRC64;

Query Match 60.6%; Score 68.5; DB 12; Length 764;
Best Local Similarity 70.0%; Pred. No. 0.21;
Matches 14; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 RRRRRWGR-RRRRPKKKR 19
| ||||| | ||||| |||
Db 12 RWRRRRRRRRRRRRRRRR 31

RESULT 26
ID Q9VVF1 PRELIMINARY; PRT; 550 AA.
AC Q9VVF1;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE CG13724 protein.
GN CG13724.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Awanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

```

```

RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,
RA Gloeck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Kusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
DR EMBL; AE003524; BAF49360.1; -.
DR FlyBase; FBgn0036707; CG13724.
SQ SEQUENCE 550 AA; 64803 MW; 60524F11BBD4FA64 CRC64;

Query Match 60.2%; Score 68; DB 5; Length 550;
Best Local Similarity 73.7%; Pred. No. 0.18;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RRRRRWGR-RRRRPKKKR 19
| ||||| | ||||| |||
Db 240 RRRRRRRRRRRRRRRRRR 258

RESULT 27
ID Q9DTD2 PRELIMINARY; PRT; 727 AA.
AC Q9DTD2;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE ORF1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=s-TTV CH71;
RA Abe K., Inami T.;
RT "simian TT virus."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=s-TTV CH71;
RA Abe K., Inami T.;
RT "simian TTV."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049608; BAB20604.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
SQ SEQUENCE 727 AA; 85212 MW; 574986EB9239D083 CRC64;

Query Match 60.2%; Score 68; DB 12; Length 727;
Best Local Similarity 56.0%; Pred. No. 0.23;
Matches 14; Conservative 3; Mismatches 2; Indels 6; Gaps 1;

QY 1 RRRRRWGR-RRRRPKKKR 19
| ||||| | ||||| |||
Db 8 RRRRRRRRRRRRRRRRRR 32

```

```
RESULT 28
Q9JG78      PRELIMINARY;      PRT;      745 AA.
AC Q9JG78;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TTVsan-S039;
RA Mishihiro S., Hijikata M., Takahashi K.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TTVsan-S039;
RX MEDLINE=20428649; PubMed=10971131;
RA Takahashi K., Hijikata M., Samokhvalov E.I., Mishihiro S.;
RT "Full or near full length nucleotide sequences of TT virus variants
   (types SANBAN and YONBAN) and the TT virus-like mini virus.";
RL Intervirology 43:119-123(2000).
DR EMBL; AB038620; BAA93581.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT ORF1.1.
SQ SEQUENCE 745 AA; 88661 MW; 14E19BD7DA9B95E3 CRC64;

Query Match      60.2%; Score 68; DB 12; Length 745;
Best Local Similarity 68.4%; Pred. No. 0.24;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPKKKR 19
Db 45 RTRRRWGRRRRRYRGWRR 63

RESULT 29
Q9WT88      PRELIMINARY;      PRT;      761 AA.
AC Q9WT88;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUS01;
RA Okamoto H.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TUS01;
RX MEDLINE=99319011; PubMed=10388667;
RA Okamoto H., Nishizawa T., Ukita M., Takahashi M., Fukuda M.,
   Iizuka H., Miyakawa Y., Mayumi M.;
RT "The entire nucleotide sequence of a TT virus isolate from the United
   States(TUS01): comparison with reported isolates and phylogenetic
   analysis.";
RL Virology 259:437-448(1999).
DR EMBL; AB017613; BAA82454.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT ORF1.1.
SQ SEQUENCE 761 AA; 90302 MW; 252662C6323A1D85 CRC64;

Query Match      60.2%; Score 68; DB 12; Length 761;
Best Local Similarity 60.0%; Pred. No. 0.24;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 RRRRRWGRRRRRPKKKR 20
Db 13 RRRRRWGRRRRRPRRTR 32

RESULT 30
Q91CV5      PRELIMINARY;      PRT;      766 AA.
AC Q91CV5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF1.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21488921; PubMed=11601907;
RA Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
   Yoshikawa A.;
RT "Heterogeneous distribution of TT virus of distinct genotypes in
   multiple tissues from infected humans.";
RL Virology 288:358-368(2001).
DR EMBL; AB060597; BAB6920.1; -.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT ORF1.1.
SQ SEQUENCE 766 AA; 91020 MW; D03DCCDFC9533E71 CRC64;

Query Match      60.2%; Score 68; DB 12; Length 766;
Best Local Similarity 75.0%; Pred. No. 0.24;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RRRRRWGRRRRRPKK 17
Db 16 RRRRRWGRRRRRPRR 31

RESULT 31
Q8V7E7      PRELIMINARY;      PRT;      57 AA.
AC Q8V7E7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF1 (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21844401; PubMed=11855633;
RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
   Okamoto H.;
RT "Analysis of the complete genomes of thirteen TT virus variants
   classifiable into the fourth and fifth genetic groups, isolated from
   viremic infants.";
RL Arch. Virol 147:21-41(2002).
DR EMBL; AB064612; BAB79368.1; -.
FT NON TER 57
SQ SEQUENCE 57 AA; 8138 MW; 61E467DDE395ACE9 CRC64;

Query Match      59.3%; Score 67; DB 12; Length 57;
Best Local Similarity 65.0%; Pred. No. 0.033;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPKKKR 20
Db 7 RRRRRWGRRRRRPRRTR 26

RESULT 32
Q8V7C6
```

```

ID Q8V7C6 PRELIMINARY; PRT; 67 AA.
AC Q8V7C6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF1 (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
NCBI_TaxID=68887;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2184403; PubMed=11855633;
RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
RA Okamoto H.;
RT "Analysis of the complete genomes of thirteen TT virus variants
RT classifiable into the fourth and fifth genetic groups, isolated from
RT viremic infants.";
RL Arch. Virol. 147:21-41(2002).
DR EMBL; AB064625; BABY9394.1; -.
FT NON TPR 67
SQ SEQUENCE 67 AA; 9511 MW; AD8271CFB79027F0 CRC64;

Query Match 59.3%; Score 67; DB 12; Length 67;
Best Local Similarity 65.0%; Pred. No. 0.038;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPPKKRK 20
Db 7 RWRRRWGRRRRRPPKLRR 26
| | | | | | | | : : :
| | | | | | | | : : :

RESULT 33
Q9QUE4 PRELIMINARY; PRT; 767 AA.
AC Q9QUE4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 90.4 kDa protein.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
NCBI_TaxID=68887;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=JA2B;
RA Erker J.C., Jeary T.P., Desai S.M., Chalmers M.I., Mushahwar I.K.;
RT "Analyses of TT virus full-length genomic sequences.";
RL J. Gen. Virol. 80:1743-1750(1999).
DR EMBL; AF122918; AAD45644.1; -.
DR InterPro; IPR004219; TVvirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
KW Hypothetical protein.
SQ SEQUENCE 767 AA; 90361 MW; 60FE8D87F4C6D8D CRC64;

Query Match 59.3%; Score 67; DB 12; Length 767;
Best Local Similarity 56.0%; Pred. No. 0.33;
Matches 14; Conservative 3; Mismatches 2; Indels 6; Gaps 1;

Qy 1 RRRRRWGCR-----RRRRPCKKR 19
Db 8 RRRRRPWRRRRRWRWRRRRRRRR 32
| | | | | | | | | | | | | |
| | | | | | | | | | | | | |

RESULT 34
Q9QUDB PRELIMINARY; PRT; 767 AA.
AC Q9QUDB;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 90.4 kDa protein.
OS TT virus.
```

```

OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-US35;
RX MEDLINE=99350006; PubMed=10423143;
RA Erker J.C., leary T.P., Desai S.M., Chalmers M.L., Mushahwar I.K.;
RT "Analyses of TT virus full-length genomic sequences.";
RL J. Gen. Virol. 80:1743-1750(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-US35;
RA Erker J.C., leary T.P., Desai S.M., Chalmers M.L., Mushahwar I.K.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DDJB databases.
DR EMBL; AF122920; AAD45650.1; -.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR004219; TTVirus_Unk.
DR Pfam; PF02956; TT_ORF1; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
KW Hypothetical protein.
SQ SEQUENCE 767 AA; 90383 MW; 6FAC515C088C1E10 CRC64;

Query Match 59.3%; Score 67; DB 12; Length 767;
Best Local Similarity 56.0%; Pred.No. 0.33; 2; Indels 6; Gaps
Matches 14; Conservative 3; Mismatches

QY 1 RRRRRWGR-----RRRRPKKKR 19
DB ||||| | | | | | | | | | | | | | | | |
8 RRRRRPWRRRRRRRRRRRRRR 32

RESULT 35
Q8V7E3 PRELIMINARY; PRT; 61 AA.
ID Q8V7E3;
AC Q8V7E3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORF1 (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21844401; PubMed=11855633;
RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
RA Okamoto H.;
RT "Analysis of the complete genomes of thirteen TT virus variants
RT classifiable into the fourth and fifth genetic groups, isolated from
RT viremic infants.";
RL Arch. Virol. 147:21-41(2002).
DR EMBL; AB064614; BAB79372.1; -.
FT NON_TER 61
SQ SEQUENCE 61 AA; 8743 MW; FA2E28332FA3657C CRC64;

Query Match 58.4%; Score 66; DB 12; Length 61;
Best Local Similarity 65.0%; Pred.No. 0.048;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps

QY 1 RRRRRWGRRRRRRRPKKKR 20
DB | | | | | | | | : | :
7 RWRRRWGRRRRRPWIRRR 26

RESULT 36
Q9A5W3 PRELIMINARY; PRT; 294 AA.
ID Q9A5W3;
AC Q9A5W3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein CC2334.
GN CC2334.

```

OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL; AE005903; AAK24305.1; -;
 DR TIGR; CC2334; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 294 AA; 34893 MW; 17F7C01F9C92BA46 CRC64;

Query Match 58.4%; Score 66; DB 16; Length 294;
 Best Local Similarity 65.0%; Pred. No. 0.19;
 Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPKKKR 20
 ||||| ||||| : : :
 Db 175 RRRRRFGRRRRRRRRR 194

RESULT 37

Q91CY9 ID Q91CY9 PRELIMINARY; PRT; 742 AA.
 AC Q91CY9;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE ORF1.
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21489921; PubMed=11601907;
 RA Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
 RA Yoshikawa A.;
 RT "Heterogeneous distribution of TT virus of distinct genotypes in
 RT multiple tissues from infected humans.";
 RL Virology 288:358-368(2001).
 DR EMBL; AB060596; BAB69916.1; -;
 DR InterPro; IPR004219; TTVirus_Unk.
 DR Pfam; PF02956; TT_ORF1; 1.
 SQ SEQUENCE 742 AA; 88541 MW; 13748D37DA86633D CRC64;

Query Match 58.4%; Score 66; DB 12; Length 742;
 Best Local Similarity 57.7%; Pred. No. 0.44;
 Matches 15; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy 1 RRRRRWGRRRRRRRPKKKR 20
 ||||| ||||| : : :
 Db 41 RVRRRRWGRRRRRRLRYTKYRRKK 66

RESULT 38

Q9YKL1 ID Q9YKL1 PRELIMINARY; PRT; 770 AA.
 AC Q9YKL1;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE ORF1 protein.
 OS TT virus.

OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TTVCHN2;
 RA Huang C.H., Zhou Y.S., Chen R.G., Dong J.F., Wang H.T.;
 RT "Cloning and sequencing of genome of TT virus isolated from a blood
 RT donor in Southern China.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF129887; AAD20024.1; -;
 DR InterPro; IPR004219; TTVirus_Unk.
 DR Pfam; PF02956; TT_ORF1; 1.
 SQ SEQUENCE 770 AA; 90342 MW; FDB00B9112D96B3A CRC64;

Query Match 58.4%; Score 66; DB 12; Length 770;
 Best Local Similarity 72.2%; Pred. No. 0.45;
 Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RRRRRWGRRRRRPKKK 18
 ||||| ||||| : : :
 Db 52 RRRRWRRRRRRRRKKK 69

RESULT 39

Q9JG32 ID Q9JG32 PRELIMINARY; PRT; 57 AA.
 AC Q9JG32;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE ORF1 (Fragment).
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20261737; PubMed=10799591;
 RA Okamoto H., Ukita M., Nishizawa T., Kishimoto J., Hoshi Y., Mizuo H.,
 RA Tanaka T., Miyakawa Y., Mayumi M.;
 RT "Circular double-stranded forms of TT virus DNA in the liver.";
 RL J. Virol. 74:5161-5167(2000).
 DR EMBL; AB040776; BAA94196.1; -;
 DR InterPro; IPR004219; TTVirus_Unk.
 DR Pfam; PF02956; TT_ORF1; 1.
 DT NON TER 57 57
 SQ SEQUENCE 57 AA; 8281 MW; 898FADC553FC8D83 CRC64;

Query Match 58.0%; Score 65.5; DB 12; Length 57;
 Best Local Similarity 73.7%; Pred. No. 0.053;
 Matches 14; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 RRRRRWGRRRRRPKKKR 19
 ||||| ||||| : : :
 Db 7 RRRRRRW-RWRRRRPWRRR 24

RESULT 40

Q91PQ4 ID Q91PQ4 PRELIMINARY; PRT; 143 AA.
 AC Q91PQ4;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Putative ORF1 spliced form.
 OS TT virus.
 OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
 OX NCBI_TaxID=68887;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1a;
 RA Yokoyama H., Yasuda J., Iwakura Y.;
 RT "Development of nephrotic syndrome with severe ascites in mice
 RT transgenic for the TT virus ORF1 gene.";

RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL: AB055937; BAB63258.1; -

DR InterPro: IPR004219; TTVirus_Unk.

DR Pfam: PF02956; TT_ORE1; 1.

SQ SEQUENCE 143 AA; 16950 MW; 80BC813E12E099FE CRC64;

Query Match 58.0%; Score 65.5; DB 12; Length 143;

Best Local Similarity 73.7%; Pred. NO. 0.12;

Matches 14; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 RRRRRWGRRRRRPKKR 19

DB 7 RRRREW-RRRRPWRR 24

Search completed: January 23, 2004, 11:18:53

Job time : 37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 24, 2004, 14:28:27 ; Search time 2723 Seconds
(without alignments)
243.583 Million cell updates/sec

Title: US-10-002-884A-5

Perfect score: 20

Sequence: 1 gttctcgctggtgatttca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 16581889874 residues

Total number of hits satisfying chosen parameters: 20836004

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Pending Patents NA Main:*

- 1: /cgn2_6/ptodata/2/pna/PCTUS COMB.seq.*
- 2: /cgn2_6/ptodata/2/pna/PCTUS COMB.seq.old.*
- 3: /cgn2_6/ptodata/2/pna/US06 COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US07 COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US080 COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US081 COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US082 COMB.seq.*
- 8: /cgn2_6/ptodata/2/pna/US083 COMB.seq.*
- 9: /cgn2_6/ptodata/2/pna/US084 COMB.seq.*
- 10: /cgn2_6/ptodata/2/pna/US085 COMB.seq.*
- 11: /cgn2_6/ptodata/2/pna/US086 COMB.seq.*
- 12: /cgn2_6/ptodata/2/pna/US087 COMB.seq.*
- 13: /cgn2_6/ptodata/2/pna/US088 COMB.seq.*
- 14: /cgn2_6/ptodata/2/pna/US089 COMB.seq.*
- 15: /cgn2_6/ptodata/2/pna/US090 COMB.seq.*
- 16: /cgn2_6/ptodata/2/pna/US091 COMB.seq.*
- 17: /cgn2_6/ptodata/2/pna/US092A COMB.seq.*
- 18: /cgn2_6/ptodata/2/pna/US092B COMB.seq.*
- 19: /cgn2_6/ptodata/2/pna/US093A COMB.seq.*
- 20: /cgn2_6/ptodata/2/pna/US093B COMB.seq.*
- 21: /cgn2_6/ptodata/2/pna/US094 COMB.seq.*
- 22: /cgn2_6/ptodata/2/pna/US095A COMB.seq.*
- 23: /cgn2_6/ptodata/2/pna/US095B COMB.seq.*
- 24: /cgn2_6/ptodata/2/pna/US095C COMB.seq.*
- 25: /cgn2_6/ptodata/2/pna/US095D COMB.seq.*
- 26: /cgn2_6/ptodata/2/pna/US096A COMB.seq.*
- 27: /cgn2_6/ptodata/2/pna/US096B COMB.seq.*
- 28: /cgn2_6/ptodata/2/pna/US096C COMB.seq.*
- 29: /cgn2_6/ptodata/2/pna/US096D COMB.seq.*
- 30: /cgn2_6/ptodata/2/pna/US096E COMB.seq.*
- 31: /cgn2_6/ptodata/2/pna/US097A COMB.seq.*
- 32: /cgn2_6/ptodata/2/pna/US097B COMB.seq.*
- 33: /cgn2_6/ptodata/2/pna/US097C COMB.seq.*
- 34: /cgn2_6/ptodata/2/pna/US098A COMB.seq.*
- 35: /cgn2_6/ptodata/2/pna/US098B COMB.seq.*
- 36: /cgn2_6/ptodata/2/pna/US098C COMB.seq.*
- 37: /cgn2_6/ptodata/2/pna/US098D COMB.seq.*
- 38: /cgn2_6/ptodata/2/pna/US099A COMB.seq.*
- 39: /cgn2_6/ptodata/2/pna/US099B COMB.seq.*
- 40: /cgn2_6/ptodata/2/pna/US099C COMB.seq.*
- 41: /cgn2_6/ptodata/2/pna/US099D COMB.seq.*
- 42: /cgn2_6/ptodata/2/pna/US099E COMB.seq.*
- 43: /cgn2_6/ptodata/2/pna/US099F COMB.seq.*

- 44: /cgn2_6/ptodata/2/pna/US100A COMB.seq.*
- 45: /cgn2_6/ptodata/2/pna/US100B COMB.seq.*
- 46: /cgn2_6/ptodata/2/pna/US101A COMB.seq.*
- 47: /cgn2_6/ptodata/2/pna/US101B COMB.seq.*
- 48: /cgn2_6/ptodata/2/pna/US102A COMB.seq.*
- 49: /cgn2_6/ptodata/2/pna/US102B COMB.seq.*
- 50: /cgn2_6/ptodata/2/pna/US103A COMB.seq.*
- 51: /cgn2_6/ptodata/2/pna/US103B COMB.seq.*
- 52: /cgn2_6/ptodata/2/pna/US104A COMB.seq.*
- 53: /cgn2_6/ptodata/2/pna/US104B COMB.seq.*
- 54: /cgn2_6/ptodata/2/pna/US6000 COMB.seq.*
- 55: /cgn2_6/ptodata/2/pna/US6001 COMB.seq.*
- 56: /cgn2_6/ptodata/2/pna/US6002 COMB.seq.*
- 57: /cgn2_6/ptodata/2/pna/US6003 COMB.seq.*
- 58: /cgn2_6/ptodata/2/pna/US6004 COMB.seq.*
- 59: /cgn2_6/ptodata/2/pna/US6005 COMB.seq.*
- 60: /cgn2_6/ptodata/2/pna/US6006 COMB.seq.*
- 61: /cgn2_6/ptodata/2/pna/US6007 COMB.seq.*
- 62: /cgn2_6/ptodata/2/pna/US6008 COMB.seq.*
- 63: /cgn2_6/ptodata/2/pna/US6009 COMB.seq.*
- 64: /cgn2_6/ptodata/2/pna/US6010 COMB.seq.*
- 65: /cgn2_6/ptodata/2/pna/US6011 COMB.seq.*
- 66: /cgn2_6/ptodata/2/pna/US6012 COMB.seq.*
- 67: /cgn2_6/ptodata/2/pna/US6013 COMB.seq.*
- 68: /cgn2_6/ptodata/2/pna/US6014 COMB.seq.*
- 69: /cgn2_6/ptodata/2/pna/US6015 COMB.seq.*
- 70: /cgn2_6/ptodata/2/pna/US6016 COMB.seq.*
- 71: /cgn2_6/ptodata/2/pna/US6017 COMB.seq.*
- 72: /cgn2_6/ptodata/2/pna/US6018 COMB.seq.*
- 73: /cgn2_6/ptodata/2/pna/US6019 COMB.seq.*
- 74: /cgn2_6/ptodata/2/pna/US6020 COMB.seq.*
- 75: /cgn2_6/ptodata/2/pna/US6021 COMB.seq.*
- 76: /cgn2_6/ptodata/2/pna/US6022 COMB.seq.*
- 77: /cgn2_6/ptodata/2/pna/US6023A COMB.seq.*
- 78: /cgn2_6/ptodata/2/pna/US6023B COMB.seq.*
- 79: /cgn2_6/ptodata/2/pna/US6024 COMB.seq.*
- 80: /cgn2_6/ptodata/2/pna/US6025 COMB.seq.*
- 81: /cgn2_6/ptodata/2/pna/US6026 COMB.seq.*
- 82: /cgn2_6/ptodata/2/pna/US6027 COMB.seq.*
- 83: /cgn2_6/ptodata/2/pna/US6028 COMB.seq.*
- 84: /cgn2_6/ptodata/2/pna/US6029 COMB.seq.*
- 85: /cgn2_6/ptodata/2/pna/US6030 COMB.seq.*
- 86: /cgn2_6/ptodata/2/pna/US6031 COMB.seq.*
- 87: /cgn2_6/ptodata/2/pna/US6032 COMB.seq.*
- 88: /cgn2_6/ptodata/2/pna/US6033 COMB.seq.*
- 89: /cgn2_6/ptodata/2/pna/US6034 COMB.seq.*
- 90: /cgn2_6/ptodata/2/pna/US6035 COMB.seq.*
- 91: /cgn2_6/ptodata/2/pna/US6036 COMB.seq.*
- 92: /cgn2_6/ptodata/2/pna/US6037 COMB.seq.*
- 93: /cgn2_6/ptodata/2/pna/US6038 COMB.seq.*
- 94: /cgn2_6/ptodata/2/pna/US6039 COMB.seq.*
- 95: /cgn2_6/ptodata/2/pna/US6040 COMB.seq.*
- 96: /cgn2_6/ptodata/2/pna/US6041 COMB.seq.*
- 97: /cgn2_6/ptodata/2/pna/US6042 COMB.seq.*
- 98: /cgn2_6/ptodata/2/pna/US6043 COMB.seq.*
- 99: /cgn2_6/ptodata/2/pna/US6044 COMB.seq.*
- 100: /cgn2_6/ptodata/2/pna/US6045 COMB.seq.*
- 101: /cgn2_6/ptodata/2/pna/US6046 COMB.seq.*
- 102: /cgn2_6/ptodata/2/pna/US6047 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	20	100.0	20	1	PCT-US00-07003-3
2	20	100.0	20	1	PCT-US00-09473-4
3	20	100.0	20	1	PCT-US00-16534-6
4	20	100.0	20	1	PCT-US00-18415-4

Sequence 3, Appli

Sequence 4, Appli

Sequence 6, Appli

Sequence 4, Appli

5	20	100.0	20	1	PCT-US01-02951-5	Sequence 5, Appli	78	20	100.0	20	25	US-09-594-387-6	Sequence 6, Appli
6	20	100.0	20	1	PCT-US01-02951-6	Sequence 6, Appli	79	20	100.0	20	27	US-09-627-787-49	Sequence 49, Appli
7	20	100.0	20	1	PCT-US02-04980-5	Sequence 5, Appli	80	20	100.0	20	28	US-09-654-373-13	Sequence 13, Appli
8	20	100.0	20	1	PCT-US03-04323-14	Sequence 14, Appli	81	20	100.0	20	31	US-09-708-224-4	Sequence 4, Appli
9	20	100.0	20	1	PCT-US03-11921-1	Sequence 1, Appli	82	20	100.0	20	31	US-09-708-224-13	Sequence 13, Appli
10	20	100.0	20	1	PCT-US97-02003-1	Sequence 1, Appli	83	20	100.0	20	31	US-09-708-224-27	Sequence 27, Appli
11	20	100.0	20	1	PCT-US98-08798-3	Sequence 3, Appli	84	20	100.0	20	31	US-09-708-224-35	Sequence 35, Appli
12	20	100.0	20	1	PCT-US99-04213-4	Sequence 4, Appli	85	20	100.0	20	31	US-09-708-224-42	Sequence 42, Appli
13	20	100.0	20	1	PCT-US99-11141-3	Sequence 3, Appli	86	20	100.0	20	32	US-09-747-009-27	Sequence 27, Appli
14	20	100.0	20	1	PCT-US99-11142-6	Sequence 6, Appli	87	20	100.0	20	32	US-09-747-009-29	Sequence 29, Appli
15	20	100.0	20	1	PCT-US99-11214-3	Sequence 3, Appli	88	20	100.0	20	32	US-09-747-009A-27	Sequence 27, Appli
16	20	100.0	20	1	PCT-US99-11267-3	Sequence 3, Appli	89	20	100.0	20	32	US-09-747-009A-28	Sequence 28, Appli
17	20	100.0	20	1	PCT-US99-11394-49	Sequence 49, Appli	90	20	100.0	20	32	US-09-747-009A-29	Sequence 29, Appli
18	20	100.0	20	1	PCT-US99-15960-3	Sequence 3, Appli	91	20	100.0	20	32	US-09-835-370-38	Sequence 38, Appli
19	20	100.0	20	1	PCT-US00-07003-3	Sequence 4, Appli	92	20	100.0	20	35	US-09-835-371-38	Sequence 5, Appli
20	20	100.0	20	2	PCT-US00-09473-4	Sequence 6, Appli	93	20	100.0	20	35	US-09-835-371-38	Sequence 5, Appli
21	20	100.0	20	2	PCT-US00-16534-6	Sequence 6, Appli	94	20	100.0	20	36	US-09-876-242-5	Sequence 13, Appli
22	20	100.0	20	2	PCT-US00-18415-4	Sequence 4, Appli	95	20	100.0	20	37	US-09-895-480A-13	Sequence 4, Appli
23	20	100.0	20	2	PCT-US01-02951-5	Sequence 5, Appli	96	20	100.0	20	38	US-09-902-953-4	Sequence 18, Appli
24	20	100.0	20	2	PCT-US01-02951-6	Sequence 6, Appli	97	20	100.0	20	39	US-09-931-732B-18	Sequence 18, Appli
25	20	100.0	20	2	PCT-US01-02951-7	Sequence 7, Appli	98	20	100.0	20	39	US-09-931-732C-18	Sequence 4, Appli
26	20	100.0	20	2	PCT-US03-04323-14	Sequence 14, Appli	99	20	100.0	20	39	US-09-931-732C-18	Sequence 4, Appli
27	20	100.0	20	2	PCT-US03-11921-1	Sequence 1, Appli	100	20	100.0	20	39	US-09-935-316-4	Sequence 4, Appli
28	20	100.0	20	2	PCT-US97-02003-1	Sequence 3, Appli	101	20	100.0	20	40	US-09-944-493-4	Sequence 4, Appli
29	20	100.0	20	2	PCT-US98-08798-3	Sequence 3, Appli	102	20	100.0	20	44	US-10-002-802A-1	Sequence 1, Appli
30	20	100.0	20	2	PCT-US99-11141-3	Sequence 3, Appli	103	20	100.0	20	44	US-10-002-884A-5	Sequence 5, Appli
31	20	100.0	20	2	PCT-US99-11142-6	Sequence 6, Appli	104	20	100.0	20	44	US-10-029-598-49	Sequence 49, Appli
32	20	100.0	20	2	PCT-US99-11214-3	Sequence 3, Appli	105	20	100.0	20	44	US-10-029-598-57	Sequence 57, Appli
33	20	100.0	20	2	PCT-US99-11267-3	Sequence 3, Appli	106	20	100.0	20	44	US-10-029-598-58	Sequence 58, Appli
34	20	100.0	20	2	PCT-US99-11394-49	Sequence 49, Appli	107	20	100.0	20	45	US-10-071-822A-4	Sequence 4, Appli
35	20	100.0	20	2	PCT-US99-15960-3	Sequence 3, Appli	108	20	100.0	20	45	US-10-080-979-22	Sequence 22, Appli
36	20	100.0	20	4	US-07-852-852-2	Sequence 4, Appli	109	20	100.0	20	46	US-10-103-906-3	Sequence 3, Appli
37	20	100.0	20	6	US-08-117-363B-22	Sequence 22, Appli	110	20	100.0	20	46	US-10-123-435-1	Sequence 1, Appli
38	20	100.0	20	8	US-08-302-672-2	Sequence 2, Appli	111	20	100.0	20	46	US-10-142-566-42	Sequence 42, Appli
39	20	100.0	20	9	US-08-464-953A-22	Sequence 22, Appli	112	20	100.0	20	49	US-10-262-318-3	Sequence 3, Appli
40	20	100.0	20	9	US-08-464-953B-22	Sequence 2, Appli	113	20	100.0	20	49	US-10-290-545-23	Sequence 23, Appli
41	20	100.0	20	9	US-08-471-967A-8	Sequence 8, Appli	114	20	100.0	20	49	US-10-290-587-4	Sequence 4, Appli
42	20	100.0	20	9	US-08-478-178-2	Sequence 2, Appli	115	20	100.0	20	49	US-10-318-628-4	Sequence 4, Appli
43	20	100.0	20	9	US-08-481-666-2	Sequence 2, Appli	116	20	100.0	20	50	US-10-318-628-13	Sequence 13, Appli
44	20	100.0	20	9	US-08-481-672-2	Sequence 2, Appli	117	20	100.0	20	50	US-10-318-628-27	Sequence 27, Appli
45	20	100.0	20	10	US-08-578-615-2	Sequence 2, Appli	118	20	100.0	20	50	US-10-318-628-35	Sequence 35, Appli
46	20	100.0	20	11	US-08-612-787-2	Sequence 2, Appli	119	20	100.0	20	50	US-10-318-628-42	Sequence 42, Appli
47	20	100.0	20	13	US-08-847-151-3	Sequence 150, App	120	20	100.0	20	50	US-10-337-004-5	Sequence 5, Appli
48	20	100.0	20	14	US-08-923-771B-150	Sequence 13, App	121	20	100.0	20	50	US-10-337-004-6	Sequence 6, Appli
49	20	100.0	20	15	US-09-078-955-13	Sequence 38, App	122	20	100.0	20	50	US-10-348-485-2	Sequence 2, Appli
50	20	100.0	20	16	US-09-108-673A-38	Sequence 4, Appli	123	20	100.0	20	51	US-10-365-623-14	Sequence 14, Appli
51	20	100.0	20	16	US-09-144-883B-4	Sequence 4, Appli	124	20	100.0	20	53	US-10-444-445-4	Sequence 4, Appli
52	20	100.0	20	16	US-09-144-922-150	Sequence 150, App	125	20	100.0	20	53	US-09-396-196F-13915	Sequence 13915, A
53	20	100.0	20	17	US-09-249-247-217	Sequence 4, Appli	126	20	100.0	20	25	US-09-396-196G-13916	Sequence 13916, A
54	20	100.0	20	18	US-09-256-515A-4	Sequence 4, Appli	127	20	100.0	20	25	US-09-396-196G-13915	Sequence 13915, A
55	20	100.0	20	18	US-09-256-515B-4	Sequence 4, Appli	128	20	100.0	20	25	US-09-396-196G-13916	Sequence 13916, A
56	20	100.0	20	19	US-09-306-278A-4	Sequence 3, Appli	129	20	100.0	20	25	US-09-396-196G-13916	Sequence 13916, A
57	20	100.0	20	19	US-09-315-292-3	Sequence 3, Appli	130	19	95.0	19	1	PCT-US98-17988-19	Sequence 19, Appli
58	20	100.0	20	19	US-09-315-292A-3	Sequence 3, Appli	131	19	95.0	19	2	PCT-US99-17988-19	Sequence 19, Appli
59	20	100.0	20	19	US-09-315-294-6	Sequence 6, Appli	132	19	95.0	19	20	US-09-370-541-19	Sequence 19, Appli
60	20	100.0	20	19	US-09-315-298-49	Sequence 49, Appli	133	19	95.0	19	31	US-09-708-224-19	Sequence 21, Appli
61	20	100.0	20	19	US-09-315-298-57	Sequence 57, Appli	134	19	95.0	19	31	US-09-708-224-21	Sequence 19, Appli
62	20	100.0	20	19	US-09-315-298-58	Sequence 58, Appli	135	19	95.0	19	50	US-10-318-628-19	Sequence 21, Appli
63	20	100.0	20	19	US-09-315-298C-49	Sequence 49, Appli	136	19	95.0	19	50	US-10-318-628-21	Sequence 5, Appli
64	20	100.0	20	19	US-09-315-299-3	Sequence 3, Appli	137	18	90.0	18	9	US-08-465-866B-5	Sequence 52, Appli
65	20	100.0	20	19	US-09-315-299A-3	Sequence 3, Appli	138	18	90.0	18	9	US-08-478-178-52	Sequence 52, Appli
66	20	100.0	20	19	US-09-315-581-3	Sequence 3, Appli	139	18	90.0	18	9	US-08-481-072-52	Sequence 52, Appli
67	20	100.0	20	19	US-09-315-581B-3	Sequence 3, Appli	140	18	90.0	18	10	US-08-578-615-52	Sequence 52, Appli
68	20	100.0	20	19	US-09-315-581C-3	Sequence 3, Appli	141	18	90.0	18	10	US-09-996-263-5	Sequence 5, Appli
69	20	100.0	20	19	US-09-315-581C-3	Sequence 3, Appli	142	18	90.0	18	43	US-10-348-485-52	Sequence 52, Appli
70	20	100.0	20	19	US-09-315-581C-14	Sequence 14, Appli	143	18	90.0	18	51	US-10-352-586-5	Sequence 5, Appli
71	20	100.0	20	19	US-09-315-581C-15	Sequence 15, Appli	144	18	90.0	18	25	US-09-396-196F-13927	Sequence 13927, A
72	20	100.0	20	19	US-09-334-130-6	Sequence 6, Appli	145	18	90.0	18	25	US-09-396-196G-13927	Sequence 6, Appli
73	20	100.0	20	19	US-09-348-106-4	Sequence 4, Appli	146	18	90.0	18	17	US-08-465-866B-6	Sequence 53, Appli
74	20	100.0	20	19	US-09-438-989-3	Sequence 3, Appli	147	17	85.0	17	9	US-08-478-178-53	Sequence 53, Appli
75	20	100.0	20	21	US-09-504-653A-19	Sequence 19, Appli	148	17	85.0	17	9	US-08-481-066-53	Sequence 53, Appli
76	20	100.0	20	22	US-09-504-653A-20	Sequence 20, Appli	149	17	85.0	17	9	US-08-481-072-53	Sequence 53, Appli
77	20	100.0	20	22	US-09-504-653A-20	Sequence 20, Appli	150	17	85.0	17	9	US-08-481-072-53	Sequence 53, Appli

151	17	85.0	17	10	US-08-578-615-53	Sequence 53, Appl	224	13.8	69.0	25	97	US-60-427-808-37913	Sequence 37913, A
152	17	85.0	17	21	US-09-498-824A-2999	Sequence 2999, Ap	225	13.8	69.0	25	97	US-60-427-808-110854	Sequence 110854, A
153	17	85.0	17	21	US-09-498-824A-3000	Sequence 3000, Ap	226	13.8	69.0	25	97	US-60-427-808-489138	Sequence 489138, A
154	17	85.0	17	21	US-09-498-824A-3001	Sequence 3001, Ap	227	13.8	69.0	25	97	US-60-427-808-549040	Sequence 549040, A
155	17	85.0	17	23	US-09-532-537B-835	Sequence 835, App	228	13.8	69.0	25	97	US-60-427-808-572713	Sequence 572713, A
156	17	85.0	17	43	US-09-996-263-6	Sequence 6, Appl	229	13.8	69.0	25	97	US-60-427-808-635348	Sequence 635348, A
157	17	85.0	17	50	US-10-348-485-53	Sequence 53, Appl	230	13.8	69.0	25	97	US-60-427-808-689514	Sequence 689514, A
158	17	85.0	17	51	US-10-352-586-6	Sequence 6, Appl	231	13.8	69.0	25	97	US-60-427-808-691286	Sequence 691286, A
159	16	80.0	17	23	US-09-532-537B-298	Sequence 6, Appl	232	13.8	69.0	25	97	US-60-427-808-851061	Sequence 851061, A
160	16	80.0	17	23	US-09-532-537B-611	Sequence 611, App	233	13.8	69.0	25	97	US-60-427-836-46281	Sequence 46281, A
161	16	80.0	17	23	US-10-142-566-38	Sequence 38, Appl	234	13.8	69.0	25	97	US-60-427-836-463441	Sequence 463441, A
162	15.4	77.0	25	51	US-10-355-577-957394	Sequence 957394, A	235	13.8	69.0	25	97	US-60-427-836-563045	Sequence 563045, A
163	15.4	77.0	25	90	US-60-353-987-957394	Sequence 957394, A	236	13.8	69.0	25	97	US-10-316-956-275	Sequence 275, App
164	15.4	77.0	25	97	US-60-427-808-549041	Sequence 549041, A	237	13.6	68.0	25	41	US-09-954-427-61211	Sequence 61211, A
165	15.2	76.0	25	97	US-60-427-808-323222	Sequence 323222, A	238	13.6	68.0	25	41	US-09-956-584-518720	Sequence 518720, A
166	15.2	76.0	25	97	US-60-427-836-137615	Sequence 137615, A	239	13.6	68.0	25	41	US-09-956-584-518720	Sequence 111814, A
167	15	75.0	17	21	US-09-498-824A-2998	Sequence 2998, Ap	240	13.6	68.0	25	45	US-10-098-263B-11814	Sequence 124042, A
168	15	75.0	37	10	US-08-578-615-108	Sequence 108, App	241	13.6	68.0	25	77	US-60-232-638-124042	Sequence 61211, A
169	14.8	74.0	25	97	US-60-427-808-552211	Sequence 552211, A	242	13.6	68.0	25	77	US-60-233-166-61211	Sequence 486666, A
170	14.4	72.0	25	97	US-60-427-808-552211	Sequence 552211, A	243	13.6	68.0	25	77	US-60-234-017-486666	Sequence 323223, A
171	14.4	72.0	25	97	US-60-437-836-158864	Sequence 158864, A	244	13.6	68.0	25	97	US-60-427-808-324894	Sequence 324894, A
172	14.4	72.0	25	97	US-60-427-836-326213	Sequence 326213, A	245	13.6	68.0	25	97	US-60-427-808-324895	Sequence 324895, A
173	14.4	72.0	25	97	US-60-427-836-540875	Sequence 540875, A	246	13.6	68.0	25	97	US-60-427-808-324895	Sequence 324895, A
174	14.2	71.0	25	49	US-10-266-090-51463	Sequence 51463, A	247	13.6	68.0	25	97	US-60-427-808-897588	Sequence 897588, A
175	14.2	71.0	25	41	US-09-953-570-97884	Sequence 97884, A	248	13.6	68.0	25	97	US-60-427-836-65590	Sequence 65590, A
176	14.2	71.0	25	41	US-09-953-570-97892	Sequence 97892, A	249	13.6	68.0	25	97	US-60-427-836-65590	Sequence 137616, A
177													

297	13.2	66.0	21	32	US-09-724-524-28	Sequence 28, Appl	C 370	13	65.0	25	51	US-10-355-577-359609	Sequence 359609,
298	13.2	66.0	21	42	US-09-966-147-28	Sequence 28, Appl	C 371	13	65.0	25	90	US-09-353-987-121334	Sequence 121334,
299	13.2	66.0	21	47	US-10-172-526-24	Sequence 24, Appl	C 372	13	65.0	25	90	US-60-353-987-359609	Sequence 359609,
300	13.2	66.0	21	51	US-10-374-469-28	Sequence 24, Appl	C 373	13	65.0	25	97	US-60-427-808-273754	Sequence 273754,
301	13.2	66.0	25	20	US-09-396-196F-89426	Sequence 89426, A	C 374	13	65.0	25	97	US-60-427-836-127198	Sequence 127198,
302	13.2	66.0	25	20	US-09-396-196F-89427	Sequence 89427, A	C 375	13	65.0	25	97	US-60-427-836-489536	Sequence 449536,
303	13.2	66.0	25	20	US-09-396-196F-92770	Sequence 92770, A	C 376	13	65.0	31	34	US-09-801-274-1799	Sequence 1799, Ap
304	13.2	66.0	25	20	US-09-396-196F-92771	Sequence 92771, A	C 377	12.8	64.0	31	34	US-10-351-951-99	Sequence 99, Appl
305	13.2	66.0	25	20	US-09-396-196F-89426	Sequence 89426, A	C 378	12.8	64.0	25	20	US-09-396-196F-7450	Sequence 7450, Ap
306	13.2	66.0	25	20	US-09-396-196F-89427	Sequence 89427, A	C 379	12.8	64.0	25	20	US-09-396-196F-40666	Sequence 40666, A
307	13.2	66.0	25	20	US-09-396-196F-92770	Sequence 92770, A	C 380	12.8	64.0	25	20	US-09-396-196F-40666	Sequence 40666, A
308	13.2	66.0	25	20	US-09-396-196F-92771	Sequence 92771, A	C 381	12.8	64.0	25	20	US-09-396-196F-40666	Sequence 139703,
309	13.2	66.0	25	29	US-09-660-222-88816	Sequence 88816, A	C 382	12.8	64.0	25	29	US-09-660-222-139703	Sequence 139703,
310	13.2	66.0	25	41	US-09-953-115-20718	Sequence 97381, A	C 383	12.8	64.0	25	41	US-09-954-427-24081	Sequence 24081, A
311	13.2	66.0	25	41	US-09-953-570-43288	Sequence 43288, A	C 384	12.8	64.0	25	41	US-09-954-427-117679	Sequence 117679,
312	13.2	66.0	25	41	US-09-954-427-121835	Sequence 43288, A	C 385	12.8	64.0	25	41	US-09-954-427-117679	Sequence 138810,
313	13.2	66.0	25	41	US-09-954-427-220203	Sequence 121835,	C 386	12.8	64.0	25	41	US-09-954-427-117679	Sequence 138810,
314	13.2	66.0	25	41	US-09-956-584-244952	Sequence 220203,	C 387	12.8	64.0	25	41	US-09-956-584-1302	Sequence 1302, Ap
315	13.2	66.0	25	41	US-09-956-584-244952	Sequence 244952,	C 388	12.8	64.0	25	41	US-09-956-584-1302	Sequence 1302, Ap
316	13.2	66.0	25	45	US-10-098-577-487359	Sequence 51446, A	C 389	12.8	64.0	25	41	US-09-956-584-68485	Sequence 68485, A
317	13.2	66.0	25	51	US-10-355-577-776331	Sequence 248342,	C 390	12.8	64.0	25	48	US-09-956-584-99262	Sequence 99262, A
318	13.2	66.0	25	51	US-10-355-577-776331	Sequence 776331,	C 391	12.8	64.0	25	51	US-10-355-577-238476	Sequence 238476,
319	13.2	66.0	25	51	US-10-355-577-776331	Sequence 776331,	C 392	12.8	64.0	25	51	US-10-355-577-343798	Sequence 343798,
320	13.2	66.0	25	51	US-10-355-577-776331	Sequence 776331,	C 393	12.8	64.0	25	51	US-10-355-577-407663	Sequence 407663,
321	13.2	66.0	25	51	US-10-355-577-776331	Sequence 776331,	C 394	12.8	64.0	25	51	US-10-355-577-41686	Sequence 441686,
322	13.2	66.0	25	51	US-10-355-577-776331	Sequence 776331,	C 395	12.8	64.0	25	51	US-10-355-577-507318	Sequence 507318,

[illegible]

c 735	12.2	61.0	25	20	US-09-396-196G-124093	Sequence 124093, A	808	12.2	61.0	25	51	US-10-355-577-467758	Sequence 467758, A
736	12.2	61.0	25	29	US-09-660-222-17736	Sequence 17736, A	809	12.2	61.0	25	51	US-10-355-577-472388	Sequence 472388, A
737	12.2	61.0	25	29	US-09-660-222-27160	Sequence 27160, A	810	12.2	61.0	25	51	US-10-355-577-482675	Sequence 482675, A
738	12.2	61.0	25	29	US-09-660-222-27165	Sequence 27165, A	c 811	12.2	61.0	25	51	US-10-355-577-523655	Sequence 523655, A
739	12.2	61.0	25	29	US-09-660-222-40502	Sequence 40502, A	812	12.2	61.0	25	51	US-10-355-577-533123	Sequence 533123, A
740	12.2	61.0	25	29	US-09-660-222-61402	Sequence 61402, A	813	12.2	61.0	25	51	US-10-355-577-533124	Sequence 533124, A
c 741	12.2	61.0	25	29	US-09-660-222-78808	Sequence 78808, A	c 814	12.2	61.0	25	51	US-10-355-577-558053	Sequence 558053, A
c 742	12.2	61.0	25	29	US-09-660-222-78809	Sequence 78809, A	c 815	12.2	61.0	25	51	US-10-355-577-631706	Sequence 631706, A
743	12.2	61.0	25	29	US-09-660-222-105849	Sequence 105849, A	816	12.2	61.0	25	51	US-10-355-577-644035	Sequence 644035, A
744	12.2	61.0	25	29	US-09-660-222-105851	Sequence 105851, A	c 817	12.2	61.0	25	51	US-10-355-577-740558	Sequence 740558, A
745	12.2	61.0	25	29	US-09-660-222-118597	Sequence 118597, A	818	12.2	61.0	25	51	US-10-355-577-785706	Sequence 785706, A
c 746	12.2	61.0	25	29	US-09-672-665-28	Sequence 28, Appl	819	12.2	61.0	25	51	US-10-355-577-877044	Sequence 877044, A
c 747	12.2	61.0	25	34	US-09-822-263-28	Sequence 28, Appl	820	12.2	61.0	25	51	US-10-355-577-877044	Sequence 877044, A
c 748	12.2	61.0	25	37	US-09-882-263-28	Sequence 28, Appl	821	12.2	61.0	25	51	US-10-355-577-947532	Sequence 947532, A
c 749	12.2	61.0	25	41	US-09-953-115-280272	Sequence 28272, A	822	12.2	61.0	25	51	US-10-355-577-954772	Sequence 954772, A
750	12.2	61.0	25	41	US-09-953-115-46077	Sequence 46077, A	823	12.2	61.0	25	51	US-10-355-577-987841	Sequence 987841, A
751	12.2	61.0	25	41	US-09-954-427-35932	Sequence 35932, A	824	12.2	61.0	25	77	US-60-232-638-46077	Sequence 35932, A
c 752	12.2	61.0	25	41	US-09-954-427-37016	Sequence 37016, A	825	12.2	61.0	25	77	US-60-233-166-35932	Sequence 37016, A
753	12.2	61.0	25	41	US-09-954-427-131957	Sequence 131957, A	c 826	12.2	61.0	25	77	US-60-233-166-37016	Sequence 131957, A
754	12.2	61.0	25	41	US-09-954-427-141455	Sequence 141455, A	827	12.2	61.0	25	77	US-60-233-166-131957	Sequence 141455, A
755	12.2	61.0	25	41	US-09-954-427-141463	Sequence 141463, A	828	12.2	61.0	25	77	US-60-233-166-141455	Sequence 141463, A
756	12.2	61.0	25	41	US-09-954-427-164868	Sequence 164868, A	829	12.2	61.0	25	77	US-60-233-166-141463	Sequence 164868, A
757	12.2	61.0	25	41	US-09-954-427-172582	Sequence 172582, A	830	12.2	61.0	25	77	US-60-233-166-164868	Sequence 172582, A
c 758	12.2	61.0	25	41	US-09-954-427-199590	Sequence 199590, A	831	12.2	61.0	25	77	US-60-233-166-172582	Sequence 199590, A
c 759	12.2	61.0	25	41	US-09-954-427-355558	Sequence 355558, A	832	12.2	61.0	25	77	US-60-233-166-199590	Sequence 355558, A
c 760	12.2	61.0	25	41	US-09-954-427-364899	Sequence 364899, A	833	12.2	61.0	25	77	US-60-233-166-364899	Sequence 364899, A
761	12.2	61.0	25	41	US-09-954-427-385320	Sequence 385320, A	834	12.2	61.0	25	77	US-60-233-166-385320	Sequence 385320, A
c 762	12.2	61.0	25	41	US-09-954-429A-9916	Sequence 9916, Ap	835	12.2	61.0	25	77	US-60-233-357-17192	Sequence 17192, A
c 763	12.2	61.0	25	41	US-09-954-445A-20937	Sequence 20937, A	836	12.2	61.0	25	77	US-60-233-620-20937	Sequence 20937, A
c 764	12.2	61.0	25	41	US-09-954-445A-54398	Sequence 54398, A	837	12.2	61.0	25	77	US-60-233-620-54398	Sequence 54398, A
c 765	12.2	61.0	25	41	US-09-954-445A-98755	Sequence 98755, A	838	12.2	61.0	25	77	US-60-233-620-98755	Sequence 98755, A
766	12.2	61.0	25	41	US-09-954-445A-116103	Sequence 116103, A	839	12.2	61.0	25	77	US-60-233-620-116103	Sequence 116103, A
767	12.2	61.0	25	41	US-09-956-584-35797	Sequence 35797, A	840	12.2	61.0	25	77	US-60-234-017-22897	Sequence 22897, A
768	12.2	61.0	25	41	US-09-956-584-35800	Sequence 35800, A	841	12.2	61.0	25	77	US-60-234-017-22910	Sequence 22910, A
769	12.2	61.0	25	41	US-09-956-584-35803	Sequence 35803, A	842	12.2	61.0	25	77	US-60-234-017-22912	Sequence 22912, A
770	12.2	61.0	25	41	US-09-956-584-46575	Sequence 46575, A	843	12.2	61.0	25	77	US-60-234-017-52690	Sequence 52690, A
c 771	12.2	61.0	25	41	US-09-956-584-46577	Sequence 46577, A	844	12.2	61.0	25	77	US-60-234-017-52692	Sequence 52692, A
c 772	12.2	61.0	25	41	US-09-956-584-127619	Sequence 127619, A	845	12.2	61.0	25	77	US-60-234-017-67327	Sequence 67327, A
c 773	12.2	61.0	25	41	US-09-956-584-127624	Sequence 127624, A	846	12.2	61.0	25	77	US-60-234-017-79038	Sequence 79038, A
c 774	12.2	61.0	25	41	US-09-956-584-128126	Sequence 128126, A	c 847	12.2	61.0	25	77	US-60-234-017-79038	Sequence 79041, A
c 775	12.2	61.0	25	41	US-09-956-584-215943	Sequence 215943, A	848	12.2	61.0	25	77	US-60-234-017-79041	Sequence 215976, A
c 776	12.2	61.0	25	41	US-09-956-584-264852	Sequence 264852, A	849	12.2	61.0	25	77	US-60-234-017-291831	Sequence 291831, A
c 777	12.2	61.0	25	41	US-09-956-584-297952	Sequence 297952, A	850	12.2	61.0	25	77	US-60-234-017-296641	Sequence 296641, A
c 778	12.2	61.0	25	41	US-09-956-584-353410	Sequence 353410, A	851	12.2	61.0	25	77	US-60-234-017-343675	Sequence 343675, A
c 779	12.2	61.0	25	41	US-09-956-584-439102	Sequence 439102, A	852	12.2	61.0	25	77	US-60-234-017-412149	Sequence 412149, A
c 780	12.2	61.0	25	41	US-09-956-584-439110	Sequence 439110, A	853	12.2	61.0	25	77	US-60-234-017-412165	Sequence 412165, A
781	12.2	61.0	25	41	US-09-956-584-518724	Sequence 518724, A	c 854	12.2	61.0	25	77	US-60-234-017-486662	Sequence 486662, A
c 782	12.2	61.0	25	41	US-09-956-604-15694	Sequence 15694, A	855	12.2	61.0	25	77	US-60-234-017-486662	Sequence 1062, Ap
c 783	12.2	61.0	25	41	US-09-956-604-34176	Sequence 34176, A	856	12.2	61.0	25	77	US-60-234-049-1084	Sequence 1084, Ap
c 784	12.2	61.0	25	41	US-09-956-604-34346	Sequence 34346, A	c 857	12.2	61.0	25	77	US-60-234-049-1086	Sequence 1086, Ap
c 785	12.2	61.0	25	41	US-09-956-604-54348	Sequence 54348, A	c 858	12.2	61.0	25	77	US-60-234-049-47677	Sequence 47677, A
c 786	12.2	61.0	25	41	US-09-956-604A-15694	Sequence 15694, A	c 859	12.2	61.0	25	77	US-60-234-049-47677	Sequence 36877, A
c 787	12.2	61.0	25	41	US-09-956-604A-54176	Sequence 54176, A	860	12.2	61.0	25	90	US-60-353-987-36878	Sequence 36878, A
c 788	12.2	61.0	25	41	US-09-956-604A-54346	Sequence 54346, A	861	12.2	61.0	25	90	US-60-353-987-36878	Sequence 86014, A
c 789	12.2	61.0	25	41	US-09-956-604A-54348	Sequence 54348, A	862	12.2	61.0	25	90	US-60-353-987-86014	Sequence 136846, A
c 790	12.2	61.0	25	41	US-09-956-604B-15694	Sequence 15694, A	863	12.2	61.0	25	90	US-60-353-987-194808	Sequence 194808, A
c 791	12.2	61.0	25	41	US-09-956-604B-54176	Sequence 54176, A	864	12.2	61.0	25	90	US-60-353-987-283709	Sequence 283709, A
c 792	12.2	61.0	25	41	US-09-956-604B-54346	Sequence 54346, A	865	12.2	61.0	25	90	US-60-353-987-283709	Sequence 328632, A
c 793	12.2	61.0	25	41	US-09-956-604B-54348	Sequence 54348, A	866	12.2	61.0	25	90	US-60-353-987-328632	Sequence 328632, A
794	12.2	61.0	25	45	US-10-098-263B-47667	Sequence 47667, A	867	12.2	61.0	25	90	US-60-353-987-352521	Sequence 352521, A
795	12.2	61.0	25	45	US-10-098-263B-51564	Sequence 51564, A	c 868	12.2	61.0	25	90	US-60-353-987-399478	Sequence 399478, A
796	12.2	61.0	25	45	US-10-098-263B-83394	Sequence 83394, A	c 869	12.2	61.0	25	90	US-60-353-987-467758	Sequence 467758, A
797	12.2	61.0	25	45	US-10-098-263B-125841	Sequence 125841, A	870	12.2	61.0	25	90	US-60-353-987-472388	Sequence 472388, A
798	12.2	61.0	25	51	US-10-355-577-36877	Sequence 36877, A	871	12.2	61.0	25	90	US-60-353-987-482675	Sequence 482675, A
799	12.2	61.0	25	51	US-10-355-577-86014	Sequence 86014, A	872	12.2	61.0	25	90	US-60-353-987-523655	Sequence 523655, A
800	12.2	61.0	25	51	US-10-355-577-136846	Sequence 136846, A	873	12.2	61.0	25	90	US-60-353-987-533123	Sequence 533123, A
801	12.2	61.0	25	51	US-10-355-577-194808	Sequence 194808, A	874	12.2	61.0	25	90	US-60-353-987-533124	Sequence 533124, A
802	12.2	61.0	25	51	US-10-355-577-209706	Sequence 209706, A	875	12.2	61.0	25	90	US-60-353-987-558053	Sequence 558053, A
803	12.2	61.0	25	51	US-10-355-577-283709	Sequence 283709, A	876	12.2	61.0	25	90	US-60-353-987-631706	Sequence 631706, A
c 804	12.2	61.0	25	51	US-10-355-577-328632	Sequence 328632, A	c 877	12.2	61.0	25	90	US-60-353-987-644035	Sequence 644035, A
c 805	12.2	61.0	25	51	US-10-355-577-32521	Sequence 32521, A	878	12.2	61.0	25	90	US-60-353-987-740558	Sequence 740558, A
c 806	12.2	61.0	25	51	US-10-355-577-399478	Sequence 399478, A	c 879	12.2	61.0	25	90	US-60-353-987-785706	Sequence 785706, A
c 807	12.2	61.0	25	51			880	12.2	61.0	25	90		

881	12.2	61.0	25	90	US-60-353-987-849172	Sequence 849172,	954	12.2	61.0	25	97	US-60-427-836-86680	Sequence 86680, A
882	12.2	61.0	25	90	US-60-353-987-877044	Sequence 877044,	c 955	12.2	61.0	25	97	US-60-427-836-867111	Sequence 86711, A
883	12.2	61.0	25	90	US-60-353-987-947532	Sequence 947532,	c 956	12.2	61.0	25	97	US-60-427-836-133675	Sequence 133675, A
884	12.2	61.0	25	90	US-60-353-987-954772	Sequence 954772,	c 957	12.2	61.0	25	97	US-60-427-836-152282	Sequence 152282, A
885	12.2	61.0	25	90	US-60-353-987-987841	Sequence 987841,	c 958	12.2	61.0	25	97	US-60-427-836-201792	Sequence 201792, A
886	12.2	61.0	25	96	US-60-417-190-39552	Sequence 39552, A	c 960	12.2	61.0	25	97	US-60-427-836-207734	Sequence 207734, A
887	12.2	61.0	25	96	US-60-417-190-39557	Sequence 39557, A	c 961	12.2	61.0	25	97	US-60-427-836-21975	Sequence 21975, A
888	12.2	61.0	25	96	US-60-417-190-58339	Sequence 58339, A	c 962	12.2	61.0	25	97	US-60-427-836-232912	Sequence 232912, A
889	12.2	61.0	25	96	US-60-417-190-58340	Sequence 58340, A	c 963	12.2	61.0	25	97	US-60-427-836-239170	Sequence 239170, A
890	12.2	61.0	25	96	US-60-417-190-58341	Sequence 58341, A	c 964	12.2	61.0	25	97	US-60-427-836-239171	Sequence 239171, A
891	12.2	61.0	25	97	US-60-427-808-1927	Sequence 1927, A	c 965	12.2	61.0	25	97	US-60-427-836-249329	Sequence 249329, A
892	12.2	61.0	25	97	US-60-427-808-1927	Sequence 1927, A	c 966	12.2	61.0	25	97	US-60-427-836-259692	Sequence 259692, A
893	12.2	61.0	25	97	US-60-427-808-27731	Sequence 27731, A	c 967	12.2	61.0	25	97	US-60-427-836-263968	Sequence 263968, A
894	12.2	61.0	25	97	US-60-427-808-36967	Sequence 36967, A	c 968	12.2	61.0	25	97	US-60-427-836-286459	Sequence 286459, A
895	12.2	61.0	25	97	US-60-427-808-37914	Sequence 37914, A	c 969	12.2	61.0	25	97	US-60-427-836-290883	Sequence 290883, A
896	12.2	61.0	25	97	US-60-427-808-77985	Sequence 77985, A	c 970	12.2	61.0	25	97	US-60-427-836-363440	Sequence 363440, A
897	12.2	61.0	25	97	US-60-427-808-106497	Sequence 106497,	c 971	12.2	61.0	25	97	US-60-427-836-375891	Sequence 375891, A
898	12.2	61.0	25	97	US-60-427-808-110853	Sequence 110853,	c 972	12.2	61.0	25	97	US-60-427-836-432764	Sequence 432764, A
899	12.2	61.0	25	97	US-60-427-808-111940	Sequence 111940,	c 973	12.2	61.0	25	97	US-60-427-836-503231	Sequence 503231, A
900	12.2	61.0	25	97	US-60-427-808-164103	Sequence 164103,	c 974	12.2	61.0	25	97	US-60-427-836-520938	Sequence 520938, A
901	12.2	61.0	25	97	US-60-427-808-196425	Sequence 196425,	c 975	12.2	61.0	25	97	US-60-427-836-537720	Sequence 537720, A
902	12.2	61.0	25	97	US-60-427-808-206903	Sequence 206903,	c 976	12.2	61.0	25	97	US-60-427-836-554207	Sequence 554207, A
903	12.2	61.0	25	97	US-60-427-808-232747	Sequence 232747,	c 977	12.2	61.0	25	97	US-60-427-836-563044	Sequence 563044, A
904	12.2	61.0	25	97	US-60-427-808-233102	Sequence 233102,	c 978	12.2	61.0	25	97	US-60-427-836-608778	Sequence 608778, A
905	12.2	61.0	25	97	US-60-427-808-248019	Sequence 248019,	c 979	12.2	61.0	25	97	US-60-427-836-634482	Sequence 634482, A
906	12.2	61.0	25	97	US-60-427-808-252461	Sequence 252461,	c 980	12.2	61.0	25	101	US-60-469-545-94873	Sequence 94873, A
907	12.2	61.0	25	97	US-60-427-808-301216	Sequence 301216,	c 981	12.2	61.0	25	101	US-60-469-545-95362	Sequence 95362, A
908	12.2	61.0	25	97	US-60-427-808-303809	Sequence 303809,	c 982	12.2	61.0	25	101	US-60-469-545-95367	Sequence 95367, A
909	12.2	61.0	25	97	US-60-427-808-347622	Sequence 347622,	c 983	12.2	61.0	25	101	US-60-469-545-95367	Sequence 116841, A
910	12.2	61.0	25	97	US-60-427-808-347623	Sequence 347623,	c 984	12.2	61.0	25	101	US-60-469-545-116841	Sequence 121336, A
911	12.2	61.0	25	97	US-60-427-808-349787	Sequence 349787,	c 985	12.2	61.0	25	101	US-60-469-545-121336	Sequence 142810, A
912	12.2	61.0	25	97	US-60-427-808-352554	Sequence 352554,	c 986	12.2	61.0	25	101	US-60-469-545-142810	Sequence 142810, A
913	12.2	61.0	25	97	US-60-427-808-352555	Sequence 352555,	c 987	12.2	61.0	25	101	US-60-469-545-142815	Sequence 143304, A
914	12.2	61.0	25	97	US-60-427-808-368866	Sequence 368866,	c 988	12.2	61.0	25	101	US-60-469-545-143304	Sequence 20411, A
915	12.2	61.0	25	97	US-60-427-808-395760	Sequence 395760,	c 989	12.2	61.0	25	102	US-60-470-475-20411	Sequence 20411, A
916	12.2	61.0	25	97	US-60-427-808-489139	Sequence 489139,	c 990	12.2	61.0	25	102	US-60-470-475-25069	Sequence 25069, A
917	12.2	61.0	25	97	US-60-427-808-503865	Sequence 503865,	c 991	12.2	61.0	25	102	US-60-470-475-80659	Sequence 80659, A
918	12.2	61.0	25	97	US-60-427-808-526135	Sequence 526135,	c 992	12.2	61.0	25	102	US-60-475-871-107838	Sequence 107838, A
919	12.2	61.0	25	97	US-60-427-808-530076	Sequence 530076,	c 993	12.2	61.0	25	35	US-09-830-902-6	Sequence 6, Appl
920	12.2	61.0	25	97	US-60-427-808-547482	Sequence 547482,	c 994	12.2	61.0	25	25	US-09-591-500-36	Sequence 36, Appl
921	12.2	61.0	25	97	US-60-427-808-572711	Sequence 572711,	c 995	12.2	61.0	25	25	US-09-591-500A-42	Sequence 42, Appl
922	12.2	61.0	25	97	US-60-427-808-593350	Sequence 593350,	c 996	12.2	61.0	25	25	US-09-591-500A-36	Sequence 36, Appl
923	12.2	61.0	25	97	US-60-427-808-630406	Sequence 630406,	c 997	12.2	61.0	30	1	PCT-US02-25940-16048	Sequence 16048, A
924	12.2	61.0	25	97	US-60-427-808-635349	Sequence 635349,	c 998	12.2	61.0	30	48	US-10-227-563-16048	Sequence 16048, A
925	12.2	61.0	25	97	US-60-427-808-635663	Sequence 635663,	c 999	12.2	61.0	30	51	US-10-367-893-16048	Sequence 1391, Ap
926	12.2	61.0	25	97	US-60-427-808-689515	Sequence 689515,	c 1000	12.2	61.0	31	32	US-09-735-271-1391	Sequence 101, App
927	12.2	61.0	25	97	US-60-427-808-691287	Sequence 691287,							
928	12.2	61.0	25	97	US-60-427-808-745602	Sequence 745602,							
929	12.2	61.0	25	97	US-60-427-808-746095	Sequence 746095,							
930	12.2	61.0	25	97	US-60-427-808-750050	Sequence 750050,							
931	12.2	61.0	25	97	US-60-427-808-754842	Sequence 754842,							
932	12.2	61.0	25	97	US-60-427-808-757389	Sequence 757389,							
933	12.2	61.0	25	97	US-60-427-808-796207	Sequence 796207,							
934	12.2	61.0	25	97	US-60-427-808-830099	Sequence 830099,							
935	12.2	61.0	25	97	US-60-427-808-834294	Sequence 834294,							
936	12.2	61.0	25	97	US-60-427-808-851062	Sequence 851062,							
937	12.2	61.0	25	97	US-60-427-808-851062	Sequence 851062,							
938	12.2	61.0	25	97	US-60-427-808-928219	Sequence 928219,							
939	12.2	61.0	25	97	US-60-427-808-928219	Sequence 928219,							
940	12.2	61.0	25	97	US-60-427-808-946603	Sequence 946603,							
941	12.2	61.0	25	97	US-60-427-808-946603	Sequence 946603,							
942	12.2	61.0	25	97	US-60-427-836-4528	Sequence 4528, Ap							
943	12.2	61.0	25	97	US-60-427-836-15382	Sequence 15382, A							
944	12.2	61.0	25	97	US-60-427-836-18067	Sequence 18067, A							
945	12.2	61.0	25	97	US-60-427-836-18068	Sequence 18068, A							
946	12.2	61.0	25	97	US-60-427-836-26024	Sequence 26024, A							
947	12.2	61.0	25	97	US-60-427-836-28959	Sequence 28959, A							
948	12.2	61.0	25	97	US-60-427-836-46282	Sequence 46282, A							
949	12.2	61.0	25	97	US-60-427-836-59743	Sequence 59743, A							
950	12.2	61.0	25	97	US-60-427-836-64642	Sequence 64642, A							
951	12.2	61.0	25	97	US-60-427-836-73571	Sequence 73571, A							
952	12.2	61.0	25	97	US-60-427-836-77804	Sequence 77804, A							
953	12.2	61.0	25	97	US-60-427-836-85475	Sequence 85475, A							

ALIGNMENTS

RESULT 1
PCT-US00-07003-3
Sequence 3, Application PC/TUS0007003
GENERAL INFORMATION:
APPLICANT: Krotz, Achim H
APPLICANT: Bethany, McElroy M
APPLICANT: Scorzari, Anthony N
TITLE OF INVENTION: Methods for Removing Dimethoxytrityl Groups from
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: ISIS4371
CURRENT APPLICATION NUMBER: PCT/US00/07003
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antisense
OTHER INFORMATION: sequence


```
PCT-US00-07003-3
Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 2
PCT-US00-09473-4
; Sequence 4, Application PC/TUS0009473
; GENERAL INFORMATION:
; APPLICANT: LEAMON, Christopher P.
; TITLE OF INVENTION: FUSOGENIC LIPIDS AND VESICLES
; FILE REFERENCE: 049202/2002
; CURRENT APPLICATION NUMBER: PCT/US00/09473
; CURRENT FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
PCT-US00-09473-4

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 3
PCT-US00-16534-6
; Sequence 6, Application PC/TUS0016534
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ligand-Conjugated Oligomeric Compounds
; FILE REFERENCE: ISIS4389
; CURRENT APPLICATION NUMBER: PCT/US00/16534
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: USSN 09/334,130
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US00-16534-6

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 4
PCT-US00-18415-4
; Sequence 4, Application PC/TUS0018415
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; TITLE OF INVENTION: Oligonucleotides Incorporating Both 2-Aminoadenine and
; FILE REFERENCE: 5-Substituted Pyrimidines
; CURRENT APPLICATION NUMBER: PCT/US00/18415
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/348,106
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US00-18415-4

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 5
PCT-US01-02951-5
; Sequence 5, Application PC/TUS0102951
; GENERAL INFORMATION:
; APPLICANT: Krotz, Achim H
; APPLICANT: Ravikumar, Vasulunga T
; TITLE OF INVENTION: Purification of Oligonucleotides
; FILE REFERENCE: ISIS4656
; CURRENT APPLICATION NUMBER: PCT/US01/02951
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US01-02951-5

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 6
PCT-US01-02951-6
; Sequence 6, Application PC/TUS0102951
; GENERAL INFORMATION:
; APPLICANT: Krotz, Achim H
; APPLICANT: Ravikumar, Vasulunga T
; TITLE OF INVENTION: Purification of Oligonucleotides
; FILE REFERENCE: ISIS4656
; CURRENT APPLICATION NUMBER: PCT/US01/02951
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US01-02951-6
```

Thu Jan 29 10:08:41 2004

us-10-002-884a-5.max.rnps

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US01-02951-6

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 7
PCT-US02-34980-5
; Sequence 5, Application PC/TUS0234980
; GENERAL INFORMATION:
; APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
; TITLE OF INVENTION: PEPTIDES THAT DELIVER ANTISENSE OLIGONUCLEOTIDES WHICH DOWNREGULATE PROTEIN EXPRESSION IN CELLS
; FILE REFERENCE: 0575/63293-pct
; CURRENT APPLICATION NUMBER: PCT/US02/34980
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: us 10/002,884
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: ANTISENSE OLIGONUCLEOTIDE
PCT-US02-34980-5

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 8
PCT-US03-04323-14
; Sequence 14, Application PC/TUS0304323
; GENERAL INFORMATION:
; APPLICANT: MEDBRIDGE, INC. and XIE, Dong
; TITLE OF INVENTION: Protein Carrier System for Therapeutic Oligonucleotides
; FILE REFERENCE: 62219.000004
; CURRENT APPLICATION NUMBER: PCT/US03/04323
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 60/356,053
; PRIOR FILING DATE: 13 February 2002
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide directed against human PKC-alpha
PCT-US03-04323-14

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20
```

```

RESULT 9
PCT-US03-11921-1
; Sequence 1, Application PC/TUS0311921
; GENERAL INFORMATION:
; APPLICANT: Uhler, Michael D.
; TITLE OF INVENTION: Surface Transfection and Expression Procedure
; FILE REFERENCE: UM-06983
; CURRENT APPLICATION NUMBER: PCT/US03/11921
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/245,892
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/305,552
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/960,454
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 10/002,802
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
PCT-US03-11921-1

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 10
PCT-US97-02003-1
; Sequence 1, Application PC/TUS9702003
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Methoxyethoxy Oligonucleotides for Modulation of Protein Kinase C Expression
; TITLE OF INVENTION: of Protein Kinase C Expression
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 720 kb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/02003
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,269
; FILING DATE: February 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISCG-0086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
```

; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 PCT-US97-02003-1

Query Match 100.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 11

PCT-US98-08798-3

; Sequence 3, Application PC/TUS9808798
 ; GENERAL INFORMATION:
 ; APPLICANT: ISIS PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED BIOAVAILABILITY
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19103

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 6.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US98/08798
 ; FILING DATE: Herewith
 ; CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/847,151
 ; FILING DATE: 30-APR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul K. Legard
 ; REGISTRATION NUMBER: 38,534
 ; REFERENCE/DOCKET NUMBER: ISIS-2988
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-568-3100
 ; TELEFAX: 215-568-3439
 ; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 PCT-US98-08798-3

Query Match 100.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 12

PCT-US99-04213-4

; Sequence 4, Application PC/TUS9904213
 ; GENERAL INFORMATION:
 ; APPLICANT: ISIS Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: IMPROVED METHODS FOR SYNTHESIS OF OLIGONUCLEOTIDES
 ; FILE REFERENCE: ISIS3404
 ; CURRENT APPLICATION NUMBER: PCT/US99/04213
 ; CURRENT FILING DATE: 1999-02-26

; EARLIER APPLICATION NUMBER: US 09/032,972
 ; EARLIER FILING DATE: 1998-02-26
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4

; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: antisense
 ; OTHER INFORMATION: oligonucleotide
 PCT-US99-04213-4

Query Match 100.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 13

PCT-US99-11141-3

; Sequence 3, Application PC/TUS9911141
 ; GENERAL INFORMATION:
 ; APPLICANT: ISIS Pharmaceuticals Inc. et al.
 ; TITLE OF INVENTION: Compositions and Methods for the Pulmonary delivery of
 ; TITLE OF INVENTION: Nucleic Acids
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: PCT/US99/11141
 ; CURRENT FILING DATE: 1999-05-20
 ; EARLIER APPLICATION NUMBER: U.S. serial no. 09/083,586
 ; EARLIER FILING DATE: 1998-05-21
 ; NUMBER OF SEQ ID NOS: 10
 ; SEQ ID NO 3

; LENGTH: 20
 ; TYPE: DNA

; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: antisense sequence
 PCT-US99-11141-3

Query Match 100.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 14

PCT-US99-11142-6

; Sequence 6, Application PC/TUS9911142
 ; GENERAL INFORMATION:
 ; APPLICANT: ISIS Pharmaceutical Inc. et al.
 ; TITLE OF INVENTION: Compositions and Methods for Topical Delivery of
 ; TITLE OF INVENTION: Oligonucleotides
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: PCT/US99/11142
 ; CURRENT FILING DATE: 1999-05-20
 ; EARLIER APPLICATION NUMBER: U.S. serial no. 09/082,336
 ; EARLIER FILING DATE: 1998-05-21
 ; NUMBER OF SEQ ID NOS: 12
 ; SEQ ID NO 6

; LENGTH: 20
 ; TYPE: DNA

; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: antisense sequence
 PCT-US99-11142-6

```

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 15
PCT-US99-11214-3
; Sequence 3, Application PC/TUS9911214
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Compositions and Methods for the Pulmonary Delivery of
; TITLE OF INVENTION: Nucleic Acids
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US99/11214
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. Ser. No. 09/083,585
; EARLIER FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US99-11214-3

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 16
PCT-US99-11267-3
; Sequence 3, Application PC/TUS9911267
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Long-Circulating Liposomal Compositions
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US99/11267
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. Serial No. 09/082,365
; EARLIER FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US99-11267-3

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 17
PCT-US99-11394-49
; Sequence 49, Application PC/TUS9911394
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals Inc. et al.
; TITLE OF INVENTION: Compositions and Methods for Non-Parenteral Delivery of
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US99/11394
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. serial no. 09/082,624
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US99-11394-49

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 18
PCT-US99-15960-3
; Sequence 3, Application PC/TUS9915960
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Oligonucleotides Having Site Specific Chiral
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US99/15960
; CURRENT FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 09/115,027
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
PCT-US99-15960-3

Query Match      100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 19
PCT-US00-07003-3
; Sequence 3, Application PC/TUS0007003
; GENERAL INFORMATION:
; APPLICANT: Krotz, Achim H
; APPLICANT: Bethany, McElroy M
; APPLICANT: Scozzari, Anthony N
; TITLE OF INVENTION: Methods for Removing Dimethoxytrityl Groups from
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: ISIS4371
; CURRENT APPLICATION NUMBER: PCT/US00/07003
; CURRENT FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 20

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
PCT-US00-07003-3

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 20
PCT-US00-09473-4
; Sequence 4, Application PC/TUS0009473
; GENERAL INFORMATION:
; APPLICANT: LEAMON, Christopher P.
; TITLE OF INVENTION: FUSOGENIC LIPIDS AND VESICLES
; FILE REFERENCE: 049202/2002
; CURRENT APPLICATION NUMBER: PCT/US00/09473
; CURRENT FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide

PCT-US00-09473-4
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 21
PCT-US00-16534-6
; Sequence 6, Application PC/TUS0016534
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ligand-Conjugated Oligomeric Compounds
; FILE REFERENCE: ISIS4389
; CURRENT APPLICATION NUMBER: PCT/US00/16534
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: USSN 09/334,130
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US00-16534-6

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 22
PCT-US00-18415-4
; Sequence 4, Application PC/TUS0018415
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; TITLE OF INVENTION: Oligonucleotides Incorporating Both 2-Aminoadenine and
; TITLE OF INVENTION: 5-Substituted Pyrimidines
; FILE REFERENCE: ISIS4398
; CURRENT APPLICATION NUMBER: PCT/US00/18415
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/348,106
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US00-18415-4

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 23
PCT-US01-02951-5
; Sequence 5, Application PC/TUS0102951
; GENERAL INFORMATION:
; APPLICANT: Krotz, Achim H
; APPLICANT: Ravikumar, Vasulunga T
; TITLE OF INVENTION: Purification of Oligonucleotides
; FILE REFERENCE: ISIS4656
; CURRENT APPLICATION NUMBER: PCT/US01/02951
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US01-02951-5

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 24
PCT-US01-02951-6
; Sequence 6, Application PC/TUS0102951
; GENERAL INFORMATION:
; APPLICANT: Krotz, Achim H
; APPLICANT: Ravikumar, Vasulunga T
; TITLE OF INVENTION: Purification of Oligonucleotides
; FILE REFERENCE: ISIS4656
; CURRENT APPLICATION NUMBER: PCT/US01/02951
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 8

us-10-002-884a-5.max.rnmpm

Thu Jan 29 10:08:41 2004

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 27

PCT-US97-02003-1
; Sequence 1, Application PC/TUS9702003
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Methoxyethoxy Oligonucleotides for Modulation
; TITLE OF INVENTION: of Protein Kinase C Expression
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSER: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 720 kb STORAGE
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/02003
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,269
; FILING DATE: February 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISCG-0086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US97-02003-1

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 28

PCT-US98-08798-3
; Sequence 3, Application PC/TUS9808798
; GENERAL INFORMATION:
; APPLICANT: ISIS PHARMACEUTICALS, INC. FOR ENHANCED BIOAVAILABILITY
; TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED BIOAVAILABILITY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence
PCT-US01-02951-6

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 25

PCT-US03-04323-14
; Sequence 14, Application PC/TUS0304323
; GENERAL INFORMATION:
; APPLICANT: MEDBRIDGE, INC. and XIE, Dong
; TITLE OF INVENTION: Protein Carrier System for Therapeutic Oligonucleotides
; FILE REFERENCE: 62219.000004
; CURRENT APPLICATION NUMBER: PCT/US03/04323
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 60/356,053
; PRIOR FILING DATE: 13 February 2002
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide directed against human PKC-alpha
PCT-US03-04323-14

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 26

PCT-US03-11921-1
; Sequence 1, Application PC/TUS0311921
; GENERAL INFORMATION:
; APPLICANT: Uhler, Michael D.
; TITLE OF INVENTION: Surface Transfection and Expression Procedure
; FILE REFERENCE: UM-06983
; CURRENT APPLICATION NUMBER: PCT/US03/11921
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/245,892
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/305,552
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/960,454
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 10/002,802
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-11921-1

```
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/08798
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/847,151
; FILING DATE: 30-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Leggaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2988
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US98-08798-3

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGTGTGAGTTTCA 20
Db 1 GTTCTCGTGTGAGTTTCA 20

RESULT 29
PCT-US99-04213-4
; Sequence 4, Application PC/TUS9904213
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc.
; TITLE OF INVENTION: IMPROVED METHODS FOR SYNTHESIS OF OLIGONUCLEOTIDES
; FILE REFERENCE: ISIS3404
; CURRENT APPLICATION NUMBER: PCT/US99/04213
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: US 09/032,972
; EARLIER FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: oligonucleotide
PCT-US99-04213-4

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGTGTGAGTTTCA 20
Db 1 GTTCTCGTGTGAGTTTCA 20

RESULT 30
PCT-US99-11141-3
; Sequence 3, Application PC/TUS9911141
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals Inc. et al.
; TITLE OF INVENTION: Compositions and Methods for the Pulmonary Delivery of
; TITLE OF INVENTION: Nucleic Acids
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US99/11141
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. serial no. 09/083,586
; EARLIER FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US99-11141-3

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGTGTGAGTTTCA 20
Db 1 GTTCTCGTGTGAGTTTCA 20

RESULT 31
PCT-US99-11142-6
; Sequence 6, Application PC/TUS9911142
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals Inc. et al.
; TITLE OF INVENTION: Compositions and Methods for Topical Delivery of
; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US99/11142
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. serial no. 09/082,336
; EARLIER FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US99-11142-6

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGTGTGAGTTTCA 20
Db 1 GTTCTCGTGTGAGTTTCA 20

RESULT 32
PCT-US99-11214-3
; Sequence 3, Application PC/TUS9911214
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals Inc. et al.
; TITLE OF INVENTION: Compositions and Methods for the Pulmonary Delivery of
; TITLE OF INVENTION: Nucleic Acids
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US99/11214
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. Ser. No. 09/083,585
; EARLIER FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US99-11214-3
```

us-10-002-884a-5.max.rnrm

Thu Jan 29 10:08:41 2004

```
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US99-11214-3
Query Match      100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 33
PCT-US99-11267-3
; Sequence 3, Application PC/TUS9911267
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Long-Circulating Liposomal Compositions
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US99/11267
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. Serial No. 09/082,365
; EARLIER FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US99-11267-3

Query Match      100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 34
PCT-US99-11394-49
; Sequence 49, Application PC/TUS9911394
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals Inc. et al.
; TITLE OF INVENTION: Compositions and Methods for Non-Parenteral Delivery of
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US99/11394
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: U.S. serial no. 09/082,624
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
PCT-US99-11394-49

Query Match      100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 35
PCT-US99-15960-3
; Sequence 3, Application PC/TUS9915960
; GENERAL INFORMATION:
; APPLICANT: ISIS Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Oligonucleotides Having Site Specific Chiral
; FILE REFERENCE: ISIS3891
; CURRENT APPLICATION NUMBER: PCT/US99/15960
; CURRENT FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 09/115,027
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
PCT-US99-15960-3

Query Match      100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 36
US-07-852-852-2
; Sequence 2, Application US/07852852
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of Protein
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/852,852
; FILING DATE: 19920316
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISIS-0508
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
```


US-07-852-852-2

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 37

US-08-117-363A-22
Sequence 22, Application US/08117363A
GENERAL INFORMATION:
APPLICANT: Manoharan, Muthiah
APPLICANT: Phillip D. Cook
TITLE OF INVENTION: AMINE-DERIVATIZED NUCLEOSIDES AND
TITLE OF INVENTION: OLIGONUCLEOSIDES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
and Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,363A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-1169
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-117-363A-22

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 11;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 38

US-08-302-672-2
Sequence 2, Application US/08302672
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
TITLE OF INVENTION: Protein Kinase C
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
and Norris

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,672
FILING DATE: herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISIS-0872
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-302-672-2

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 39

US-08-464-953A-22
Sequence 22, Application US/08464953A
GENERAL INFORMATION:
APPLICANT: Cook and Manoharan
TITLE OF INVENTION: AMINE-DERIVATIZED NUCLEOSIDES AND
TITLE OF INVENTION: OLIGONUCLEOSIDES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,953A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100

us-10-002-884a-5.max.rnpm

Thu Jan 29 10:08:41 2004

TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-464-953A-22

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 11;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GUTCTCGCTGGTGAGTTTCA 20

RESULT 40

US-08-464-953B-22
Sequence 22. Application US/08464953B

GENERAL INFORMATION:
APPLICANT: Cook and Manoharan
TITLE OF INVENTION: AMINE-DERIVATIZED NUCLEOSIDES AND
TITLE OF INVENTION: OLIGONUCLEOSIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: Norris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.4 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,953B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-464-953B-22

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 11;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GUTCTCGCTGGTGAGTTTCA 20

Search completed: January 24, 2004, 16:23:08
Job time : 2743 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 24, 2004, 14:32:27 ; Search time 301 Seconds
(without alignments)
186.890 Million cell updates/sec

Title: US-10-002-884A-5

Perfect score: 20

Sequence: 1 gttctcggtggtgatttca 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4868162 seqs, 1406344122 residues

Total number of hits satisfying chosen parameters: 6770940

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Pending Patents NA.New.*

1: /cgn2_6/ptodata/1/pna/PCT NEW COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06 NEW COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07 NEW COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08 NEW COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09 NEW COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US10 NEW COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US10 NEW COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US10 NEW COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	100.0	20	1	PCT-US03-25935-268
2	20	100.0	20	1	PCT-US03-25935-269
3	20	100.0	20	5	US-09-546-596A-22
4	20	100.0	20	7	US-10-437-275-23
5	20	100.0	20	7	US-10-447-136-217
6	20	100.0	20	7	US-10-437-263-23
7	20	100.0	20	7	US-10-437-258-23
8	20	100.0	20	7	US-10-181-200-4
9	20	100.0	20	7	US-10-181-200-4
10	19	95.0	19	1	PCT-US03-23344-2
11	15.4	77.0	25	5	US-10-719-900-549041
12	15.2	76.0	25	5	US-09-954-427A-364371
13	15.2	76.0	25	7	US-10-719-956-137615
14	15.2	76.0	25	7	US-10-719-900-323222
15	14.8	74.0	25	7	US-10-719-900-251427
16	14.4	72.0	25	7	US-10-719-956-158864
17	14.4	72.0	25	7	US-10-719-956-326213
18	14.4	72.0	25	7	US-10-719-956-540875
19	14.4	72.0	25	7	US-10-719-900-552211
20	14.2	71.0	25	5	US-09-954-427A-94322
21	14.2	71.0	25	5	US-09-954-427A-342631
22	14.2	71.0	25	7	US-10-719-956-500175
23	14.2	71.0	25	7	US-10-719-956-628121
24	14.2	71.0	25	7	US-10-719-900-493573
25	14.2	71.0	25	7	US-10-719-900-688991

26	14.2	71.0	25	7	US-10-719-900-822309	Sequence 822309,
27	14.2	71.0	25	8	US-60-507-511-8335	Sequence 8135, Ap
28	14.2	71.0	25	8	US-60-507-481-172187	Sequence 172187,
29	13.8	69.0	25	5	US-09-956-604D-114030	Sequence 114030,
30	13.8	69.0	25	5	US-09-954-427A-286389	Sequence 286389,
31	13.8	69.0	25	5	US-09-954-427A-369103	Sequence 369103,
32	13.8	69.0	25	7	US-10-719-956-46281	Sequence 46281, A
33	13.8	69.0	25	7	US-10-719-956-363441	Sequence 363441,
34	13.8	69.0	25	7	US-10-719-956-563045	Sequence 563045,
35	13.8	69.0	25	7	US-10-719-900-37913	Sequence 37913, A
36	13.8	69.0	25	7	US-10-719-900-110854	Sequence 110854,
37	13.8	69.0	25	7	US-10-719-900-489138	Sequence 489138,
38	13.8	69.0	25	7	US-10-719-900-548040	Sequence 548040,
39	13.8	69.0	25	7	US-10-719-900-572713	Sequence 572713,
40	13.8	69.0	25	7	US-10-719-900-635348	Sequence 635348,
41	13.8	69.0	25	7	US-10-719-900-689514	Sequence 689514,
42	13.8	69.0	25	7	US-10-719-900-691286	Sequence 691286,
43	13.8	69.0	25	7	US-10-719-900-851061	Sequence 851061,
44	13.8	69.0	25	8	US-60-507-511-49787	Sequence 49787, A
45	13.8	69.0	25	8	US-60-507-511-69566	Sequence 69566, A
46	13.8	69.0	25	8	US-60-507-511-105084	Sequence 105084,
47	13.8	69.0	25	8	US-60-507-481-115458	Sequence 115458,
48	13.6	68.0	25	5	US-09-956-604D-71047	Sequence 71047, A
49	13.6	68.0	25	5	US-09-954-427A-58553	Sequence 58553, A
50	13.6	68.0	25	5	US-09-954-427A-301501	Sequence 301501,
51	13.6	68.0	25	7	US-10-719-956-65590	Sequence 65590, A
52	13.6	68.0	25	7	US-10-719-956-137616	Sequence 137616,
53	13.6	68.0	25	7	US-10-719-956-155392	Sequence 155392,
54	13.6	68.0	25	7	US-10-719-956-189767	Sequence 189767,
55	13.6	68.0	25	7	US-10-719-956-275050	Sequence 275050,
56	13.6	68.0	25	7	US-10-719-956-643684	Sequence 643684,
57	13.6	68.0	25	7	US-10-719-900-323223	Sequence 323223,
58	13.6	68.0	25	7	US-10-719-900-324894	Sequence 324894,
59	13.6	68.0	25	7	US-10-719-900-324895	Sequence 324895,
60	13.6	68.0	25	7	US-10-719-900-656929	Sequence 656929,
61	13.6	68.0	25	7	US-10-719-900-897588	Sequence 897588,
62	13.4	67.0	25	7	US-10-719-956-286357	Sequence 286357,
63	13.4	67.0	25	7	US-10-719-956-286358	Sequence 286358,
64	13.4	67.0	25	7	US-10-719-956-663609	Sequence 663609,
65	13.4	67.0	25	7	US-10-719-900-9496	Sequence 9496, Ap
66	13.4	67.0	25	7	US-10-719-900-473028	Sequence 473028,
67	13.4	67.0	25	7	US-10-719-900-524021	Sequence 524021,
68	13.4	67.0	25	7	US-10-719-900-565541	Sequence 565541,
69	13.4	67.0	25	7	US-10-719-900-587722	Sequence 587722,
70	13.4	67.0	25	7	US-10-719-900-830249	Sequence 830249,
71	13.4	67.0	25	8	US-60-507-511-157676	Sequence 157676,
72	13.4	67.0	25	8	US-60-507-511-196343	Sequence 196343,
73	13.4	67.0	25	8	US-60-507-481-23225	Sequence 23225, A
74	13.2	66.0	21	6	US-10-751-736-14419	Sequence 14419, A
75	13.2	66.0	21	6	US-10-751-736-14420	Sequence 14420, A
76	13.2	66.0	21	6	US-10-751-736-15022	Sequence 15022, A
77	13.2	66.0	21	6	US-10-751-736-15023	Sequence 15023, A
78	13.2	66.0	21	6	US-10-751-736-15025	Sequence 15025, A
79	13.2	66.0	21	6	US-10-751-736-15310	Sequence 15310, A
80	13.2	66.0	21	6	US-10-751-736-15311	Sequence 15311, A
81	13.2	66.0	21	6	US-10-751-736-15397	Sequence 15397, A
82	13.2	66.0	21	6	US-10-751-736-15398	Sequence 15398, A
83	13.2	66.0	21	6	US-10-751-736-15400	Sequence 15400, A
84	13.2	66.0	21	6	US-10-698-597-28	Sequence 28, Appl
85	13.2	66.0	25	5	US-09-956-604D-42346	Sequence 42346, A
86	13.2	66.0	25	5	US-09-956-604D-51088	Sequence 51088, A
87	13.2	66.0	25	5	US-09-956-604D-130670	Sequence 130670, A
88	13.2	66.0	25	5	US-09-953-570A-32660	Sequence 32660, A
89	13.2	66.0	25	5	US-09-954-427A-17089	Sequence 135755,
90	13.2	66.0	25	5	US-09-954-427A-36447	Sequence 17089, A
91	13.2	66.0	25	5	US-09-954-427A-252772	Sequence 36447, A
92	13.2	66.0	25	5	US-09-954-427A-354149	Sequence 252772,
93	13.2	66.0	25	5	US-10-719-956-67250	Sequence 354149, A
94	13.2	66.0	25	7	US-10-719-956-172309	Sequence 67250, A
95	13.2	66.0	25	7	US-10-719-956-172310	Sequence 172309,
96	13.2	66.0	25	7	US-10-719-956-185995	Sequence 172310,
97	13.2	66.0	25	7	US-10-719-956-185995	Sequence 185995,
98	13.2	66.0	25	7	US-10-719-956-207830	Sequence 207830,

C 99	13.2	66.0	25	7	US-10-719-956-214533, Sequence 214533,	C 172	12.8	64.0	25	7	US-10-719-900-820890 Sequence 820890,
C 100	13.2	66.0	25	7	Sequence 279848,	C 173	12.8	64.0	25	7	Sequence 841441,
C 101	13.2	66.0	25	7	Sequence 279848,	C 174	12.8	64.0	25	7	Sequence 841441,
C 102	13.2	66.0	25	7	Sequence 286583,	C 175	12.8	64.0	25	7	Sequence 910039,
C 103	13.2	66.0	25	7	Sequence 286584,	C 176	12.8	64.0	25	8	US-60-507-511-135085 Sequence 35085, A
C 104	13.2	66.0	25	7	Sequence 363557,	C 177	12.8	64.0	25	8	US-60-507-511-143996 Sequence 53002, A
C 105	13.2	66.0	25	7	Sequence 385174,	C 178	12.8	64.0	25	8	US-60-507-481-530027 Sequence 100227,
C 106	13.2	66.0	25	7	Sequence 150115,	C 179	12.8	64.0	25	8	US-60-507-481-100227 Sequence 145671,
C 107	13.2	66.0	25	7	Sequence 150116,	C 180	12.8	64.0	25	8	US-60-507-481-145671 Sequence 3019, Ap
C 108	13.2	66.0	25	7	Sequence 151428,	C 181	12.6	63.0	20	1	PCT-US03-25389-3019 Sequence 3307, Ap
C 109	13.2	66.0	25	7	Sequence 324760,	C 182	12.6	63.0	21	6	US-10-751-736-46378 Sequence 46378, A
C 110	13.2	66.0	25	7	Sequence 352186,	C 183	12.6	63.0	21	6	Sequence 46379, A
C 111	13.2	66.0	25	7	Sequence 396382,	C 184	12.6	63.0	21	6	Sequence 46627, A
C 112	13.2	66.0	25	7	Sequence 446270,	C 185	12.6	63.0	21	6	Sequence 46774, A
C 113	13.2	66.0	25	7	Sequence 446271,	C 186	12.6	63.0	21	6	Sequence 46775, A
C 114	13.2	66.0	25	7	Sequence 697852,	C 187	12.6	63.0	25	5	US-09-956-604D-48460 Sequence 48460, A
C 115	13.2	66.0	25	7	Sequence 847690,	C 188	12.6	63.0	25	5	US-09-956-604D-53093 Sequence 53093, A
C 116	13.2	66.0	25	7	Sequence 867397,	C 189	12.6	63.0	25	5	US-09-956-604D-70498 Sequence 70498, A
C 117	13.2	66.0	25	7	Sequence 941239,	C 190	12.6	63.0	25	5	Sequence 78072, A
C 118	13.2	66.0	25	7	Sequence 969774,	C 191	12.6	63.0	25	5	Sequence 78625, A
C 119	13.2	66.0	25	8	Sequence 143976,	C 192	12.6	63.0	25	5	Sequence 133859, A
C 120	13.2	66.0	25	8	Sequence 69972, A	C 193	12.6	63.0	25	5	Sequence 66215, A
C 121	13.2	66.0	25	8	Sequence 118146,	C 194	12.6	63.0	25	5	Sequence 89137, A
C 122	13	65.0	25	8	Sequence 134083,	C 195	12.6	63.0	25	5	Sequence 115681,
C 123	13	65.0	25	5	Sequence 83432, A	C 196	12.6	63.0	25	5	Sequence 125697,
C 124	13	65.0	25	5	Sequence 15027, A	C 197	12.6	63.0	25	5	Sequence 191304,
C 125	13	65.0	25	5	Sequence 32704, A	C 198	12.6	63.0	25	5	Sequence 264443,
C 126	13	65.0	25	5	Sequence 93594, A	C 199	12.6	63.0	25	5	Sequence 264460,
C 127	13	65.0	25	5	Sequence 247233,	C 200	12.6	63.0	25	5	Sequence 331732,
C 128	13	65.0	25	5	Sequence 247234,	C 201	12.6	63.0	25	5	Sequence 36782, A
C 129	13	65.0	25	5	Sequence 247235,	C 202	12.6	63.0	25	5	Sequence 61754, A
C 130	13	65.0	25	5	Sequence 247373,	C 203	12.6	63.0	25	5	Sequence 95528, A
C 131	13	65.0	25	5	Sequence -27198,	C 204	12.6	63.0	25	7	Sequence 10266,
C 132	13	65.0	25	7	Sequence 449536,	C 205	12.6	63.0	25	7	Sequence 105428,
C 133	12.8	64.0	25	5	Sequence 273754,	C 206	12.6	63.0	25	7	Sequence 150740,
C 134	12.8	64.0	25	5	Sequence 5306, A	C 207	12.6	63.0	25	7	Sequence 176242,
C 135	12.8	64.0	25	5	Sequence 5307, A	C 208	12.6	63.0	25	7	Sequence 176242,
C 136	12.8	64.0	25	5	Sequence 55317, A	C 209	12.6	63.0	25	7	Sequence 194955,
C 137	12.8	64.0	25	5	Sequence 55330, A	C 210	12.6	63.0	25	7	Sequence 195174,
C 138	12.8	64.0	25	5	Sequence 82630, A	C 211	12.6	63.0	25	7	Sequence 202340,
C 139	12.8	64.0	25	5	Sequence 82630, A	C 212	12.6	63.0	25	7	Sequence 312435,
C 140	12.8	64.0	25	5	Sequence 82630, A	C 213	12.6	63.0	25	7	Sequence 312435,
C 141	12.8	64.0	25	5	Sequence 106379, A	C 214	12.6	63.0	25	7	Sequence 373457,
C 142	12.8	64.0	25	5	Sequence 11759, A	C 215	12.6	63.0	25	7	Sequence 500174,
C 143	12.8	64.0	25	5	Sequence 19910, A	C 216	12.6	63.0	25	7	Sequence 526469,
C 144	12.8	64.0	25	5	Sequence 19916, A	C 217	12.6	63.0	25	7	Sequence 526469,
C 145	12.8	64.0	25	5	Sequence 403816, A	C 218	12.6	63.0	25	7	Sequence 572106,
C 146	12.8	64.0	25	5	Sequence 20778, A	C 219	12.6	63.0	25	7	Sequence 609465,
C 147	12.8	64.0	25	7	Sequence 30021, A	C 220	12.6	63.0	25	7	Sequence 609465,
C 148	12.8	64.0	25	7	Sequence 68470, A	C 221	12.6	63.0	25	7	Sequence 625585,
C 149	12.8	64.0	25	7	Sequence 114920, A	C 222	12.6	63.0	25	7	Sequence 625585,
C 150	12.8	64.0	25	7	Sequence 158863, A	C 223	12.6	63.0	25	7	Sequence 628122,
C 151	12.8	64.0	25	7	Sequence 186013, A	C 224	12.6	63.0	25	7	Sequence 673243,
C 152	12.8	64.0	25	7	Sequence 285172, A	C 225	12.6	63.0	25	7	Sequence 70598, A
C 153	12.8	64.0	25	7	Sequence 326215, A	C 226	12.6	63.0	25	7	Sequence 140015,
C 154	12.8	64.0	25	7	Sequence 347772, A	C 227	12.6	63.0	25	7	Sequence 140016,
C 155	12.8	64.0	25	7	Sequence 497698, A	C 228	12.6	63.0	25	7	Sequence 156563,
C 156	12.8	64.0	25	7	Sequence 540874, A	C 229	12.6	63.0	25	7	Sequence 156563,
C 157	12.8	64.0	25	7	Sequence 573031, A	C 230	12.6	63.0	25	7	Sequence 184095,
C 158	12.8	64.0	25	7	Sequence 138054, A	C 231	12.6	63.0	25	7	Sequence 184095,
C 159	12.8	64.0	25	7	Sequence 243906, A	C 232	12.6	63.0	25	7	Sequence 221156,
C 160	12.8	64.0	25	7	Sequence 244016, A	C 233	12.6	63.0	25	7	Sequence 237158,
C 161	12.8	64.0	25	7	Sequence 359204, A	C 234	12.6	63.0	25	7	Sequence 274714, A
C 162	12.8	64.0	25	7	Sequence 432778, A	C 235	12.6	63.0	25	7	Sequence 278876, A
C 163	12.8	64.0	25	7	Sequence 461442, A	C 236	12.6	63.0	25	7	Sequence 281070, A
C 164	12.8	64.0	25	7	Sequence 474931, A	C 237	12.6	63.0	25	7	Sequence 325038, A
C 165	12.8	64.0	25	7	Sequence 495051, A	C 238	12.6	63.0	25	7	Sequence 325039, A
C 166	12.8	64.0	25	7	Sequence 502128, A	C 239	12.6	63.0	25	7	Sequence 350339, A
C 167	12.8	64.0	25	7	Sequence 552210, A	C 240	12.6	63.0	25	7	Sequence 401482, A
C 168	12.8	64.0	25	7	Sequence 552210, A	C 241	12.6	63.0	25	7	Sequence 466298, A
C 169	12.8	64.0	25	7	Sequence 654667, A	C 242	12.6	63.0	25	7	Sequence 493572, A
C 170	12.8	64.0	25	7	Sequence 740425, A	C 243	12.6	63.0	25	7	Sequence 500070, A
C 171	12.8	64.0	25	7	Sequence 795463, A	C 244	12.6	63.0	25	7	Sequence 500071, A

C 245	12.6	63.0	25	7	US-10-719-900-728498	Sequence 728498,	318	12.2	61.0	25	5	US-09-954-429B-547	Sequence 547, App
C 246	12.6	63.0	25	7	US-10-719-900-733453	Sequence 733453,	C 319	12.2	61.0	25	5	US-09-953-115A-25345	Sequence 25345, A
C 247	12.6	63.0	25	7	US-10-719-900-767120	Sequence 767120,	C 320	12.2	61.0	25	5	US-09-953-570A-54531	Sequence 54531, A
C 248	12.6	63.0	25	7	US-10-719-900-822308	Sequence 822308,	C 321	12.2	61.0	25	5	US-09-953-570A-54538	Sequence 54538, A
C 249	12.6	63.0	25	7	US-10-719-900-876350	Sequence 876350,	C 322	12.2	61.0	25	5	US-09-953-570A-58198	Sequence 58198, A
C 250	12.6	63.0	25	7	US-10-719-900-977892	Sequence 977892,	C 323	12.2	61.0	25	5	US-09-953-570A-102051	Sequence 102051,
C 251	12.6	63.0	25	8	US-60-507-481-78631	Sequence 78631, A	C 324	12.2	61.0	25	5	US-09-953-570A-102053	Sequence 102053,
C 252	12.6	63.0	25	8	US-60-507-481-132884	Sequence 132884, A	C 325	12.2	61.0	25	5	US-09-953-570A-131795	Sequence 131795,
C 253	12.4	62.0	15	1	PCT-US02-38216-13434	Sequence 13434, A	C 326	12.2	61.0	25	5	US-09-954-427A-8033	Sequence 8033, Ap
C 254	12.4	62.0	24	1	PCT-US02-38216-69244	Sequence 69244, A	C 327	12.2	61.0	25	5	US-09-954-427A-17084	Sequence 17084, A
C 255	12.4	62.0	25	5	US-09-956-604D-45522	Sequence 45522, A	C 328	12.2	61.0	25	5	US-09-954-427A-36491	Sequence 36491, A
C 256	12.4	62.0	25	5	US-09-956-604D-61098	Sequence 61098, A	C 329	12.2	61.0	25	5	US-09-954-427A-48355	Sequence 48355, A
C 257	12.4	62.0	25	5	US-09-956-604D-68943	Sequence 68943, A	C 330	12.2	61.0	25	5	US-09-954-427A-49168	Sequence 49168, A
C 258	12.4	62.0	25	5	US-09-953-115A-15387	Sequence 15387, A	C 331	12.2	61.0	25	5	US-09-954-427A-118761	Sequence 118761,
C 259	12.4	62.0	25	5	US-09-953-115A-15392	Sequence 15392, A	C 332	12.2	61.0	25	5	US-09-954-427A-121372	Sequence 121372,
C 260	12.4	62.0	25	5	US-09-953-115A-16513	Sequence 16513, A	C 333	12.2	61.0	25	5	US-09-954-427A-151621	Sequence 151621,
C 261	12.4	62.0	25	5	US-09-954-427A-19915	Sequence 19915, A	C 334	12.2	61.0	25	5	US-09-954-427A-151715	Sequence 151715,
C 262	12.4	62.0	25	5	US-09-954-427A-19939	Sequence 19939, A	C 335	12.2	61.0	25	5	US-09-954-427A-238438	Sequence 238438,
C 263	12.4	62.0	25	5	US-09-954-427A-104064	Sequence 104064, A	C 336	12.2	61.0	25	5	US-09-954-427A-275143	Sequence 275143,
C 264	12.4	62.0	25	5	US-09-954-427A-170722	Sequence 170722, A	C 337	12.2	61.0	25	5	US-09-954-427A-275584	Sequence 275584,
C 265	12.4	62.0	25	5	US-09-954-427A-170742	Sequence 170742, A	C 338	12.2	61.0	25	5	US-09-954-427A-275610	Sequence 275610,
C 266	12.4	62.0	25	5	US-09-954-427A-217393	Sequence 217393, A	C 339	12.2	61.0	25	5	US-09-954-427A-298175	Sequence 298175,
C 267	12.4	62.0	25	5	US-09-954-427A-398688	Sequence 398688, A	C 340	12.2	61.0	25	5	US-09-954-427A-298573	Sequence 298573,
C 268	12.4	62.0	25	7	US-10-719-956-11458	Sequence 11458, A	C 341	12.2	61.0	25	5	US-09-954-427A-307158	Sequence 307158,
C 269	12.4	62.0	25	7	US-10-719-956-178994	Sequence 178994, A	C 342	12.2	61.0	25	5	US-09-954-427A-348421	Sequence 348421,
C 270	12.4	62.0	25	7	US-10-719-956-183313	Sequence 183313, A	C 343	12.2	61.0	25	5	US-09-954-427A-368772	Sequence 368772,
C 271	12.4	62.0	25	7	US-10-719-956-186952	Sequence 186952, A	C 344	12.2	61.0	25	7	US-10-681-773-20411	Sequence 20411, A
C 272	12.4	62.0	25	7	US-10-719-956-223698	Sequence 223698, A	C 345	12.2	61.0	25	7	US-10-681-773-25069	Sequence 25069, A
C 273	12.4	62.0	25	7	US-10-719-956-336424	Sequence 336424, A	C 346	12.2	61.0	25	7	US-10-681-773-80659	Sequence 80659, A
C 274	12.4	62.0	25	7	US-10-719-956-350429	Sequence 350429, A	C 347	12.2	61.0	25	7	US-10-719-956-4528	Sequence 4528, Ap
C 275	12.4	62.0	25	7	US-10-719-956-396042	Sequence 396042, A	C 348	12.2	61.0	25	7	US-10-719-956-15382	Sequence 15382, A
C 276	12.4	62.0	25	7	US-10-719-956-402045	Sequence 402045, A	C 349	12.2	61.0	25	7	US-10-719-956-18067	Sequence 18067, A
C 277	12.4	62.0	25	7	US-10-719-956-496830	Sequence 496830, A	C 350	12.2	61.0	25	7	US-10-719-956-18068	Sequence 18068, A
C 278	12.4	62.0	25	7	US-10-719-956-553396	Sequence 553396, A	C 351	12.2	61.0	25	7	US-10-719-956-26024	Sequence 26024, A
C 279	12.4	62.0	25	7	US-10-719-956-630887	Sequence 630887, A	C 352	12.2	61.0	25	7	US-10-719-956-28959	Sequence 28959, A
C 280	12.4	62.0	25	7	US-10-719-956-647919	Sequence 647919, A	C 353	12.2	61.0	25	7	US-10-719-956-46282	Sequence 46282, A
C 281	12.4	62.0	25	7	US-10-719-956-56205	Sequence 56205, A	C 354	12.2	61.0	25	7	US-10-719-956-59743	Sequence 59743, A
C 282	12.4	62.0	25	7	US-10-719-900-56208	Sequence 56208, A	C 355	12.2	61.0	25	7	US-10-719-956-64642	Sequence 64642, A
C 283	12.4	62.0	25	7	US-10-719-900-203569	Sequence 203569, A	C 356	12.2	61.0	25	7	US-10-719-956-73571	Sequence 73571, A
C 284	12.4	62.0	25	7	US-10-719-900-203571	Sequence 203571, A	C 357	12.2	61.0	25	7	US-10-719-956-77804	Sequence 77804, A
C 285	12.4	62.0	25	7	US-10-719-900-497730	Sequence 497730, A	C 358	12.2	61.0	25	7	US-10-719-956-85475	Sequence 85475, A
C 286	12.4	62.0	25	7	US-10-719-900-567215	Sequence 567215, A	C 359	12.2	61.0	25	7	US-10-719-956-86680	Sequence 86680, A
C 287	12.4	62.0	25	7	US-10-719-900-746176	Sequence 746176, A	C 360	12.2	61.0	25	7	US-10-719-956-86711	Sequence 86711, A
C 288	12.4	62.0	25	7	US-10-719-900-822706	Sequence 822706, A	C 361	12.2	61.0	25	7	US-10-719-956-133675	Sequence 133675, A
C 289	12.4	62.0	25	7	US-10-719-900-822707	Sequence 822707, A	C 362	12.2	61.0	25	7	US-10-719-956-152282	Sequence 152282,
C 290	12.4	62.0	25	7	US-10-719-900-848005	Sequence 848005, A	C 363	12.2	61.0	25	7	US-10-719-956-201792	Sequence 201792,
C 291	12.4	62.0	25	7	US-10-719-900-848005	Sequence 848005, A	C 364	12.2	61.0	25	7	US-10-719-956-207734	Sequence 207734,
C 292	12.4	62.0	25	7	US-10-719-900-882601	Sequence 882601, A	C 365	12.2	61.0	25	7	US-10-719-956-211975	Sequence 211975,
C 293	12.4	62.0	25	7	US-10-719-900-933895	Sequence 933895, A	C 366	12.2	61.0	25	7	US-10-719-956-232912	Sequence 232912,
C 294	12.4	62.0	25	7	US-10-719-900-933895	Sequence 933895, A	C 367	12.2	61.0	25	7	US-10-719-956-239170	Sequence 239170,
C 295	12.4	62.0	25	8	US-60-507-511-117735	Sequence 117735, A	C 368	12.2	61.0	25	7	US-10-719-956-239171	Sequence 239171,
C 296	12.4	62.0	25	8	US-60-507-511-179232	Sequence 179232, A	C 369	12.2	61.0	25	7	US-10-719-956-249329	Sequence 249329,
C 297	12.4	62.0	25	8	US-60-507-511-179840	Sequence 179840, A	C 370	12.2	61.0	25	7	US-10-719-956-259692	Sequence 259692,
C 298	12.4	62.0	25	8	US-60-507-511-180274	Sequence 180274, A	C 371	12.2	61.0	25	7	US-10-719-956-263968	Sequence 263968,
C 299	12.2	61.0	17	7	US-10-138-674A-5390	Sequence 5390, Ap	C 372	12.2	61.0	25	7	US-10-719-956-520323	Sequence 520323,
C 300	12.2	61.0	20	7	US-10-677-943-34	Sequence 34, Appl	C 373	12.2	61.0	25	7	US-10-719-956-520938	Sequence 520938,
C 301	12.2	61.0	21	6	US-10-751-736-31612	Sequence 31612, A	C 374	12.2	61.0	25	7	US-10-719-956-634482	Sequence 634482,
C 302	12.2	61.0	21	6	US-10-751-736-31613	Sequence 31613, A	C 375	12.2	61.0	25	7	US-10-719-956-375891	Sequence 375891,
C 303	12.2	61.0	21	6	US-10-751-736-36559	Sequence 36559, A	C 376	12.2	61.0	25	7	US-10-719-956-432764	Sequence 432764,
C 304	12.2	61.0	21	6	US-10-751-736-37057	Sequence 37057, A	C 377	12.2	61.0	25	7	US-10-719-956-503231	Sequence 503231,
C 305	12.2	61.0	21	6	US-10-751-736-37228	Sequence 37228, A	C 378	12.2	61.0	25	7	US-10-719-956-520938	Sequence 520938,
C 306	12.2	61.0	23	6	US-10-617-070-265	Sequence 265, App	C 379	12.2	61.0	25	7	US-10-719-956-537720	Sequence 537720,
C 307	12.2	61.0	23	6	US-10-617-070-336	Sequence 336, App	C 380	12.2	61.0	25	7	US-10-719-956-554207	Sequence 554207,
C 308	12.2	61.0	23	7	US-10-411-954-285	Sequence 285, App	C 381	12.2	61.0	25	7	US-10-719-956-563044	Sequence 563044,
C 309	12.2	61.0	23	7	US-10-411-954-336	Sequence 336, App	C 382	12.2	61.0	25	7	US-10-719-956-601749	Sequence 601749,
C 310	12.2	61.0	25	5	US-09-956-604D-20605	Sequence 20605, A	C 383	12.2	61.0	25	7	US-10-719-956-608778	Sequence 608778,
C 311	12.2	61.0	25	5	US-09-956-604D-32438	Sequence 32438, A	C 384	12.2	61.0	25	7	US-10-719-956-634482	Sequence 634482,
C 312	12.2	61.0	25	5	US-09-956-604D-53522	Sequence 53522, A	C 385	12.2	61.0	25	7	US-10-719-900-1925	Sequence 1925, Ap
C 313	12.2	61.0	25	5	US-09-956-604D-104710	Sequence 104710, A	C 386	12.2	61.0	25	7	US-10-719-900-1927	Sequence 1927, Ap
C 314	12.2	61.0	25	5	US-09-956-604D-122217	Sequence 122217, A	C 387	12.2	61.0	25	7	US-10-719-900-27731	Sequence 27731, A
C 315	12.2	61.0	25	5	US-09-956-604D-123870	Sequence 123870, A	C 388	12.2	61.0	25	7	US-10-719-900-36967	Sequence 36967, A
C 316	12.2	61.0	25	5	US-09-956-604D-136596	Sequence 136596, A	C 389	12.2	61.0	25	7	US-10-719-900-37914	Sequence 37914, A
C 317	12.2	61.0	25	5	US-09-954-429B-547	Sequence 547, App	C 390	12.2	61.0	25	7	US-10-719-900-77985	Sequence 77985, A

C 391	12.2	61.0	25	7	US-10-719-900-106497	Sequence 106497,	454	12	60.0	25	5	US-09-953-570A-52600	Sequence 52600, A
C 392	12.2	61.0	25	7	US-10-719-900-110853	Sequence 110853,	C 455	12	60.0	25	5	US-09-953-570A-122247	Sequence 122247,
C 393	12.2	61.0	25	7	US-10-719-900-111940	Sequence 111940,	C 456	12	60.0	25	5	US-09-953-570A-138364	Sequence 138364, A
C 394	12.2	61.0	25	7	US-10-719-900-114413	Sequence 114413,	C 457	12	60.0	25	5	US-09-954-427A-62661	Sequence 62661, A
C 395	12.2	61.0	25	7	US-10-719-900-136425	Sequence 136425,	C 458	12	60.0	25	5	US-09-954-427A-106184	Sequence 106184,
C 396	12.2	61.0	25	7	US-10-719-900-206903	Sequence 206903,	C 459	12	60.0	25	5	US-09-954-427A-144621	Sequence 144621,
C 397	12.2	61.0	25	7	US-10-719-900-212747	Sequence 212747,	C 470	12	60.0	25	5	US-09-954-427A-17980	Sequence 17980,
C 398	12.2	61.0	25	7	US-10-719-900-233102	Sequence 233102,	C 471	12	60.0	25	5	US-09-954-427A-198375	Sequence 198375,
C 399	12.2	61.0	25	7	US-10-719-900-248019	Sequence 248019,	C 472	12	60.0	25	5	US-09-954-427A-233594	Sequence 233594,
C 400	12.2	61.0	25	7	US-10-719-900-252461	Sequence 252461,	C 473	12	60.0	25	5	US-09-954-427A-240574	Sequence 240574,
C 401	12.2	61.0	25	7	US-10-719-900-301216	Sequence 301216,	C 474	12	60.0	25	5	US-09-954-427A-243208	Sequence 243208,
C 402	12.2	61.0	25	7	US-10-719-900-303809	Sequence 303809,	C 475	12	60.0	25	5	US-09-954-427A-258578	Sequence 258578,
C 403	12.2	61.0	25	7	US-10-719-900-347622	Sequence 347622,	C 476	12	60.0	25	5	US-09-954-427A-302998	Sequence 302998,
C 404	12.2	61.0	25	7	US-10-719-900-347623	Sequence 347623,	C 477	12	60.0	25	5	US-09-954-427A-338483	Sequence 338483,
C 405	12.2	61.0	25	7	US-10-719-900-349787	Sequence 349787,	C 478	12	60.0	25	5	US-09-954-427A-354886	Sequence 354886,
C 406	12.2	61.0	25	7	US-10-719-900-352554	Sequence 352554,	C 479	12	60.0	25	5	US-09-954-427A-368959	Sequence 368959,
C 407	12.2	61.0	25	7	US-10-719-900-352555	Sequence 352555,	C 480	12	60.0	25	5	US-09-954-427A-372020	Sequence 372020,
C 408	12.2	61.0	25	7	US-10-719-900-368866	Sequence 368866,	C 481	12	60.0	25	5	US-09-954-427A-394546	Sequence 394546,
C 409	12.2	61.0	25	7	US-10-719-900-395760	Sequence 395760,	C 482	12	60.0	25	7	US-10-717-597-4175	Sequence 4175, Ap
C 410	12.2	61.0	25	7	US-10-719-900-420692	Sequence 420692,	C 483	12	60.0	25	7	US-10-719-956-1415	Sequence 1415, Ap
C 411	12.2	61.0	25	7	US-10-719-900-489139	Sequence 489139,	C 484	12	60.0	25	7	US-10-719-956-14235	Sequence 14235, A
C 412	12.2	61.0	25	7	US-10-719-900-503865	Sequence 503865,	C 485	12	60.0	25	7	US-10-719-956-54546	Sequence 54546, A
C 413	12.2	61.0	25	7	US-10-719-900-530076	Sequence 530076,	C 486	12	60.0	25	7	US-10-719-956-65589	Sequence 65589, A
C 414	12.2	61.0	25	7	US-10-719-900-547482	Sequence 547482,	C 487	12	60.0	25	7	US-10-719-956-153423	Sequence 153423,
C 415	12.2	61.0	25	7	US-10-719-900-572711	Sequence 572711,	C 488	12	60.0	25	7	US-10-719-956-153424	Sequence 153424,
C 416	12.2	61.0	25	7	US-10-719-900-593350	Sequence 593350,	C 489	12	60.0	25	7	US-10-719-956-155391	Sequence 155391,
C 417	12.2	61.0	25	7	US-10-719-900-630406	Sequence 630406,	C 490	12	60.0	25	7	US-10-719-956-189768	Sequence 189768,
C 418	12.2	61.0	25	7	US-10-719-900-635349	Sequence 635349,	C 491	12	60.0	25	7	US-10-719-956-204178	Sequence 204178,
C 419	12.2	61.0	25	7	US-10-719-900-635663	Sequence 635663,	C 492	12	60.0	25	7	US-10-719-956-231722	Sequence 231722,
C 420	12.2	61.0	25	7	US-10-719-900-689515	Sequence 689515,	C 493	12	60.0	25	7	US-10-719-956-255337	Sequence 255337,
C 421	12.2	61.0	25	7	US-10-719-900-691287	Sequence 691287,	C 494	12	60.0	25	7	US-10-719-956-275049	Sequence 275049,
C 422	12.2	61.0	25	7	US-10-719-900-745602	Sequence 745602,	C 495	12	60.0	25	7	US-10-719-956-363384	Sequence 363384,
C 423	12.2	61.0	25	7	US-10-719-900-746095	Sequence 746095,	C 496	12	60.0	25	7	US-10-719-956-405683	Sequence 405683,
C 424	12.2	61.0	25	7	US-10-719-900-750050	Sequence 750050,	C 497	12	60.0	25	7	US-10-719-956-521402	Sequence 521402,
C 425	12.2	61.0	25	7	US-10-719-900-754842	Sequence 754842,	C 498	12	60.0	25	7	US-10-719-956-580693	Sequence 580693,
C 426	12.2	61.0	25	7	US-10-719-900-757389	Sequence 757389,	C 499	12	60.0	25	7	US-10-719-956-581511	Sequence 581511,
C 427	12.2	61.0	25	7	US-10-719-900-796207	Sequence 796207,	C 500	12	60.0	25	7	US-10-719-956-604022	Sequence 604022,
C 428	12.2	61.0	25	7	US-10-719-900-830099	Sequence 830099,	C 501	12	60.0	25	7	US-10-719-956-607106	Sequence 607106,
C 429	12.2	61.0	25	7	US-10-719-900-834294	Sequence 834294,	C 502	12	60.0	25	7	US-10-719-956-635444	Sequence 635444,
C 430	12.2	61.0	25	7	US-10-719-900-851082	Sequence 851082,	C 503	12	60.0	25	7	US-10-719-956-643683	Sequence 643683,
C 431	12.2	61.0	25	7	US-10-719-900-943611	Sequence 943611,	C 504	12	60.0	25	7	US-10-719-956-643683	Sequence 643683,
C 432	12.2	61.0	25	7	US-10-719-900-946603	Sequence 946603,	C 505	12	60.0	25	7	US-10-719-956-68547	Sequence 68547,
C 433	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 506	12	60.0	25	7	US-10-719-956-688548	Sequence 688548,
C 434	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 507	12	60.0	25	7	US-10-719-900-17939	Sequence 17939, A
C 435	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 508	12	60.0	25	7	US-10-719-900-29962	Sequence 29962, A
C 436	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 509	12	60.0	25	7	US-10-719-900-48630	Sequence 48630, A
C 437	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 510	12	60.0	25	7	US-10-719-900-204226	Sequence 204226,
C 438	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 511	12	60.0	25	7	US-10-719-900-277629	Sequence 277629,
C 439	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 512	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 440	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 513	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 441	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 514	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 442	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 515	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 443	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 516	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 444	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 517	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 445	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 518	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 446	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 519	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 447	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 520	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 448	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 521	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 449	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 522	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 450	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 523	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 451	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 524	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 452	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 525	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 453	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 526	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 454	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 527	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 455	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 528	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 456	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 529	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 457	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 530	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 458	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 531	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 459	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 532	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 460	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 533	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 461	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 534	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 462	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 535	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,
C 463	12.2	61.0	25	7	US-10-719-900-948959	Sequence 948959,	C 536	12	60.0	25	7	US-10-719-900-313792	Sequence 313792,

C 537	12	60.0	25	8	US-60-507-511-196036	Sequence 196036, A	C 610	11.8	59.0	25	7	US-10-719-956-144965	Sequence 144965,
C 538	12	60.0	25	8	US-60-507-481-32650	Sequence 32650, A	611	11.8	59.0	25	7	US-10-719-956-154442	Sequence 154442,
C 539	12	60.0	25	8	US-60-507-481-68791	Sequence 68791, A	612	11.8	59.0	25	7	US-10-719-956-160063	Sequence 160063,
C 540	12	60.0	25	8	US-60-507-481-112450	Sequence 112450, A	613	11.8	59.0	25	7	US-10-719-956-160059	Sequence 160059,
C 541	12	60.0	25	8	US-60-507-481-138778	Sequence 138778, A	C 614	11.8	59.0	25	7	US-10-719-956-264744	Sequence 264744,
C 542	12	60.0	25	8	US-60-507-481-145606	Sequence 145606, A	615	11.8	59.0	25	7	US-10-719-956-267693	Sequence 267693,
C 543	12	60.0	25	8	US-60-507-481-145606	Sequence 145606, A	616	11.8	59.0	25	7	US-10-719-956-268384	Sequence 268384,
C 544	12	60.0	25	8	US-60-507-481-183375	Sequence 183375, A	617	11.8	59.0	25	7	US-10-719-956-268384	Sequence 268384,
C 545	12	60.0	25	8	US-60-507-481-192697	Sequence 192697, A	C 618	11.8	59.0	25	7	US-10-719-956-313870	Sequence 313870,
C 546	12	60.0	25	8	US-60-507-481-192697	Sequence 192697, A	619	11.8	59.0	25	7	US-10-719-956-322366	Sequence 322366,
C 547	12	60.0	25	8	US-60-507-481-192697	Sequence 192697, A	C 620	11.8	59.0	25	7	US-10-719-956-327046	Sequence 327046,
C 548	12	60.0	25	8	US-60-507-481-192697	Sequence 192697, A	C 621	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 549	12	60.0	25	8	US-60-507-481-192697	Sequence 192697, A	C 622	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 550	11.8	59.0	25	7	US-10-712-633-1355	Sequence 1355, Ap	C 623	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 551	11.8	59.0	25	7	US-10-138-674A-1031	Sequence 1031, Ap	C 624	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 552	11.8	59.0	25	7	US-10-138-674A-8115	Sequence 8115, Ap	C 625	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 553	11.8	59.0	25	7	US-10-751-736-28112	Sequence 28112, A	C 626	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 554	11.8	59.0	25	7	US-10-751-736-32045	Sequence 32045, A	C 627	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 555	11.8	59.0	25	7	US-10-110-707A-42	Sequence 42, Appl	C 628	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 556	11.8	59.0	25	5	US-09-956-604D-10406	Sequence 10406, A	C 629	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 557	11.8	59.0	25	5	US-09-956-604D-51316	Sequence 51316, A	C 630	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 558	11.8	59.0	25	5	US-09-956-604D-53342	Sequence 53342, A	C 631	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 559	11.8	59.0	25	5	US-09-956-604D-55309	Sequence 55309, A	C 632	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 560	11.8	59.0	25	5	US-09-956-604D-55329	Sequence 55329, A	C 633	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 561	11.8	59.0	25	5	US-09-956-604D-78325	Sequence 78325, A	C 634	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 562	11.8	59.0	25	5	US-09-956-604D-106721	Sequence 106721, A	C 635	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 563	11.8	59.0	25	5	US-09-956-604D-123763	Sequence 123763, A	C 636	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 564	11.8	59.0	25	5	US-09-956-604D-139263	Sequence 139263, A	C 637	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 565	11.8	59.0	25	5	US-09-954-42B-3450	Sequence 3450, Ap	C 638	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 566	11.8	59.0	25	5	US-09-954-42B-3450	Sequence 3450, Ap	C 639	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 567	11.8	59.0	25	5	US-09-953-115A-26699	Sequence 26699, A	C 640	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 568	11.8	59.0	25	5	US-09-953-570A-26005	Sequence 26005, A	C 641	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 569	11.8	59.0	25	5	US-09-953-570A-40191	Sequence 40191, A	C 642	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 570	11.8	59.0	25	5	US-09-953-570A-57883	Sequence 57883, A	C 643	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 571	11.8	59.0	25	5	US-09-953-570A-57884	Sequence 57884, A	C 644	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 572	11.8	59.0	25	5	US-09-953-570A-129228	Sequence 129228, A	C 645	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 573	11.8	59.0	25	5	US-09-953-570A-129231	Sequence 129231, A	C 646	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 574	11.8	59.0	25	5	US-09-954-427A-39723	Sequence 39723, A	C 647	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 575	11.8	59.0	25	5	US-09-954-427A-39724	Sequence 39724, A	C 648	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 576	11.8	59.0	25	5	US-09-954-427A-48017	Sequence 48017, A	C 649	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 577	11.8	59.0	25	5	US-09-954-427A-68109	Sequence 68109, A	C 650	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 578	11.8	59.0	25	5	US-09-954-427A-136454	Sequence 136454, A	C 651	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 579	11.8	59.0	25	5	US-09-954-427A-216416	Sequence 216416, A	C 652	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 580	11.8	59.0	25	5	US-09-954-427A-235517	Sequence 235517, A	C 653	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 581	11.8	59.0	25	5	US-09-954-427A-268872	Sequence 268872, A	C 654	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 582	11.8	59.0	25	5	US-09-954-427A-268914	Sequence 268914, A	C 655	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 583	11.8	59.0	25	5	US-09-954-427A-284489	Sequence 284489, A	C 656	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 584	11.8	59.0	25	5	US-09-954-427A-284909	Sequence 284909, A	C 657	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 585	11.8	59.0	25	5	US-09-954-427A-287458	Sequence 287458, A	C 658	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 586	11.8	59.0	25	5	US-09-954-427A-287610	Sequence 287610, A	C 659	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 587	11.8	59.0	25	5	US-09-954-427A-298414	Sequence 298414, A	C 660	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 588	11.8	59.0	25	5	US-09-954-427A-319249	Sequence 319249, A	C 661	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 589	11.8	59.0	25	5	US-09-954-427A-319254	Sequence 319254, A	C 662	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 590	11.8	59.0	25	5	US-09-954-427A-343409	Sequence 343409, A	C 663	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 591	11.8	59.0	25	5	US-09-954-427A-346226	Sequence 346226, A	C 664	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 592	11.8	59.0	25	5	US-09-954-427A-372007	Sequence 372007, A	C 665	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 593	11.8	59.0	25	5	US-09-954-427A-416145	Sequence 416145, A	C 666	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 594	11.8	59.0	25	6	US-10-681-113-88	Sequence 88, Appl	C 667	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 595	11.8	59.0	25	7	US-10-681-773-51493	Sequence 51493, A	C 668	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 596	11.8	59.0	25	7	US-10-681-773-60303	Sequence 60303, A	C 669	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 597	11.8	59.0	25	7	US-10-681-773-115641	Sequence 115641, A	C 670	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 598	11.8	59.0	25	7	US-10-681-773-120822	Sequence 120822, A	C 671	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 599	11.8	59.0	25	7	US-10-719-956-7462	Sequence 7462, Ap	C 672	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 600	11.8	59.0	25	7	US-10-719-956-7560	Sequence 7560, Ap	C 673	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 601	11.8	59.0	25	7	US-10-719-956-57078	Sequence 57078, A	C 674	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 602	11.8	59.0	25	7	US-10-719-956-66483	Sequence 66483, A	C 675	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 603	11.8	59.0	25	7	US-10-719-956-66483	Sequence 66483, A	C 676	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 604	11.8	59.0	25	7	US-10-719-956-66869	Sequence 66869, A	C 677	11.8	59.0	25	7	US-10-719-956-327842	Sequence 327842,
C 605	11.8	59.0	25	7	US-10-719-956-77945	Sequence 77945, A	C 678	11.8	59.0	25	8	US-60-507-511-10400	Sequence 10400, A
C 606	11.8	59.0	25	7	US-10-719-956-88831	Sequence 88831, A	C 679	11.8	59.0	25	8	US-60-507-511-13066	Sequence 13066, A
C 607	11.8	59.0	25	7	US-10-719-956-96069	Sequence 96069, A	C 680	11.8	59.0	25	8	US-60-507-511-78554	Sequence 78554, A
C 608	11.8	59.0	25	7	US-10-719-956-129914	Sequence 129914, A	C 681	11.8	59.0	25	8	US-60-507-511-116749	Sequence 116749, A
C 609	11.8	59.0	25	7	US-10-719-956-129914	Sequence 129914, A	C 682	11.8	59.0	25	8	US-60-507-511-116749	Sequence 116749, A

us-10-002-884a-5.max.rnpn

Thu Jan 29 10:08:41 2004

683	11.8	59.0	25	8	US-60-507-511-123628	Sequence 123628,	756	11.6	58.0	25	5	US-09-954-429B-10401	Sequence 10401, A
684	11.8	59.0	25	8	US-60-507-511-136646	Sequence 136646,	757	11.6	58.0	25	5	US-09-954-429B-16244	Sequence 16244, A
685	11.8	59.0	25	8	US-60-507-511-158897	Sequence 158897,	c 758	11.6	58.0	25	5	US-09-953-115A-6124	Sequence 6124, Ap
686	11.8	59.0	25	8	US-60-507-511-184440	Sequence 184440,	c 759	11.6	58.0	25	5	US-09-953-115A-24430	Sequence 24430, A
687	11.8	59.0	25	8	US-60-507-481-19015	Sequence 19015, A	c 760	11.6	58.0	25	5	US-09-953-570A-22351	Sequence 22351, A
688	11.8	59.0	25	8	US-60-507-481-23841	Sequence 23841, A	c 761	11.6	58.0	25	5	US-09-953-570A-31305	Sequence 31305, A
689	11.8	59.0	25	8	US-60-507-481-50030	Sequence 50030, A	c 762	11.6	58.0	25	5	US-09-953-570A-37372	Sequence 37372, A
690	11.8	59.0	25	8	US-60-507-481-66786	Sequence 66786, A	c 763	11.6	58.0	25	5	US-09-953-570A-37400	Sequence 37400, A
691	11.8	59.0	25	8	US-60-507-481-72712	Sequence 72712, A	c 764	11.6	58.0	25	5	US-09-953-570A-51518	Sequence 51518, A
692	11.8	59.0	25	8	US-60-507-481-80181	Sequence 80181, A	c 765	11.6	58.0	25	5	US-09-953-570A-52610	Sequence 52610, A
693	11.8	59.0	25	8	US-60-507-481-80563	Sequence 80563, A	c 766	11.6	58.0	25	5	US-09-953-570A-107810	Sequence 107810, A
694	11.8	59.0	25	8	US-60-507-481-83370	Sequence 83370, A	c 767	11.6	58.0	25	5	US-09-953-570A-116531	Sequence 116531, A
695	11.8	59.0	25	8	US-60-507-481-102034	Sequence 102034,	c 768	11.6	58.0	25	5	US-09-954-427A-7819	Sequence 7819, Ap
696	11.8	59.0	25	8	US-60-507-481-111208	Sequence 111208,	c 769	11.6	58.0	25	5	US-09-954-427A-13277	Sequence 13277, A
697	11.8	59.0	25	8	US-60-507-481-112723	Sequence 112723,	c 770	11.6	58.0	25	5	US-09-954-427A-21687	Sequence 21687, A
698	11.8	59.0	25	8	US-60-507-481-145913	Sequence 145913,	c 771	11.6	58.0	25	5	US-09-954-427A-22164	Sequence 22164, A
699	11.8	59.0	25	8	US-60-507-481-148129	Sequence 148129,	c 772	11.6	58.0	25	5	US-09-954-427A-33417	Sequence 33417, A
700	11.8	59.0	25	8	US-60-507-481-149260	Sequence 149260,	c 773	11.6	58.0	25	5	US-09-954-427A-46098	Sequence 46098, A
701	11.8	59.0	25	8	US-60-507-481-159274	Sequence 159274,	c 774	11.6	58.0	25	5	US-09-954-427A-47699	Sequence 47699, A
702	11.8	59.0	25	8	US-60-507-481-206833	Sequence 206833,	c 775	11.6	58.0	25	5	US-09-954-427A-47725	Sequence 47725, A
703	11.8	59.0	25	8	US-60-507-481-208388	Sequence 208388,	c 776	11.6	58.0	25	5	US-09-954-427A-54556	Sequence 54556, A
704	11.8	59.0	28	5	US-09-955-225B-25	Sequence 25, Appl	c 777	11.6	58.0	25	5	US-09-954-427A-58412	Sequence 58412, A
705	11.8	59.0	32	7	US-10-707-147-5317	Sequence 5317, Ap	c 778	11.6	58.0	25	5	US-09-954-427A-80413	Sequence 80413, A
706	11.8	59.0	32	7	US-10-707-147-15657	Sequence 15657, A	c 779	11.6	58.0	25	5	US-09-954-427A-90080	Sequence 90080, A
707	11.8	59.0	37	5	US-09-581-286A-673	Sequence 673, App	c 780	11.6	58.0	25	5	US-09-954-427A-106175	Sequence 106175, A
708	11.8	59.0	38	7	US-10-471-271-5777	Sequence 5777, Ap	c 781	11.6	58.0	25	5	US-09-954-427A-172967	Sequence 172967, A
709	11.8	59.0	38	7	US-10-471-271-7123	Sequence 7123, Ap	c 782	11.6	58.0	25	5	US-09-954-427A-182285	Sequence 182285, A
710	11.8	59.0	38	7	US-10-471-271-7598	Sequence 7598, Ap	c 783	11.6	58.0	25	5	US-09-954-427A-187137	Sequence 187137, A
711	11.8	59.0	38	7	US-10-471-271-9951	Sequence 9951, Ap	c 784	11.6	58.0	25	5	US-09-954-427A-211376	Sequence 211376, A
712	11.8	59.0	38	7	US-10-669-841-7847	Sequence 7847, Ap	c 785	11.6	58.0	25	5	US-09-954-427A-213177	Sequence 213177, A
713	11.8	59.0	38	7	US-10-712-672-3750	Sequence 3750, Ap	c 786	11.6	58.0	25	5	US-09-954-427A-213183	Sequence 213183, A
714	11.8	59.0	38	7	US-10-138-674A-9954	Sequence 9954, Ap	c 787	11.6	58.0	25	5	US-09-954-427A-224027	Sequence 224027, A
715	11.8	59.0	38	7	US-10-138-674A-11203	Sequence 11203, A	c 788	11.6	58.0	25	5	US-09-954-427A-224636	Sequence 224636, A
716	11.8	59.0	38	7	US-10-138-674A-11578	Sequence 11578, A	c 789	11.6	58.0	25	5	US-09-954-427A-224648	Sequence 224648, A
717	11.8	59.0	38	7	US-10-138-674A-11903	Sequence 11903, A	c 790	11.6	58.0	25	5	US-09-954-427A-229966	Sequence 229966, A
718	11.8	59.0	38	7	US-10-138-674A-12853	Sequence 12853, A	c 791	11.6	58.0	25	5	US-09-954-427A-255388	Sequence 255388, A
719	11.6	58.0	18	1	PCT-US02-38216-51499	Sequence 51499, A	c 792	11.6	58.0	25	5	US-09-954-427A-258579	Sequence 258579, A
720	11.6	58.0	19	6	US-10-746-556-19	Sequence 19, Appl	c 793	11.6	58.0	25	5	US-09-954-427A-261464	Sequence 261464, A
721	11.6	58.0	20	1	PCT-US03-25389-3109	Sequence 3109, Ap	c 794	11.6	58.0	25	5	US-09-954-427A-261502	Sequence 261502, A
722	11.6	58.0	20	1	PCT-US03-25389-3274	Sequence 3274, Ap	c 795	11.6	58.0	25	5	US-09-954-427A-261701	Sequence 261701, A
723	11.6	58.0	21	6	US-10-751-736-24890	Sequence 24890, A	c 796	11.6	58.0	25	5	US-09-954-427A-300719	Sequence 300719, A
724	11.6	58.0	21	6	US-10-751-736-24890	Sequence 24890, A	c 797	11.6	58.0	25	5	US-09-954-427A-300724	Sequence 300724, A
725	11.6	58.0	23	5	US-09-852-238A-3	Sequence 4234, A	c 798	11.6	58.0	25	5	US-09-954-427A-308337	Sequence 308337, A
726	11.6	58.0	23	6	US-10-739-904-59	Sequence 3, Appl	c 799	11.6	58.0	25	5	US-09-954-427A-310044	Sequence 310044, A
727	11.6	58.0	23	6	US-10-707-147-503	Sequence 59, Appl	c 800	11.6	58.0	25	5	US-09-954-427A-320485	Sequence 320485, A
728	11.6	58.0	24	7	US-10-457-839-52	Sequence 503, App	c 801	11.6	58.0	25	5	US-09-954-427A-320485	Sequence 320485, A
729	11.6	58.0	25	1	PCT-US02-38216-17708	Sequence 52, Appl	c 802	11.6	58.0	25	5	US-09-954-427A-335269	Sequence 335269, A
730	11.6	58.0	25	5	US-09-956-604D-729	Sequence 17708, A	c 803	11.6	58.0	25	5	US-09-954-427A-335269	Sequence 335269, A
731	11.6	58.0	25	5	US-09-956-604D-791	Sequence 729, App	c 804	11.6	58.0	25	5	US-09-954-427A-335444	Sequence 335444, A
732	11.6	58.0	25	5	US-09-956-604D-811	Sequence 791, App	c 805	11.6	58.0	25	5	US-09-954-427A-354592	Sequence 354592, A
733	11.6	58.0	25	5	US-09-956-604D-811	Sequence 811, App	c 806	11.6	58.0	25	5	US-09-954-427A-355420	Sequence 355420, A
734	11.6	58.0	25	5	US-09-956-604D-7851	Sequence 8105, Ap	c 807	11.6	58.0	25	5	US-09-954-427A-391786	Sequence 391786, A
735	11.6	58.0	25	5	US-09-956-604D-17912	Sequence 7851, Ap	c 808	11.6	58.0	25	5	US-09-954-427A-391809	Sequence 391809, A
736	11.6	58.0	25	5	US-09-956-604D-18317	Sequence 17932, A	c 809	11.6	58.0	25	5	US-09-954-427A-398843	Sequence 398843, A
737	11.6	58.0	25	5	US-09-956-604D-29661	Sequence 18317, A	c 810	11.6	58.0	25	5	US-09-954-427A-401040	Sequence 401040, A
738	11.6	58.0	25	5	US-09-956-604D-29729	Sequence 29661, A	c 811	11.6	58.0	25	5	US-10-681-773-8998	Sequence 8998, Ap
739	11.6	58.0	25	5	US-09-956-604D-31771	Sequence 29729, A	c 812	11.6	58.0	25	7	US-10-681-773-31485	Sequence 31485, A
740	11.6	58.0	25	5	US-09-956-604D-46322	Sequence 31771, A	c 813	11.6	58.0	25	7	US-10-681-773-48251	Sequence 48251, A
741	11.6	58.0	25	5	US-09-956-604D-49164	Sequence 46322, A	c 814	11.6	58.0	25	7	US-10-681-773-64196	Sequence 64196, A
742	11.6	58.0	25	5	US-09-956-604D-49994	Sequence 49164, A	c 815	11.6	58.0	25	7	US-10-719-956-2695	Sequence 2695, Ap
743	11.6	58.0	25	5	US-09-956-604D-49994	Sequence 49994, A	c 816	11.6	58.0	25	7	US-10-719-956-7548	Sequence 7548, Ap
744	11.6	58.0	25	5	US-09-956-604D-63681	Sequence 63681, A	c 817	11.6	58.0	25	7	US-10-719-956-12294	Sequence 12294, A
745	11.6	58.0	25	5	US-09-956-604D-76447	Sequence 76447, A	c 818	11.6	58.0	25	7	US-10-719-956-12296	Sequence 12296, A
746	11.6	58.0	25	5	US-09-956-604D-96656	Sequence 96656, A	c 819	11.6	58.0	25	7	US-10-719-956-13969	Sequence 13969, A
747	11.6	58.0	25	5	US-09-956-604D-96714	Sequence 96714, A	c 820	11.6	58.0	25	7	US-10-719-956-13970	Sequence 13970, A
748	11.6	58.0	25	5	US-09-956-604D-115420	Sequence 115420, A	c 821	11.6	58.0	25	7	US-10-719-956-16374	Sequence 16374, A
749	11.6	58.0	25	5	US-09-956-604D-115426	Sequence 115426, A	c 822	11.6	58.0	25	7	US-10-719-956-27575	Sequence 27575, A
750	11.6	58.0	25	5	US-09-956-604D-125430	Sequence 125430, A	c 823	11.6	58.0	25	7	US-10-719-956-45208	Sequence 45208, A
751	11.6	58.0	25	5	US-09-956-604D-131259	Sequence 131259, A	c 824	11.6	58.0	25	7	US-10-719-956-49071	Sequence 49071, A
752	11.6	58.0	25	5	US-09-956-604D-138382	Sequence 138382, A	c 825	11.6	58.0	25	7	US-10-719-956-51903	Sequence 51903, A
753	11.6	58.0	25	5	US-09-956-604D-139545	Sequence 139545, A	c 826	11.6	58.0	25	7	US-10-719-956-56222	Sequence 56222, A
754	11.6	58.0	25	5	US-09-954-429-10401	Sequence 10401, A	c 827	11.6	58.0	25	7	US-10-719-956-67248	Sequence 67248, A
755	11.6	58.0	25	5	US-09-954-429-16244	Sequence 16244, A	c 828	11.6	58.0	25	7	US-10-719-956-71154	Sequence 71154, A

C 829	11.6	58.0	25	7	US-10-719-956-82917	Sequence 82917, A	902	11.6	58.0	25	7	US-10-719-900-152782	Sequence 152782,
C 830	11.6	58.0	25	7	US-10-719-956-110034	Sequence 110034,	C 903	11.6	58.0	25	7	US-10-719-900-176848	Sequence 176848,
C 831	11.6	58.0	25	7	US-10-719-956-117963	Sequence 117963,	904	11.6	58.0	25	7	US-10-719-900-179446	Sequence 179446,
C 832	11.6	58.0	25	7	US-10-719-956-146113	Sequence 146113,	C 905	11.6	58.0	25	7	US-10-719-900-185023	Sequence 185023,
C 833	11.6	58.0	25	7	US-10-719-956-147801	Sequence 147801,	C 906	11.6	58.0	25	7	US-10-719-900-189452	Sequence 189452,
C 834	11.6	58.0	25	7	US-10-719-956-163394	Sequence 163394,	C 907	11.6	58.0	25	7	US-10-719-900-210751	Sequence 210751,
C 835	11.6	58.0	25	7	US-10-719-956-170347	Sequence 170347,	C 908	11.6	58.0	25	7	US-10-719-900-230909	Sequence 230909,
C 836	11.6	58.0	25	7	US-10-719-956-175549	Sequence 175549,	909	11.6	58.0	25	7	US-10-719-900-247957	Sequence 247957,
C 837	11.6	58.0	25	7	US-10-719-956-175549	Sequence 175549,	910	11.6	58.0	25	7	US-10-719-900-262332	Sequence 262332,
C 838	11.6	58.0	25	7	US-10-719-956-184839	Sequence 184839,	911	11.6	58.0	25	7	US-10-719-900-270411	Sequence 270411,
C 839	11.6	58.0	25	7	US-10-719-956-184839	Sequence 184839,	912	11.6	58.0	25	7	US-10-719-900-275068	Sequence 275068,
C 840	11.6	58.0	25	7	US-10-719-956-185996	Sequence 185996,	C 913	11.6	58.0	25	7	US-10-719-900-292504	Sequence 292504,
C 841	11.6	58.0	25	7	US-10-719-956-187649	Sequence 187649,	C 914	11.6	58.0	25	7	US-10-719-900-315418	Sequence 315418,
C 842	11.6	58.0	25	7	US-10-719-956-187757	Sequence 187757,	915	11.6	58.0	25	7	US-10-719-900-317105	Sequence 317105,
C 843	11.6	58.0	25	7	US-10-719-956-194362	Sequence 194362,	916	11.6	58.0	25	7	US-10-719-900-322734	Sequence 322734,
C 844	11.6	58.0	25	7	US-10-719-956-201541	Sequence 201541,	917	11.6	58.0	25	7	US-10-719-900-322735	Sequence 322735,
C 845	11.6	58.0	25	7	US-10-719-956-207829	Sequence 207829,	918	11.6	58.0	25	7	US-10-719-900-324761	Sequence 324761,
C 846	11.6	58.0	25	7	US-10-719-956-214534	Sequence 214534,	919	11.6	58.0	25	7	US-10-719-900-325025	Sequence 325025,
C 847	11.6	58.0	25	7	US-10-719-956-235147	Sequence 235147,	920	11.6	58.0	25	7	US-10-719-900-327007	Sequence 327007,
C 848	11.6	58.0	25	7	US-10-719-956-279847	Sequence 279847,	921	11.6	58.0	25	7	US-10-719-900-335061	Sequence 335061,
C 849	11.6	58.0	25	7	US-10-719-956-281204	Sequence 281204,	922	11.6	58.0	25	7	US-10-719-900-352187	Sequence 352187,
C 850	11.6	58.0	25	7	US-10-719-956-302141	Sequence 302141,	923	11.6	58.0	25	7	US-10-719-900-390214	Sequence 390214,
C 851	11.6	58.0	25	7	US-10-719-956-319841	Sequence 319841,	924	11.6	58.0	25	7	US-10-719-900-396381	Sequence 396381,
C 852	11.6	58.0	25	7	US-10-719-956-323365	Sequence 323365,	925	11.6	58.0	25	7	US-10-719-900-399667	Sequence 399667,
C 853	11.6	58.0	25	7	US-10-719-956-329086	Sequence 329086,	926	11.6	58.0	25	7	US-10-719-900-401635	Sequence 401635,
C 854	11.6	58.0	25	7	US-10-719-956-342162	Sequence 342162,	C 927	11.6	58.0	25	7	US-10-719-900-406651	Sequence 406651,
C 855	11.6	58.0	25	7	US-10-719-956-342163	Sequence 342163,	C 928	11.6	58.0	25	7	US-10-719-900-406652	Sequence 406652,
C 856	11.6	58.0	25	7	US-10-719-956-363556	Sequence 363556,	929	11.6	58.0	25	7	US-10-719-900-437390	Sequence 437390,
C 857	11.6	58.0	25	7	US-10-719-956-385175	Sequence 385175,	930	11.6	58.0	25	7	US-10-719-900-441643	Sequence 441643,
C 858	11.6	58.0	25	7	US-10-719-956-386616	Sequence 386616,	931	11.6	58.0	25	7	US-10-719-900-444236	Sequence 444236,
C 859	11.6	58.0	25	7	US-10-719-956-401407	Sequence 401407,	C 932	11.6	58.0	25	7	US-10-719-900-471751	Sequence 471751,
C 860	11.6	58.0	25	7	US-10-719-956-402056	Sequence 402056,	933	11.6	58.0	25	7	US-10-719-900-487021	Sequence 487021,
C 861	11.6	58.0	25	7	US-10-719-956-403069	Sequence 403069,	934	11.6	58.0	25	7	US-10-719-900-509769	Sequence 509769,
C 862	11.6	58.0	25	7	US-10-719-956-406592	Sequence 406592,	935	11.6	58.0	25	7	US-10-719-900-511305	Sequence 511305,
C 863	11.6	58.0	25	7	US-10-719-956-416768	Sequence 416768,	936	11.6	58.0	25	7	US-10-719-900-514433	Sequence 514433,
C 864	11.6	58.0	25	7	US-10-719-956-416769	Sequence 416769,	C 937	11.6	58.0	25	7	US-10-719-900-527558	Sequence 527558,
C 865	11.6	58.0	25	7	US-10-719-956-421775	Sequence 421775,	C 938	11.6	58.0	25	7	US-10-719-900-534690	Sequence 534690,
C 866	11.6	58.0	25	7	US-10-719-956-421775	Sequence 421775,	C 939	11.6	58.0	25	7	US-10-719-900-534691	Sequence 534691,
C 867	11.6	58.0	25	7	US-10-719-956-450425	Sequence 450425,	940	11.6	58.0	25	7	US-10-719-900-540247	Sequence 540247,
C 868	11.6	58.0	25	7	US-10-719-956-479682	Sequence 479682,	941	11.6	58.0	25	7	US-10-719-900-557378	Sequence 557378,
C 869	11.6	58.0	25	7	US-10-719-956-479869	Sequence 479869,	C 942	11.6	58.0	25	7	US-10-719-900-582249	Sequence 582249,
C 870	11.6	58.0	25	7	US-10-719-956-493679	Sequence 493679,	C 943	11.6	58.0	25	7	US-10-719-900-617279	Sequence 617279,
C 871	11.6	58.0	25	7	US-10-719-956-501990	Sequence 501990,	944	11.6	58.0	25	7	US-10-719-900-648673	Sequence 648673,
C 872	11.6	58.0	25	7	US-10-719-956-506298	Sequence 506298,	C 945	11.6	58.0	25	7	US-10-719-900-655261	Sequence 655261,
C 873	11.6	58.0	25	7	US-10-719-956-506797	Sequence 506797,	C 946	11.6	58.0	25	7	US-10-719-900-697853	Sequence 697853,
C 874	11.6	58.0	25	7	US-10-719-956-508489	Sequence 508489,	947	11.6	58.0	25	7	US-10-719-900-705611	Sequence 705611,
C 875	11.6	58.0	25	7	US-10-719-956-517711	Sequence 517711,	C 948	11.6	58.0	25	7	US-10-719-900-720031	Sequence 720031,
C 876	11.6	58.0	25	7	US-10-719-956-540378	Sequence 540378,	949	11.6	58.0	25	7	US-10-719-900-729965	Sequence 729965,
C 877	11.6	58.0	25	7	US-10-719-956-540379	Sequence 540379,	C 950	11.6	58.0	25	7	US-10-719-900-731053	Sequence 731053,
C 878	11.6	58.0	25	7	US-10-719-956-552141	Sequence 552141,	C 951	11.6	58.0	25	7	US-10-719-900-733942	Sequence 733942,
C 879	11.6	58.0	25	7	US-10-719-956-571043	Sequence 571043,	C 952	11.6	58.0	25	7	US-10-719-900-734151	Sequence 734151,
C 880	11.6	58.0	25	7	US-10-719-956-585816	Sequence 585816,	953	11.6	58.0	25	7	US-10-719-900-738696	Sequence 738696,
C 881	11.6	58.0	25	7	US-10-719-956-589063	Sequence 589063,	954	11.6	58.0	25	7	US-10-719-900-742431	Sequence 742431,
C 882	11.6	58.0	25	7	US-10-719-956-623403	Sequence 623403,	955	11.6	58.0	25	7	US-10-719-900-761761	Sequence 761761,
C 883	11.6	58.0	25	7	US-10-719-956-627506	Sequence 627506,	956	11.6	58.0	25	7	US-10-719-900-786823	Sequence 786823,
C 884	11.6	58.0	25	7	US-10-719-956-639736	Sequence 639736,	C 957	11.6	58.0	25	7	US-10-719-900-807260	Sequence 807260,
C 885	11.6	58.0	25	7	US-10-719-956-646418	Sequence 646418,	C 958	11.6	58.0	25	7	US-10-719-900-841280	Sequence 841280,
C 886	11.6	58.0	25	7	US-10-719-956-672091	Sequence 672091,	959	11.6	58.0	25	7	US-10-719-900-842733	Sequence 842733,
C 887	11.6	58.0	25	7	US-10-719-956-673473	Sequence 673473,	C 960	11.6	58.0	25	7	US-10-719-900-847689	Sequence 847689,
C 888	11.6	58.0	25	7	US-10-719-956-682060	Sequence 682060,	961	11.6	58.0	25	7	US-10-719-900-867398	Sequence 867398,
C 889	11.6	58.0	25	7	US-10-719-956-683690	Sequence 683690,	C 962	11.6	58.0	25	7	US-10-719-900-868117	Sequence 868117,
C 890	11.6	58.0	25	7	US-10-719-956-692517	Sequence 692517,	963	11.6	58.0	25	7	US-10-719-900-874461	Sequence 874461,
C 891	11.6	58.0	25	7	US-10-719-956-693783	Sequence 693783,	C 964	11.6	58.0	25	7	US-10-719-900-874462	Sequence 874462,
C 892	11.6	58.0	25	7	US-10-719-956-693946	Sequence 693946,	C 965	11.6	58.0	25	7	US-10-719-900-911927	Sequence 911927,
C 893	11.6	58.0	25	7	US-10-719-900-5274	Sequence 5274, Ap	966	11.6	58.0	25	7	US-10-719-900-912854	Sequence 912854,
C 894	11.6	58.0	25	7	US-10-719-900-44588	Sequence 44588, A	967	11.6	58.0	25	7	US-10-719-900-941240	Sequence 941240,
C 895	11.6	58.0	25	7	US-10-719-900-59277	Sequence 59277, A	968	11.6	58.0	25	7	US-10-719-900-941513	Sequence 941513,
C 896	11.6	58.0	25	7	US-10-719-900-74972	Sequence 74972, A	C 969	11.6	58.0	25	7	US-10-719-900-944666	Sequence 944666,
C 897	11.6	58.0	25	7	US-10-719-900-79074	Sequence 79074, A	970	11.6	58.0	25	7	US-10-719-900-952911	Sequence 952911,
C 898	11.6	58.0	25	7	US-10-719-900-110915	Sequence 110915,	C 971	11.6	58.0	25	7	US-10-719-900-952911	Sequence 952911,
C 899	11.6	58.0	25	7	US-10-719-900-137080	Sequence 137080,	972	11.6	58.0	25	8	US-60-507-511-7000	Sequence 7000, Ap
C 900	11.6	58.0	25	7	US-10-719-900-143332	Sequence 143332,	C 973	11.6	58.0	25	8	US-60-507-511-27940	Sequence 27940, A
C 901	11.6	58.0	25	7	US-10-719-900-149958	Sequence 149958,	C 974	11.6	58.0	25	8	US-60-507-511-42159	Sequence 42159, A

Thu Jan 29 10:08:41 2004

us-10-002-884a-5.max.rnpn

```

975 11.6 58.0 25 8 US-60-507-511-73067
976 11.6 58.0 25 8 US-60-507-511-73068
977 11.6 58.0 25 8 US-60-507-511-73069
978 11.6 58.0 25 8 US-60-507-511-83110
979 11.6 58.0 25 8 US-60-507-511-83768
980 11.6 58.0 25 8 US-60-507-511-102966
981 11.6 58.0 25 8 US-60-507-511-115772
982 11.6 58.0 25 8 US-60-507-511-115778
983 11.6 58.0 25 8 US-60-507-511-135778
984 11.6 58.0 25 8 US-60-507-511-160150
985 11.6 58.0 25 8 US-60-507-511-166096
986 11.6 58.0 25 8 US-60-507-511-167242
987 11.6 58.0 25 8 US-60-507-511-170000
988 11.6 58.0 25 8 US-60-507-511-170893
989 11.6 58.0 25 8 US-60-507-511-174135
990 11.6 58.0 25 8 US-60-507-511-176768
991 11.6 58.0 25 8 US-60-507-511-176769
992 11.6 58.0 25 8 US-60-507-511-195152
993 11.6 58.0 25 8 US-60-507-511-202453
994 11.6 58.0 25 8 US-60-507-481-19442
995 11.6 58.0 25 8 US-60-507-481-30249
996 11.6 58.0 25 8 US-60-507-481-42669
997 11.6 58.0 25 8 US-60-507-481-45811
998 11.6 58.0 25 8 US-60-507-481-49796
999 11.6 58.0 25 8 US-60-507-481-70512
1000 11.6 58.0 25 8 US-60-507-481-83028
1001 11.6 58.0 25 8 US-60-507-481-203738

```

ALIGNMENTS

```

RESULT 1
PCT-US03-25935-268
; Sequence 268, Application PC/TUS0325935
; GENERAL INFORMATION:
; APPLICANT: COLEY PHARMACEUTICAL GROUP, INC.
; APPLICANT: COLEY PHARMACEUTICAL GMBH
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS
; FILE REFERENCE: C01037.70048 US
; CURRENT APPLICATION NUMBER: PCT/US03/25935
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,479
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/447,377
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/404,820
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 268
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligodeoxynucleotide
PCT-US03-25935-268

```

```

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

```

```

RESULT 2
PCT-US03-25935-269
; Sequence 269, Application PC/TUS0325935
; GENERAL INFORMATION:
; APPLICANT: COLEY PHARMACEUTICAL GROUP, INC.
; APPLICANT: COLEY PHARMACEUTICAL GMBH
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACIDS

```

```

; FILE REFERENCE: C01037.70048 US
; CURRENT APPLICATION NUMBER: PCT/US03/25935
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,479
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/447,377
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/404,820
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 269
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligodeoxynucleotide
PCT-US03-25935-269

```

```

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

```

```

RESULT 3
US-09-546-596A-22
; Sequence 22, Application US/09546596A
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; Cook, Phillip D.
; Bennett, C. Frank
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; ENHANCED BIOTABILITY AND ALTERED BIODISTRIBUTION OF
; OLIGONUCLEOTIDES IN MAMMALS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; and Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/546,596A
; APPLICATION NUMBER: US/09/546,596A
; FILING DATE: 10-Apr-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lucchi, Joseph
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2707
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-546-596A-22

```

Query Match 100.0%; Score 20; DB 5; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.4;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|:|||||
Db 1 GUTCTCGCTGGTGAGTTTCA 20

RESULT 4

US-10-437-275-23
; Sequence 23, Application US/10437275
; GENERAL INFORMATION:
; APPLICANT: Tam, Ying K.
; APPLICANT: Semple, Sean
; APPLICANT: Klimuk, Sandra
; APPLICANT: Chikh, Ghania
; TITLE OF INVENTION: METHYLATED IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND METHODS OF
; FILE REFERENCE: A-72159/TAL
; CURRENT APPLICATION NUMBER: US/10/437,275
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/290,545
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-437-275-23

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|:|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 5

US-10-447-136-217
; Sequence 217, Application US/10447136
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; FILE REFERENCE: 032396-023
; CURRENT APPLICATION NUMBER: US/10/447,136
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/249,247
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/023,040
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/039,959
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/904,901
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-10-447-136-217

Query Match 100.0%; Score 20; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|:|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 6

US-10-437-263-23
; Sequence 23, Application US/10437263
; GENERAL INFORMATION:
; APPLICANT: Semple, Sean
; APPLICANT: Tam, Ying K.
; APPLICANT: Chikh, Ghania
; APPLICANT: Hope, Michael J.
; TITLE OF INVENTION: PATHOGEN VACCINES AND METHODS FOR USING THE SAME
; FILE REFERENCE: A-72216/TAL
; CURRENT APPLICATION NUMBER: US/10/437,263
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/454,298
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-437-263-23

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|:|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 7

US-10-437-258-23
; Sequence 23, Application US/10437258
; GENERAL INFORMATION:
; APPLICANT: Tam, Ying K.
; APPLICANT: Semple, Sean
; APPLICANT: Klimuk, Sandra
; APPLICANT: Chikh, Ghania
; TITLE OF INVENTION: CANCER VACCINES AND METHODS OF USING THE SAME
; FILE REFERENCE: A-72252/TAL
; CURRENT APPLICATION NUMBER: US/10/437,258
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/454,298
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-437-258-23

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Thu Jan 29 10:08:41 2004

us-10-002-884a-5.max.rnpn

Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGGATTCA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GTTCTCGCTGGTGGATTCA 20

RESULT 10
PCT-US03-23344-2
; Sequence 2, Application PC/TUS0323344
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; TITLE OF INVENTION: Universal Support Media for Synthesis of Oligomeric Compounds
; FILE REFERENCE: ISIS-5242
; CURRENT APPLICATION NUMBER: PCT/US03/23344
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/400,312
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 10/260,076
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 10/364,034
; PRIOR FILING DATE: 2003-02-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
PCT-US03-23344-2

Query Match 95.0%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.5; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGGATTTC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GTTCTCGCTGGTGGATTTC 19

RESULT 11
US-10-719-900-549041/c
; Sequence 549041, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; FILE REFERENCE: 3528.1
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 549041
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-549041

Query Match 77.0%; Score 15.4; DB 7; Length 25;
Best Local Similarity 94.1%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGGATT 17
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GTTCTCGCTGGTGGATT 4

RESULT 12
US-09-954-427A-364371/c
; Sequence 364371, Application US/09954427A

QY 1 GTTCTCGCTGGTGGATTCA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GTTCTCGCTGGTGGATTCA 20

RESULT 8
US-10-181-200-4
; Sequence 4, Application US/10181200
; GENERAL INFORMATION:
; APPLICANT: Cole, Douglas L.
; APPLICANT: Ravikumar, Vasulunga T.
; APPLICANT: Cheruvallath, Zacharia S.
; TITLE OF INVENTION: IMPROVED SYNTHESIS OF SULFURIZED OLIGONUCLEOTIDES
; FILE REFERENCE: ISIS-4709
; CURRENT APPLICATION NUMBER: US/10/181,200
; CURRENT FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: PCT/US01/00715
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 09/481,486
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; LOCATION: (1)-(20)
; OTHER INFORMATION: phosphorothioate 20-mer
US-10-181-200-4

Query Match 100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGGATTCA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GTTCTCGCTGGTGGATTCA 20

RESULT 9
US-10-181-200-4
; Sequence 4, Application US/10181200
; GENERAL INFORMATION:
; APPLICANT: Cole, Douglas L.
; APPLICANT: Ravikumar, Vasulunga T.
; APPLICANT: Cheruvallath, Zacharia S.
; TITLE OF INVENTION: IMPROVED SYNTHESIS OF SULFURIZED OLIGONUCLEOTIDES
; FILE REFERENCE: ISIS-4709
; CURRENT APPLICATION NUMBER: US/10/181,200
; CURRENT FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: PCT/US01/00715
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 09/481,486
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; LOCATION: (1)-(20)
; OTHER INFORMATION: phosphorothioate 20-mer
US-10-181-200-4

Query Match 100.0%; Score 20; DB 7; Length 20;

```
; GENERAL INFORMATION:
; APPLICANT: Michael Wittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 364371
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-364371

Query Match          76.0%; Score 15.2; DB 5; Length 25;
Best Local Similarity 85.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    ||||| ||||| |||||
Db 21 GTTCTGGATGGTCAGTTTCA 2

RESULT 13
US-10-719-956-137615
; Sequence 137615, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 137615
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-137615

Query Match          76.0%; Score 15.2; DB 7; Length 25;
Best Local Similarity 85.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    ||||| ||||| |||||
Db 6 GGTCTCCCTAGTGAGTTTCA 25

RESULT 14
US-10-719-900-323222/c
; Sequence 323222, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 323222
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-323222

Query Match          76.0%; Score 15.2; DB 7; Length 25;

; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 251427
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-251427

Query Match          74.0%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 9.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCTCGCTGGTGAGTTTCA 20
    ||||| ||||| |||||
Db 25 TTTCGCTGGTGAGTTTCA 8

RESULT 16
US-10-719-956-158864/c
; Sequence 158864, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 158864
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-158864

Query Match          72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTT 17
    ||||| ||||| |||||
Db 25 TTCTCGCTGGTGAGTT 10

RESULT 17
US-10-719-956-326213/c
; Sequence 326213, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2003-11-20
```

Thu Jan 29 10:08:41 2004

```
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 326213
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-326213

Query Match      72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCGCTGGTGAGT 16
Db 17 GTTCGCTGGTGAGT 2

RESULT 18
US-10-719-956-540875/c
; Sequence 540875, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 540875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-540875

Query Match      72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTT 17
Db 17 TTCTCGCAGGTGAGTT 2

RESULT 19
US-10-719-900-552211
; Sequence 552211, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 552211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-552211

Query Match      72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTCGCTGGTGAGTTTC 19
Db 4 CTGCTGGTGAGTTTC 19

; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 326213
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-326213

Query Match      72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCGCTGGTGAGT 16
Db 17 GTTCGCTGGTGAGT 2

RESULT 18
US-10-719-956-540875/c
; Sequence 540875, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 540875
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-540875

Query Match      72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTT 17
Db 17 TTCTCGCAGGTGAGTT 2

RESULT 19
US-10-719-900-552211
; Sequence 552211, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 552211
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-552211

Query Match      72.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTCGCTGGTGAGTTTC 19
Db 4 CTGCTGGTGAGTTTC 19

; Sequence 94322, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94322
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-94322

Query Match      71.0%; Score 14.2; DB 5; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTTTCA 20
Db 4 TTCTCTCTGGTGCTTTTCA 22

RESULT 21
US-09-954-427A-342631/c
; Sequence 342631, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 342631
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-342631

Query Match      71.0%; Score 14.2; DB 5; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTTTCA 20
Db 21 TTCTCGCTGGTGAGTGCA 3

RESULT 22
US-10-719-956-500175
; Sequence 500175, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 500175
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-500175

Query Match          71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTTTCA 20
   ||||| ||||| ||||| |||||
Db 4 TTGTCGGTGGTGAGTTTCA 22

RESULT 23
US-10-719-956-628121/c
; Sequence 628121, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 628121
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-628121

Query Match          71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTC 19
   ||||| ||||| ||||| |||||
Db 21 GTTCTTGTGCTGAGTTTC 3

RESULT 24
US-10-719-900-493573
; Sequence 493573, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 493573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-493573

Query Match          71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTTTCA 20
   ||||| ||||| ||||| |||||
Db 6 TACTCGCTGTGATTTC 24

RESULT 25
US-10-719-900-688991/c
; Sequence 688991, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 688991
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-688991

Query Match          71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTC 19
   ||||| ||||| ||||| |||||
Db 24 GTTCTTGTGCTGAGTTTC 6

RESULT 26
US-10-719-900-822309
; Sequence 822309, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 822309
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-822309

Query Match          71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTC 19
   ||||| ||||| ||||| |||||
Db 24 GTTCTTGTGCTGAGTTTC 6

RESULT 27
US-60-507-511-8135
; Sequence 8135, Application US/60507511
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: AM 101081
; CURRENT APPLICATION NUMBER: US/60/507,511
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 203623
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8135
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-507-511-8135

Query Match          71.0%; Score 14.2; DB 8; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
```

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTTTCA 20
DB 2 TTTTCGCTGGTGAGTTTCA 20

RESULT 28

US-60-507-481-172187
; Sequence 172187, Application US/60507481
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: AM101084
; CURRENT APPLICATION NUMBER: US/60/507,481
; CURRENT FILING DATE: 2003-10-02
; NUMBER OF SEQ ID NOS: 210107
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 172187
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Canis familiaris
US-60-507-481-172187

Query Match 71.0%; Score 14.2; DB 8; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTTTCA 20
DB 4 TTCTCACTGGTGAGTTTCA 22

RESULT 29

US-09-956-604D-114030/c
; Sequence 114030, Application US/09956604D
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia Coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604D
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.2
; SEQ ID NO 114030
; LENGTH: 25
; TYPE: DNA
; ORGANISM: E. coli
US-09-956-604D-114030

Query Match 69.0%; Score 13.8; DB 5; Length 25;
Best Local Similarity 88.2%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTTT 18
DB 21 TTCTCGCGGGGAGTTT 5

RESULT 30

US-09-954-427A-286389
; Sequence 286389, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166

; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 286389
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-286389

Query Match 69.0%; Score 13.8; DB 5; Length 25;
Best Local Similarity 88.2%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTT 17
DB 7 GTTCTCTCTGGTGGGTTT 23

RESULT 31

US-09-954-427A-369103/c
; Sequence 369103, Application US/09954427A
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat Genome
; FILE REFERENCE: 3112.1
; CURRENT APPLICATION NUMBER: US/09/954,427A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,166
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 369103
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-09-954-427A-369103

Query Match 69.0%; Score 13.8; DB 5; Length 25;
Best Local Similarity 88.2%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCTCGCTGGTGAGTTTC 19
DB 19 TCTTGTCTGTGAGTTTC 3

RESULT 32

US-10-719-956-46281/c
; Sequence 46281, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 46281
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-46281

Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCTCGCTGGTGAGTTTC 19
DB 25 TGTCTGTGGGAGTTTC 9


```
RESULT 33
US-10-719-956-363441/c
; Sequence 363441, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 363441
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-363441
Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCTCGTGTGAGTT 17
Db 18 GTTCTCGTGTGAGAT 2

RESULT 34
US-10-719-956-563045
; Sequence 563045, Application US/10719956
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 563045
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-563045
Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCTCGTGTGAGTT 17
Db 18 GTTCTCGTGTGAGAT 2

RESULT 35
US-10-719-956-37913
; Sequence 37913, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 37913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-37913
Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCTCGCTGTGAGTTTC 19
Db 4 TCTCCTGTGTGAGTTTC 20

RESULT 36
US-10-719-900-110854
; Sequence 110854, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 110854
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-110854
Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTCGCTGTGAGTTTCA 20
Db 3 CTCACCTGTGACTTTCA 19

RESULT 37
US-10-719-900-489138/c
; Sequence 489138, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 489138
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-489138
Query Match 69.0%; Score 13.8; DB 7; Length 25;
Best Local Similarity 88.2%; Pred. No. 3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTCGCTGTGAGTTTCA 20
Db 6 CTGCTGTGAGTTTCA 22

RESULT 38
US-10-719-900-549040/c
; Sequence 549040, Application US/10719900
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
```

Thu Jan 29 10:08:41 2004

;; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

;; FILE REFERENCE: 3528.1
 ;; CURRENT APPLICATION NUMBER: US/10/719,900
 ;; CURRENT FILING DATE: 2003-11-20
 ;; PRIOR APPLICATION NUMBER: 60/427,808
 ;; PRIOR FILING DATE: 2002 11 20
 ;; NUMBER OF SEQ ID NOS: 982914
 ;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ;; SEQ ID NO 549040
 ;; LENGTH: 25
 ;; TYPE: DNA
 ;; ORGANISM: Mus musculus
 US-10-719-900-549040

Query Match 69.0%; Score 13.8; DB 7; Length 25;
 Best Local Similarity 88.2%; Pred. No. 3e+03; 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GTTCTCGTGGTGAGTT 17
 Db 20 GTTCTCGTGGTGAGAT 4

RESULT 39

US-10-719-900-572713
 ; Sequence 572713, Application US/10719900
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 572713
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-572713

Query Match 69.0%; Score 13.8; DB 7; Length 25;
 Best Local Similarity 88.2%; Pred. No. 3e+03; 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Gaps 0;

Qy 4 CTCGCTGGTGAGTTTCA 20
 Db 2 CTGGCTGGTGAGTCTCA 18

RESULT 40

US-10-719-900-635348/c
 ; Sequence 635348, Application US/10719900
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002 11 20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 635348
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-635348

Query Match 69.0%; Score 13.8; DB 7; Length 25;
 Best Local Similarity 88.2%; Pred. No. 3e+03; 2; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GTTCTCGTGGTGAGTT 17
 Db 23 GTTCTCTCTGGTGGTT 7
 Search completed: January 24, 2004, 16:28:27
 Job time : 318 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 24, 2004, 13:25:56 ; Search time 1954 Seconds
(without alignments)
418.727 Million cell updates/sec

Title: US-10-002-884A-5

Perfect score: 20
Sequence: 1 gttctcgctggtgagtttca 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 1204238

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl:*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.ma.*

20: em.mu.*

21: em.ov.*

22: em.or.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	20	100.0	20	6	A52133	A52133 Sequence 6
2	20	100.0	20	6	AR003720	AR003720 Sequence
3	20	100.0	20	6	AR073302	AR073302 Sequence
4	20	100.0	20	6	AR076637	AR076637 Sequence
5	20	100.0	20	6	AR110486	AR110486 Sequence
6	20	100.0	20	6	AR120090	AR120090 Sequence
7	20	100.0	20	6	AR121944	AR121944 Sequence
8	20	100.0	20	6	AR142474	AR142474 Sequence
9	20	100.0	20	6	AR165299	AR165299 Sequence
10	20	100.0	20	6	AR165308	AR165308 Sequence
11	20	100.0	20	6	AR165322	AR165322 Sequence
12	20	100.0	20	6	AR165330	AR165330 Sequence
13	20	100.0	20	6	AR165337	AR165337 Sequence
14	20	100.0	20	6	AR167447	AR167447 Sequence
15	20	100.0	20	6	AR176025	AR176025 Sequence
16	20	100.0	20	6	AR179699	AR179699 Sequence
17	20	100.0	20	6	AR182694	AR182694 Sequence
18	20	100.0	20	6	AR207553	AR207553 Sequence
19	20	100.0	20	6	AR212317	AR212317 Sequence
20	20	100.0	20	6	AR212511	AR212511 Sequence
21	20	100.0	20	6	AR224789	AR224789 Sequence
22	20	100.0	20	6	AR231438	AR231438 Sequence
23	20	100.0	20	6	AR237041	AR237041 Sequence
24	20	100.0	20	6	AR279796	AR279796 Sequence
25	20	100.0	20	6	AR300774	AR300774 Sequence
26	20	100.0	20	6	AX081370	AX081370 Sequence
27	20	100.0	20	6	AX224865	AX224865 Sequence
28	20	100.0	20	6	AX224866	AX224866 Sequence
29	20	100.0	20	6	AX226292	AX226292 Sequence
30	20	100.0	20	6	AX283200	AX283200 Sequence
31	20	100.0	20	6	AX283268	AX283268 Sequence
32	20	100.0	20	6	AX556256	AX556256 Sequence
33	20	100.0	20	6	BD014068	BD014068 Oligonuc1
34	20	100.0	20	6	BD014107	BD014107 High-chim
35	20	100.0	20	6	BD015993	BD015993 Oligonuc1
36	20	100.0	20	6	BD016112	BD016112 Oligonuc1
37	20	100.0	20	6	BD017264	BD017264 Oligonuc1
38	20	100.0	20	6	BD076448	BD076448 Combined
39	20	100.0	20	6	BD106496	BD106496 High effi
40	20	100.0	20	6	I29012	I29012 Sequence 8
41	20	100.0	20	6	I32395	I32395 Sequence 8
42	20	100.0	20	6	I36648	I36648 Sequence 8
43	20	100.0	20	6	I40397	I40397 Sequence 8
44	20	100.0	20	6	I59719	I59719 Sequence 8
45	20	100.0	20	6	I63128	I63128 Sequence 8
46	20	100.0	20	6	I87106	I87106 Sequence 2
47	19	95.0	19	6	A65240	A65240 Sequence 4
48	19	95.0	19	6	A68211	A68211 Sequence 6
49	19	95.0	19	6	AR124872	AR124872 Sequence
50	19	95.0	19	6	AR124874	AR124874 Sequence
51	19	95.0	19	6	AR124876	AR124876 Sequence
52	19	95.0	19	6	AR124878	AR124878 Sequence
53	19	95.0	19	6	AR165314	AR165314 Sequence
54	19	95.0	19	6	AR165316	AR165316 Sequence
55	18	90.0	18	6	AR029129	AR029129 Sequence
56	18	90.0	18	6	AR036513	AR036513 Sequence
57	18	90.0	18	6	AR076687	AR076687 Sequence
58	18	90.0	18	6	AR096046	AR096046 Sequence
59	18	90.0	18	6	AR182744	AR182744 Sequence
60	18	90.0	18	6	AR212279	AR212279 Sequence
61	18	90.0	18	6	AR231413	AR231413 Sequence
62	18	90.0	18	6	AR237091	AR237091 Sequence
63	18	90.0	18	6	AR300824	AR300824 Sequence
64	18	90.0	18	6	BD016043	BD016043 Oligonuc1
65	18	90.0	18	6	BD016162	BD016162 Oligonuc1

Pred. No. is the number of results predicted by chance to have a

66	18	90.0	18	6	BD017314	BD017314 Oligonucle	C 139	12	60.0	18	6	I30616	I30616 Sequence 54
67	18	90.0	18	6	I87156	I87156 Sequence 52	C 140	12	60.0	18	6	I30617	I30617 Sequence 55
68	17	85.0	17	6	AR029130	AR029130 Sequence	C 141	12	60.0	18	6	I30618	I30618 Sequence 56
69	17	85.0	17	6	AR036514	AR036514 Sequence	C 142	12	60.0	18	6	I30619	I30619 Sequence 57
70	17	85.0	17	6	AR076688	AR076688 Sequence	C 143	12	60.0	18	6	I30620	I30620 Sequence 58
71	17	85.0	17	6	AR096047	AR096047 Sequence	C 144	12	60.0	18	6	I30621	I30621 Sequence 59
72	17	85.0	17	6	AR182745	AR182745 Sequence	C 145	12	60.0	18	6	I30622	I30622 Sequence 60
73	17	85.0	17	6	AR212280	AR212280 Sequence	C 146	12	60.0	18	6	I46062	I46062 Sequence 41
74	17	85.0	17	6	AR231414	AR231414 Sequence	C 147	12	60.0	18	6	I46063	I46063 Sequence 42
75	17	85.0	17	6	AR237092	AR237092 Sequence	C 148	12	60.0	18	6	I46064	I46064 Sequence 43
76	17	85.0	17	6	AR3000825	AR3000825 Sequence	C 149	12	60.0	18	6	I46065	I46065 Sequence 44
77	17	85.0	17	6	BD016044	BD016044 Oligonucle	C 150	12	60.0	18	6	I46066	I46066 Sequence 45
78	17	85.0	17	6	BD016163	BD016163 Oligonucle	C 151	12	60.0	18	6	I46067	I46067 Sequence 46
79	17	85.0	17	6	BD017315	BD017315 Oligonucle	C 152	12	60.0	18	6	I46068	I46068 Sequence 47
80	17	85.0	17	6	I87157	I87157 Sequence 53	C 153	12	60.0	18	6	I46069	I46069 Sequence 48
81	16	80.0	17	6	AR279792	AR279792 Sequence	C 154	12	60.0	18	6	I46070	I46070 Sequence 49
82	15	75.0	37	6	BD016099	BD016099 Oligonucle	C 155	12	60.0	18	6	I46071	I46071 Sequence 50
83	15	75.0	37	6	BD016218	BD016218 Oligonucle	C 156	12	60.0	18	6	I46072	I46072 Sequence 51
84	15	75.0	37	6	BD017370	BD017370 Oligonucle	C 157	12	60.0	18	6	I46073	I46073 Sequence 52
85	15	75.0	37	6	I71415	I71415 Sequence 5	C 158	12	60.0	18	6	I46074	I46074 Sequence 53
86	14.8	74.0	18	6	AR140632	AR140632 Sequence	C 159	12	60.0	18	6	I46075	I46075 Sequence 54
87	13.8	69.0	18	6	AR140631	AR140631 Sequence	C 160	12	60.0	18	6	I46076	I46076 Sequence 55
88	13.8	69.0	20	6	AR140633	AR140633 Sequence	C 161	12	60.0	18	6	I46077	I46077 Sequence 56
89	13.8	69.0	20	6	AR162570	AR162570 Sequence	C 162	12	60.0	18	6	I46078	I46078 Sequence 57
90	13.4	67.0	22	6	AR242481	AR242481 Sequence	C 163	12	60.0	18	6	I46079	I46079 Sequence 58
91	13.4	67.0	24	6	AX445744	AX445744 Sequence	C 164	12	60.0	18	6	I46080	I46080 Sequence 59
92	13.4	67.0	38	6	I37770	I37770 Sequence 78	C 165	12	60.0	18	6	I46081	I46081 Sequence 60
93	13.4	67.0	38	6	I94620	I94620 Sequence 78	C 166	12	60.0	18	6	AR254387	AR254387 Sequence
94	13.2	66.0	21	6	AR063174	AR063174 Sequence	C 167	12	60.0	21	6	AX698670	AX698670 Sequence
95	13.2	66.0	21	6	AR071370	AR071370 Sequence	C 168	12	60.0	22	6	AR086171	AR086171 Sequence
96	13.2	66.0	21	6	AR119356	AR119356 Sequence	C 169	12	60.0	22	6	AR089590	AR089590 Sequence
97	13	65.0	31	6	AR249720	AR249720 Sequence	C 170	12	60.0	22	6	AR093686	AR093686 Sequence
98	12.8	64.0	18	6	AR140630	AR140630 Sequence	C 171	12	60.0	22	6	AR153328	AR153328 Sequence
99	12.8	64.0	24	6	AR173806	AR173806 Sequence	C 172	12	60.0	22	6	AR179781	AR179781 Sequence
100	12.8	64.0	30	6	AX207286	AX207286 Sequence	C 173	12	60.0	22	6	AR193625	AR193625 Sequence
101	12.6	63.0	27	6	AR028332	AR028332 Sequence 2	C 174	12	60.0	22	6	AR266721	AR266721 Sequence
102	12.6	63.0	27	6	I24930	I24930 Sequence	C 175	12	60.0	22	6	AR308921	AR308921 Sequence
103	12.6	63.0	29	6	AR214574	AR214574 Sequence	C 176	12	60.0	22	6	AX045396	AX045396 Sequence
104	12.6	63.0	29	6	AX074009	AX074009 Sequence	C 177	12	60.0	22	6	AX045443	AX045443 Sequence
105	12.4	62.0	20	6	AR173849	AR173849 Sequence	C 178	12	60.0	22	6	AX045741	AX045741 Sequence
106	12.4	62.0	38	6	AX273655	AX273655 Sequence	C 179	12	60.0	22	6	AX045805	AX045805 Sequence
107	12.2	61.0	20	6	AR314980	AR314980 Sequence	C 180	12	60.0	22	6	AX298067	AX298067 Sequence
108	12.2	61.0	20	6	BD134928	BD134928 High-affi	C 181	12	60.0	22	6	AX299033	AX299033 Sequence
109	12.2	61.0	20	6	BOVDIK38	D44539 Bovine DNA,	C 182	12	60.0	22	6	AX554544	AX554544 Sequence
110	12.2	61.0	21	6	AX241224	AX241224 Sequence	C 183	12	60.0	22	6	BD095843	BD095843 FEN-1 end
111	12.2	61.0	22	6	AX487825	AX487825 Sequence	C 184	12	60.0	25	6	AX196738	AX196738 FEN-1 end
112	12.2	61.0	22	6	AX527884	AX527884 Sequence	C 185	12	60.0	25	6	I33607	I33607 Sequence 29
113	12.2	61.0	23	6	AX598496	AX598496 Sequence	C 186	12	60.0	25	6	BD076444	BD076444 Combined
114	12.2	61.0	23	6	BD009761	BD009761 Mini-aden	C 187	12	60.0	29	6	AX553589	AX553589 Sequence
115	12.2	61.0	24	6	A07517	A07517 Primer TG 1	C 188	12	60.0	30	6	AX553590	AX553590 Sequence
116	12.2	61.0	24	6	AX111687	AX111687 Sequence	C 189	12	60.0	30	6	E49667	E49667 Insect cell
117	12.2	61.0	25	6	AX093476	AX093476 Sequence	C 190	12	60.0	30	6	I08952	I08952 Sequence 18
118	12.2	61.0	27	6	BD139740	BD139740 Gene fami	C 191	12	60.0	36	6	BD075510	BD075510 Secretary
119	12.2	61.0	29	6	BD107126	BD107126 Monoclonal	C 192	12	60.0	37	6	BD172370	BD172370 Secreted
120	12.2	61.0	30	6	E05837	E05837 DNA sequence	C 193	12	60.0	37	6	BD172689	BD172689 Secreted
121	12.2	61.0	30	6	AX183638	AX183638 Sequence	C 194	12	60.0	37	6	BD173008	BD173008 Secreted
122	12.2	61.0	31	6	BD012658	BD012658 Novel Yea	C 195	12	60.0	37	6	BD173327	BD173327 Secreted
123	12.2	61.0	32	6	BD013658	BD013658 Sequence	C 196	12	60.0	37	6	BD175361	BD175361 Secretary
124	12.2	61.0	39	6	BD171763	BD171763 Method fo	C 197	12	60.0	37	6	A51622	A51622 Sequence 32
125	12	60.0	18	6	I30603	I30603 Sequence 41	C 198	11.8	59.0	39	6	A51623	A51623 Sequence 33
126	12	60.0	18	6	I30604	I30604 Sequence 42	C 199	11.8	59.0	39	6	AR187019	AR187019 Sequence
127	12	60.0	18	6	I30605	I30605 Sequence 43	C 200	11.8	59.0	17	6	AX724431	AX724431 Sequence
128	12	60.0	18	6	I30606	I30606 Sequence 44	C 201	11.8	59.0	17	6	AX737546	AX737546 Sequence
129	12	60.0	18	6	I30607	I30607 Sequence 45	C 202	11.8	59.0	18	6	AR140629	AR140629 Sequence
130	12	60.0	18	6	I30608	I30608 Sequence 46	C 203	11.8	59.0	20	6	AR311144	AR311144 Sequence
131	12	60.0	18	6	I30609	I30609 Sequence 47	C 204	11.8	59.0	20	6	E40648	E40648 Antihuman F
132	12	60.0	18	6	I30610	I30610 Sequence 48	C 205	11.8	59.0	20	6	AR222884	AR222884 Sequence
133	12	60.0	18	6	I30611	I30611 Sequence 49	C 206	11.8	59.0	21	6	BD003266	BD003266 Therapeut
134	12	60.0	18	6	I30612	I30612 Sequence 50	C 207	11.8	59.0	21	6	AX012657	AX012657 Sequence
135	12	60.0	18	6	I30613	I30613 Sequence 51	C 208	11.8	59.0	23	6	AX290937	AX290937 Sequence
136	12	60.0	18	6	I30614	I30614 Sequence 52	C 209	11.8	59.0	24	6	AX571771	AX571771 Sequence
137	12	60.0	18	6	I30615	I30615 Sequence 53	C 210	11.8	59.0	24	6	E21962	E21962 Thermus hav
138	12	60.0	18	6			C 211	11.8	59.0	24	6		

C 212	11.8	59.0	24	6	E21964	E21964 Thermus hav	C 285	11.6	58.0	25	6	AX598245	AX598245 Sequence
C 213	11.8	59.0	25	6	AX659533	AX659533 Sequence	286	11.6	58.0	25	6	BD014685	BD014685 Method fo
C 214	11.8	59.0	26	6	AX091035	AX091035 Sequence	C 287	11.6	58.0	25	6	E12422	E12422 PCR primer
C 215	11.8	59.0	28	6	AX198070	AX198070 Sequence	C 288	11.6	58.0	26	6	AR221678	AR221678 Sequence
C 216	11.8	59.0	28	6	AX260224	AX260224 Sequence	C 289	11.6	58.0	26	6	AR239322	AR239322 Sequence
C 217	11.8	59.0	28	6	AX498202	AX498202 Sequence	C 290	11.6	58.0	26	6	AR279124	AR279124 Sequence
C 218	11.8	59.0	29	6	AX259885	AX259885 Sequence	C 291	11.6	58.0	26	6	AR026200	AR026200 Sequence
C 219	11.8	59.0	30	6	AX611548	AX611548 Sequence	C 292	11.6	58.0	27	6	AR026280	AR026280 Sequence
C 220	11.8	59.0	33	6	AR217985	AR217985 Sequence	C 293	11.6	58.0	27	6	AR035435	AR035435 Sequence
C 221	11.8	59.0	33	6	BD134931	BD134931 High-affi	C 294	11.6	58.0	27	6	AR035436	AR035436 Sequence
C 222	11.8	59.0	36	6	AR056619	AR056619 Sequence	C 295	11.6	58.0	27	6	E61343	E61343 Probe for d
C 223	11.8	59.0	36	6	AR056975	AR056975 Sequence	C 296	11.6	58.0	27	6	I82942	I82942 Sequence 44
C 224	11.8	59.0	36	6	AR057081	AR057081 Sequence	C 297	11.6	58.0	27	6	I83022	I83022 Sequence 12
C 225	11.8	59.0	36	6	AR114377	AR114377 Sequence	C 298	11.6	58.0	27	6	A40180	A40180 Sequence 2
C 226	11.8	59.0	36	6	AR114733	AR114733 Sequence	C 299	11.6	58.0	28	6	AR136053	AR136053 Sequence
C 227	11.8	59.0	36	6	AR114839	AR114839 Sequence	C 300	11.6	58.0	28	6	BD007567	BD007567 Process o
C 228	11.8	59.0	36	6	AR131986	AR131986 Sequence	C 301	11.6	58.0	29	6	AR183747	AR183747 Sequence
C 229	11.8	59.0	36	6	AR133412	AR133412 Sequence	C 302	11.6	58.0	29	6	AR236056	AR236056 Sequence
C 230	11.8	59.0	36	6	AR133475	AR133475 Sequence	C 303	11.6	58.0	29	6	AR241295	AR241295 Sequence
C 231	11.8	59.0	36	6	AX633678	AX633678 Sequence	C 304	11.6	58.0	29	6	AX099766	AX099766 Sequence
C 232	11.8	59.0	36	6	AX634034	AX634034 Sequence	C 305	11.6	58.0	29	6	AX188648	AX188648 Sequence
C 233	11.8	59.0	36	6	AX634140	AX634140 Sequence	C 306	11.6	58.0	29	6	AX188649	AX188649 Sequence
C 234	11.8	59.0	36	6	AX636273	AX636273 Sequence	C 307	11.6	58.0	29	6	BD062064	BD062064 Apo-2 rec
C 235	11.8	59.0	36	6	AX636462	AX636462 Sequence	C 308	11.6	58.0	29	6	BD085996	BD085996 Tumor nec
C 236	11.8	59.0	36	6	I61867	I61867 Sequence 42	C 309	11.6	58.0	29	6	BD090957	BD090957 Apo-3 119
C 237	11.8	59.0	36	6	I62056	I62056 Sequence 61	C 310	11.6	58.0	29	6	BD132797	BD132797 Apo-2DcR.
C 238	11.8	59.0	36	6	I85764	I85764 Sequence 3	C 311	11.6	58.0	30	6	A51870	A51870 Sequence 34
C 239	11.8	59.0	36	6	I85765	I85765 Sequence 4	C 312	11.6	58.0	30	6	A51872	A51872 Sequence 36
C 240	11.8	59.0	38	6	AR045740	AR045740 Sequence	C 313	11.6	58.0	30	6	AR085837	AR085837 Sequence
C 241	11.8	59.0	38	6	AR046907	AR046907 Sequence	C 314	11.6	58.0	30	6	AR085837	AR085837 Sequence
C 242	11.8	59.0	38	6	AR047627	AR047627 Sequence	C 315	11.6	58.0	30	6	AX525150	AX525150 Sequence
C 243	11.8	59.0	38	6	AR047783	AR047783 Sequence	C 316	11.6	58.0	30	6	A51634	A51634 Sequence 44
C 244	11.8	59.0	38	6	AR057840	AR057840 Sequence	C 317	11.6	58.0	30	6	AR032342	AR032342 Sequence
C 245	11.8	59.0	38	6	AR057877	AR057877 Sequence	C 318	11.6	58.0	30	6	AR032343	AR032343 Sequence
C 246	11.8	59.0	38	6	AR115598	AR115598 Sequence	C 319	11.6	58.0	30	6	BD081630	BD081630 Inhibitio
C 247	11.8	59.0	38	6	AR115635	AR115635 Sequence	C 320	11.6	58.0	30	6	I09458	I09458 Sequence 2
C 248	11.8	59.0	38	6	AR201859	AR201859 Sequence	C 321	11.6	58.0	30	6	AR049839	AR049839 Sequence
C 249	11.8	59.0	38	6	AR217984	AR217984 Sequence	C 322	11.6	58.0	30	6	AR149733	AR149733 Sequence
C 250	11.8	59.0	38	6	AX219157	AX219157 Sequence	C 323	11.6	58.0	30	6	A40179	A40179 Sequence 1
C 251	11.8	59.0	38	6	AX222484	AX222484 Sequence	C 324	11.6	58.0	30	6	AR035466	AR035466 Sequence
C 252	11.8	59.0	38	6	AX228278	AX228278 Sequence	C 325	11.6	58.0	30	6	AR088703	AR088703 Sequence
C 253	11.8	59.0	38	6	AX2423867	AX2423867 Sequence	C 326	11.6	58.0	30	6	AX103956	AX103956 Sequence
C 254	11.8	59.0	38	6	AX424009	AX424009 Sequence	C 327	11.6	58.0	30	6	AX355389	AX355389 Sequence
C 255	11.8	59.0	38	6	AX580868	AX580868 Sequence	C 328	11.6	58.0	30	6	AX547009	AX547009 Sequence
C 256	11.8	59.0	38	6	AX581227	AX581227 Sequence	C 329	11.6	58.0	30	6	AR005185	AR005185 Sequence
C 257	11.8	59.0	38	6	AX581262	AX581262 Sequence	C 330	11.6	58.0	30	6	AR005186	AR005186 Sequence
C 258	11.8	59.0	38	6	AX634899	AX634899 Sequence	C 331	11.6	58.0	30	6	AR038395	AR038395 Sequence
C 259	11.8	59.0	38	6	AX634936	AX634936 Sequence	C 332	11.6	58.0	30	6	AR038396	AR038396 Sequence
C 260	11.8	59.0	38	6	BD134930	BD134930 High-affi	C 333	11.6	58.0	30	6	AR067696	AR067696 Sequence
C 261	11.8	59.0	38	6	I52792	I52792 Sequence 53	C 334	11.6	58.0	30	6	AR067697	AR067697 Sequence
C 262	11.8	59.0	38	6	I53959	I53959 Sequence 17	C 335	11.6	58.0	30	6	AR178131	AR178131 Sequence
C 263	11.8	59.0	38	6	I54679	I54679 Sequence 24	C 336	11.6	58.0	30	6	AR178132	AR178132 Sequence
C 264	11.8	59.0	38	6	I54835	I54835 Sequence 25	C 337	11.6	58.0	30	6	I58471	I58471 Sequence 43
C 265	11.8	59.0	40	6	AR217983	AR217983 Sequence	C 338	11.6	58.0	30	6	I58472	I58472 Sequence 44
C 266	11.8	59.0	40	6	BD134929	BD134929 High-affi	C 339	11.6	58.0	30	6	I66589	I66589 Sequence 43
C 267	11.8	59.0	40	6	BD134932	BD134932 High-affi	C 340	11.6	58.0	30	6	I66590	I66590 Sequence 44
C 268	11.6	58.0	18	6	AR232702	AR232702 Sequence	C 341	11.6	58.0	30	6	I68237	I68237 Sequence 44
C 269	11.6	58.0	20	6	AR230403	AR230403 Sequence	C 342	11.6	58.0	30	6	AX268415	AX268415 Sequence
C 270	11.6	58.0	20	6	AR310098	AR310098 Sequence	C 343	11.4	57.0	13	6	AR306750	AR306750 Sequence
C 271	11.6	58.0	20	6	A22675	A22675 Oligonucleo	C 344	11.4	57.0	13	6	A0527	A0527 Sequence 64
C 272	11.6	58.0	21	6	AX095164	AX095164 Sequence	C 345	11.4	57.0	14	6	A89054	A89054 Sequence 12
C 273	11.6	58.0	21	6	I21799	I21799 Sequence 13	C 346	11.4	57.0	14	6	AR232807	AR232807 Sequence
C 274	11.6	58.0	21	6	BD063893	BD063893 Nucleic a	C 347	11.4	57.0	14	6	AX030102	AX030102 Sequence
C 275	11.6	58.0	22	6	BD063915	BD063915 Nucleic a	C 348	11.4	57.0	14	6	AX316423	AX316423 Sequence
C 276	11.6	58.0	23	6	AR106267	AR106267 Sequence	C 349	11.4	57.0	14	6	BD066567	BD066567 An antise
C 277	11.6	58.0	23	6	AX229593	AX229593 Sequence	C 350	11.4	57.0	14	6	BD066567	BD066567 An antise
C 278	11.6	58.0	23	6	BD008835	BD008835 Uses of a	C 351	11.4	57.0	16	6	A89430	A89430 Sequence 15
C 279	11.6	58.0	23	6	AR212941	AR212941 Sequence	C 352	11.4	57.0	16	6	BD066943	BD066943 An antise
C 280	11.6	58.0	24	6	AX229601	AX229601 Sequence	C 353	11.4	57.0	19	6	AX132691	AX132691 Sequence
C 281	11.6	58.0	24	6	AX107811	AX107811 Sequence	C 354	11.4	57.0	20	6	AR023735	AR023735 Sequence
C 282	11.6	58.0	25	6	AX299019	AX299019 Sequence	C 355	11.4	57.0	20	6	AX361141	AX361141 Sequence
C 283	11.6	58.0	25	6	AX299020	AX299020 Sequence	C 356	11.4	57.0	20	6	BD144758	BD144758 Use of ph
C 284	11.6	58.0	25	6	AX299020	AX299020 Sequence	C 357	11.4	57.0	20	6	AX472036	AX472036 Sequence

C 358	11.4	57.0	22	6	AR002307 Sequence	C 431	11	55.0	19	6	I30701 Sequence 13
C 359	11.4	57.0	22	6	AR053158 Sequence	C 432	11	55.0	19	6	I30706 Sequence 14
C 360	11.4	57.0	22	6	AX180600 Sequence	C 433	11	55.0	19	6	I46148 Sequence 12
C 361	11.4	57.0	22	6	AX180611 Sequence	C 434	11	55.0	19	6	I46149 Sequence 12
C 362	11.4	57.0	23	6	E36478	C 435	11	55.0	19	6	I46156 Sequence 13
C 363	11.4	57.0	23	6	E36478 Luciferase	C 436	11	55.0	19	6	I46160 Sequence 13
C 364	11.4	57.0	24	6	AX444224 Sequence	C 437	11	55.0	19	6	I46165 Sequence 14
C 365	11.4	57.0	25	6	AX207953 Sequence	C 438	11	55.0	20	6	AR076751 Sequence
C 366	11.4	57.0	25	6	AX448190 Sequence	C 439	11	55.0	20	6	AR182808 Sequence
C 367	11.4	57.0	25	6	AX473058 Sequence	C 440	11	55.0	20	6	AR300888 Sequence
C 368	11.4	57.0	27	6	E26666 Improved me	C 441	11	55.0	20	6	AX224688 Sequence
C 369	11.4	57.0	28	6	AR275790 Sequence	C 442	11	55.0	20	6	AX255031 Sequence
C 370	11.4	57.0	30	6	AX613002 Sequence	C 443	11	55.0	20	6	BD016069 Oligonuc
C 371	11.4	57.0	31	6	AR195918 Sequence	C 444	11	55.0	20	6	BD016188 Oligonuc
C 372	11.4	57.0	33	6	AR174229 Sequence	C 445	11	55.0	20	6	BD017340 Oligonuc
C 373	11.4	57.0	33	6	AR174266 Sequence	C 446	11	55.0	20	6	E40745
C 374	11.4	57.0	33	6	AR179161 Sequence	C 447	11	55.0	21	6	AX153839 Sequence
C 375	11.4	57.0	33	6	AR274165 Sequence	C 448	11	55.0	21	6	AX375565 Sequence
C 376	11.4	57.0	36	6	AR211370 Sequence	C 449	11	55.0	22	6	AX182207 Sequence
C 377	11.4	57.0	36	6	AR213279 Sequence	C 450	11	55.0	22	6	AX382016 Sequence
C 378	11.4	57.0	40	6	AX424791 Sequence	C 451	11	55.0	22	6	AX382055 Sequence
C 379	11.2	56.0	17	6	BD180787 Array of	C 452	11	55.0	23	6	AR255303 Sequence
C 380	11.2	56.0	17	6	AX227082 Sequence	C 453	11	55.0	23	6	AR255304 Sequence
C 381	11.2	56.0	17	6	AX227730 Sequence	C 454	11	55.0	23	6	AX487363 Sequence
C 382	11.2	56.0	17	6	AX227731 Sequence	C 455	11	55.0	23	6	BD056798 Method an
C 383	11.2	56.0	18	6	AX578293 Sequence	C 456	11	55.0	24	6	AR230097 Sequence
C 384	11.2	56.0	18	6	AX378484 Sequence	C 457	11	55.0	24	6	AR230098 Sequence
C 385	11.2	56.0	19	6	AR294516 Sequence	C 458	11	55.0	24	6	AX022199 Sequence
C 386	11.2	56.0	19	6	BD080214 Tango-72	C 459	11	55.0	24	6	AX022200 Sequence
C 387	11.2	56.0	20	6	AR009520 Sequence	C 460	11	55.0	24	6	AX030725 Sequence
C 388	11.2	56.0	20	6	AR062092 Sequence	C 461	11	55.0	24	6	AX030726 Sequence
C 389	11.2	56.0	20	6	AR089612 Sequence	C 462	11	55.0	24	6	AX115718 Sequence
C 390	11.2	56.0	20	6	AR172132 Sequence	C 463	11	55.0	24	6	AX133735 Sequence
C 391	11.2	56.0	20	6	AR308968 Sequence	C 464	11	55.0	24	6	BD008646 Stable ex
C 392	11.2	56.0	20	6	AR313237 Sequence	C 465	11	55.0	24	6	BD008647
C 393	11.2	56.0	20	6	AX555481 Sequence	C 466	11	55.0	24	8	ATH529109 Arabidops
C 394	11.2	56.0	20	6	BD095892 FEN-1 end	C 467	11	55.0	25	6	AR239218 Sequence
C 395	11.2	56.0	20	6	BD165772 Immunorea	C 468	11	55.0	25	6	AX279020 Sequence
C 396	11.2	56.0	20	6	I66194 Sequence 1	C 469	11	55.0	25	6	AX612814 Sequence
C 397	11.2	56.0	21	6	I66207 Sequence 1	C 470	11	55.0	25	6	AX614085 Sequence
C 398	11.2	56.0	21	6	AR136193 Sequence	C 471	11	55.0	27	6	AR184583 Sequence
C 399	11.2	56.0	21	6	AR145683 Sequence	C 472	11	55.0	27	6	AR203466 Sequence
C 400	11.2	56.0	21	6	AR174507 Sequence	C 473	11	55.0	27	6	AR207740 Sequence
C 401	11.2	56.0	21	6	AR257141 Sequence	C 474	11	55.0	27	6	AR257877 Sequence
C 402	11.2	56.0	21	6	AX038806 Sequence	C 475	11	55.0	27	6	AX034682 Sequence
C 403	11.2	56.0	21	6	BD070076 Oligonuc	C 476	11	55.0	27	6	AX455732 Sequence
C 404	11.2	56.0	21	6	BD096028 Use of di	C 477	11	55.0	27	6	E33644 Protein bin
C 405	11.2	56.0	21	6	BD128303 Utilizati	C 478	11	55.0	27	6	I15299 Sequence 7
C 406	11.2	56.0	22	6	AX534714 Sequence	C 479	11	55.0	27	6	I28735 Sequence 3
C 407	11.2	56.0	22	6	AX534730 Sequence	C 480	11	55.0	27	6	I84647 Sequence 7
C 408	11.2	56.0	22	6	BD089187 A method	C 481	11	55.0	29	6	AR3977 Sequence 4
C 409	11.2	56.0	24	6	AX444080 Sequence	C 482	11	55.0	29	6	AR165372 Sequence
C 410	11.2	56.0	25	6	AR157073 Sequence	C 483	11	55.0	29	6	AR173093 Sequence 8
C 411	11.2	56.0	25	6	AR268391 Sequence	C 484	11	55.0	30	6	A65152 Sequence
C 412	11.2	56.0	25	6	I81179 Sequence 35	C 485	11	55.0	30	6	AR125689 Sequence
C 413	11.2	56.0	26	6	AX441302 Sequence	C 486	11	55.0	30	6	AR125726 Sequence
C 414	11.2	56.0	26	6	BD171602 Method fo	C 487	11	55.0	30	6	AR206866 Sequence
C 415	11.2	56.0	27	6	E22917 Method for	C 488	11	55.0	30	6	AR287286 Sequence
C 416	11.2	56.0	29	6	AR083298 Sequence	C 489	11	55.0	30	6	AR287288 Sequence
C 417	11.2	56.0	29	6	AX099642 Sequence	C 490	11	55.0	30	6	AX089410 Sequence
C 418	11.2	56.0	30	6	BD056714 Secreted	C 491	11	55.0	30	6	AX089412 Sequence
C 419	11.2	56.0	30	6	AX281012 Sequence	C 492	11	55.0	30	6	AX136895 Sequence
C 420	11.2	56.0	30	6	AX590804 Sequence	C 493	11	55.0	30	6	AX472650 Sequence
C 421	11.2	56.0	31	6	AX249374 Sequence	C 494	11	55.0	30	6	AX472652 Sequence
C 422	11.2	56.0	32	6	AX024596 Sequence	C 495	11	55.0	30	6	AX553583 Sequence
C 423	11.2	56.0	34	6	A93583 Sequence 13	C 496	11	55.0	30	6	AX553585 Sequence
C 424	11.2	56.0	36	6	I01742 Sequence 8	C 497	11	55.0	30	6	AX553591 Sequence
C 425	11.2	56.0	38	6	AX076649 Sequence	C 498	11	55.0	30	6	AX553592 Sequence
C 426	11.2	56.0	40	6	AR059126 Sequence	C 499	11	55.0	30	6	BD006821 N-Acetyl
C 427	11	55.0	17	6	AX674448 Sequence	C 500	11	55.0	30	6	I47101 Sequence 31
C 428	11	55.0	19	6	AX117818 Sequence	C 501	11	55.0	30	6	I47138 Sequence 68
C 429	11	55.0	19	6	I30689 Sequence 12	C 502	11	55.0	31	6	AX069251 Sequence
C 430	11	55.0	19	6	I30690 Sequence 12	C 503	11	55.0	31	6	AX467530 Sequence
					I30697 Sequence 13						

504	11	55.0	31	6	AX589486	AX589486 Sequence	577	10.8	54.0	24	6	AX289312	AX289312 Sequence
505	11	55.0	32	6	I46968	I46968 Sequence 61	c 578	10.8	54.0	24	6	AX447183	AX447183 Sequence
506	11	55.0	33	6	AR031518	AR031518 Sequence	579	10.8	54.0	24	6	AX487258	AX487258 Sequence
507	11	55.0	33	6	AR144028	AR144028 Sequence	580	10.8	54.0	24	6	AX613241	AX613241 Sequence
508	11	55.0	33	6	E32990	E32990 Novel greA	581	10.8	54.0	24	6	BD075219	BD075219 Methods f
509	11	55.0	35	6	AR230018	AR230018 Sequence	582	10.8	54.0	24	6	I39908	I39908 Sequence 13
510	11	55.0	35	6	AX134149	AX134149 Sequence	583	10.8	54.0	25	6	AX196914	AX196914 Sequence
511	11	55.0	35	6	I11546	I11546 Sequence 15	c 584	10.8	54.0	25	6	AX598376	AX598376 Sequence
512	11	55.0	36	6	A51627	A51627 Sequence 37	c 585	10.8	54.0	25	6	BD057620	BD057620 Chimeric
513	11	55.0	36	6	I44805	I44805 Sequence 29	586	10.8	54.0	26	6	A92189	A92189 Sequence 23
514	11	55.0	37	6	A91225	A91225 Sequence 17	587	10.8	54.0	26	6	AR087984	AR087984 Sequence
515	11	55.0	37	6	AR000551	AR000551 Sequence	c 588	10.8	54.0	26	6	AX497386	AX497386 Sequence
516	11	55.0	37	6	AR076146	AR076146 Sequence	589	10.8	54.0	26	6	BD009164	BD009164 Herbicide
517	11	55.0	37	6	AR078178	AR078178 Sequence	590	10.8	54.0	26	6	I80202	I80202 Sequence 91
518	11	55.0	37	6	AR145092	AR145092 Sequence	591	10.8	54.0	27	6	AR039250	AR039250 Sequence
519	11	55.0	37	6	AX101156	AX101156 Sequence	592	10.8	54.0	27	6	AR040186	AR040186 Sequence
520	11	55.0	37	6	AX464506	AX464506 Sequence	593	10.8	54.0	27	6	AR185071	AR185071 Sequence
521	11	55.0	37	6	BD056483	BD056483 Proteins	594	10.8	54.0	27	6	AR187869	AR187869 Sequence
522	11	55.0	38	6	AR301255	AR301255 Sequence	595	10.8	54.0	27	6	AR188244	AR188244 Sequence
523	11	55.0	38	6	AX027274	AX027274 Sequence	596	10.8	54.0	27	6	AR189297	AR189297 Sequence
524	11	55.0	38	6	E31316	E31316 Process for	597	10.8	54.0	27	6	AR191225	AR191225 Sequence
525	11	55.0	38	6	I11547	I11547 Sequence 16	598	10.8	54.0	27	6	AR196503	AR196503 Sequence
526	11	55.0	38	6	I60258	I60258 Sequence 3	599	10.8	54.0	27	6	AR196585	AR196585 Sequence
527	11	55.0	39	6	E26161	E26161 Novel brain	600	10.8	54.0	27	6	AR196838	AR196838 Sequence
528	11	55.0	40	6	AR053614	AR053614 Sequence	601	10.8	54.0	27	6	AX306924	AX306924 Sequence
529	11	55.0	40	6	AR100697	AR100697 Sequence	602	10.8	54.0	27	6	BD068081	BD068081 Enzymatic
530	11	55.0	40	6	AR258549	AR258549 Sequence	603	10.8	54.0	27	6	BD068156	BD068156 Enzymatic
531	11	55.0	40	6	AX032940	AX032940 Sequence	604	10.8	54.0	27	6	BD068280	BD068280 Enzymatic
532	11	55.0	40	6	AX467226	AX467226 Sequence	605	10.8	54.0	28	6	AR139142	AR139142 Sequence
533	10.8	54.0	14	6	A21089	A21089 Synthetic o	606	10.8	54.0	28	6	AR231706	AR231706 Sequence
534	10.8	54.0	14	6	AR104331	AR104331 Sequence	607	10.8	54.0	28	6	E10501	E10501 Primer. 9/1
535	10.8	54.0	14	6	AR137618	AR137618 Sequence	608	10.8	54.0	28	6	I71343	I71343 Sequence 15
536	10.8	54.0	15	6	AX635647	AX635647 Sequence	609	10.8	54.0	29	6	AX020879	AX020879 Sequence
537	10.8	54.0	15	6	AX635649	AX635649 Sequence	610	10.8	54.0	29	6	AX107815	AX107815 Sequence
538	10.8	54.0	15	6	AX635651	AX635651 Sequence	611	10.8	54.0	29	6	BD014689	BD014689 Method fo
539	10.8	54.0	15	6	I39343	I39343 Sequence 38	612	10.8	54.0	29	6	BD140094	BD140094 RANTES mu
540	10.8	54.0	15	6	I39344	I39344 Sequence 38	613	10.8	54.0	30	6	AR193843	AR193843 Sequence
541	10.8	54.0	15	6	I39345	I39345 Sequence 38	614	10.8	54.0	30	6	AR214250	AR214250 Sequence
542	10.8	54.0	18	6	AR083944	AR083944 Sequence	615	10.8	54.0	30	6	AR214252	AR214252 Sequence
543	10.8	54.0	18	6	AR140628	AR140628 Sequence	616	10.8	54.0	30	6	AX012380	AX012380 Sequence
544	10.8	54.0	18	6	AR216242	AR216242 Sequence	617	10.8	54.0	30	6	AX012382	AX012382 Sequence
545	10.8	54.0	19	6	AX129923	AX129923 Sequence	618	10.8	54.0	30	6	AX553589	AX553589 Sequence
546	10.8	54.0	19	6	AX130676	AX130676 Sequence	619	10.8	54.0	30	6	AX553590	AX553590 Sequence
547	10.8	54.0	19	6	AX131789	AX131789 Sequence	620	10.8	54.0	30	6	BD022558	BD022558 Multi-fun
548	10.8	54.0	19	6	AX356969	AX356969 Sequence	621	10.8	54.0	30	6	E59986	E59986 Highly acti
549	10.8	54.0	19	6	E33110	E33110 Primer for	622	10.8	54.0	30	6	E59988	E59988 Highly acti
550	10.8	54.0	20	6	AX234746	AX234746 Sequence	623	10.8	54.0	31	6	A12962	A12962 Nucleotide
551	10.8	54.0	20	6	AX010222	AX010222 Sequence	624	10.8	54.0	31	6	A13346	A13346 B-pertussis
552	10.8	54.0	20	6	AX443254	AX443254 Sequence	625	10.8	54.0	31	6	A13347	A13347 Modified DN
553	10.8	54.0	20	6	AX662893	AX662893 Sequence	626	10.8	54.0	31	6	AR195850	AR195850 Sequence
554	10.8	54.0	20	6	BD097096	BD097096 Therapeut	627	10.8	54.0	31	6	AX248862	AX248862 Sequence
555	10.8	54.0	20	6	E40649	E40649 Antihuman F	628	10.8	54.0	32	6	AR177550	AR177550 Sequence
556	10.8	54.0	20	6	E40665	E40665 Antihuman F	629	10.8	54.0	32	6	AR177551	AR177551 Sequence
557	10.8	54.0	21	6	A38324	A38324 Sequence 58	630	10.8	54.0	32	6	AR217746	AR217746 Sequence
558	10.8	54.0	21	6	AR037240	AR037240 Sequence	631	10.8	54.0	32	6	AR217747	AR217747 Sequence
559	10.8	54.0	21	6	AR048709	AR048709 Sequence	632	10.8	54.0	32	6	AR256957	AR256957 Sequence
560	10.8	54.0	21	6	AR079379	AR079379 Sequence	633	10.8	54.0	32	6	AR256958	AR256958 Sequence
561	10.8	54.0	21	6	AR110044	AR110044 Sequence	634	10.8	54.0	32	6	E59066	E59066 Novel carbo
562	10.8	54.0	21	6	AX054676	AX054676 Sequence	635	10.8	54.0	32	6	E59067	E59067 Novel carbo
563	10.8	54.0	21	6	BD008908	BD008908 High leve	636	10.8	54.0	33	6	A49028	A49028 Sequence 10
564	10.8	54.0	21	6	BD022946	BD022946 Specie-g-s	637	10.8	54.0	33	6	A51628	A51628 Sequence 38
565	10.8	54.0	21	6	BD124110	BD124110 Novel GAB	638	10.8	54.0	34	6	AR094424	AR094424 Sequence
566	10.8	54.0	22	6	AX351493	AX351493 Sequence	639	10.8	54.0	34	6	AR095744	AR095744 Sequence
567	10.8	54.0	22	6	AX641678	AX641678 Sequence	640	10.8	54.0	34	6	AX048305	AX048305 Sequence
568	10.8	54.0	22	6	I86604	I86604 Sequence 6	641	10.8	54.0	34	6	AX711213	AX711213 Sequence
569	10.8	54.0	22	6	AR202536	AR202536 Sequence	642	10.8	54.0	35	6	AR094446	AR094446 Sequence
570	10.8	54.0	23	6	AR219529	AR219529 Sequence	643	10.8	54.0	35	6	AR266279	AR266279 Sequence
571	10.8	54.0	23	6	AX718099	AX718099 Sequence	c 644	10.8	54.0	35	6	AX575278	AX575278 Sequence
572	10.8	54.0	23	6	AX718102	AX718102 Sequence	645	10.8	54.0	36	6	AR041685	AR041685 Sequence
573	10.8	54.0	23	6	BD008663	BD008663 Assays an	646	10.8	54.0	36	6	AR056676	AR056676 Sequence
574	10.8	54.0	24	6	AR137345	AR137345 Sequence	647	10.8	54.0	36	6	AR114434	AR114434 Sequence
575	10.8	54.0	24	6	AX037467	AX037467 Sequence	648	10.8	54.0	36	6	AR132669	AR132669 Sequence
576	10.8	54.0	24	6	AX111681	AX111681 Sequence	649	10.8	54.0	36	6	AR132670	AR132670 Sequence

650	10.8	54.0	36	6	AR133123	Sequence	723	10.6	53.0	18	6	BD166303	BD166303 Process f
651	10.8	54.0	36	6	AR133786	Sequence	724	10.6	53.0	18	6	BD170930	BD170930 Process f
652	10.8	54.0	36	6	AR133983	Sequence	725	10.6	53.0	18	6	BD171041	BD171041 Process f
653	10.8	54.0	36	6	AR133984	Sequence	726	10.6	53.0	18	6	BD171102	BD171102 Process f
c 654	10.8	54.0	36	6	AR236142	Sequence	c 727	10.6	53.0	18	6	I17363	I17363 Sequence 13
655	10.8	54.0	36	6	AR237337	Sequence	728	10.6	53.0	19	6	AR295676	AR295676 Sequence 13
656	10.8	54.0	36	6	AR237375	Sequence	729	10.6	53.0	20	6	AR295676	AR295676 Sequence 17
657	10.8	54.0	36	6	AR237375	Sequence	c 730	10.6	53.0	20	6	AR315652	AR315652 Sequence
c 658	10.8	54.0	36	6	AR237143	Sequence	c 731	10.6	53.0	20	6	AR315652	AR315652 Sequence
659	10.8	54.0	36	6	BD006280	Artificia	c 732	10.6	53.0	21	6	AR070888	AR070888 Sequence
660	10.8	54.0	36	6	I39520	Sequence 55	c 733	10.6	53.0	21	6	AR103633	AR103633 Sequence
661	10.8	54.0	36	6	AR045526	Sequence	c 734	10.6	53.0	21	6	BD129863	BD129863 Asthma-as
662	10.8	54.0	36	6	AR045782	Sequence	c 735	10.6	53.0	21	6	I46528	I46528 Sequence 50
663	10.8	54.0	36	6	AR045864	Sequence	c 736	10.6	53.0	22	6	AR1989	AR1989 Synthetic H
664	10.8	54.0	36	6	AR045874	Sequence	c 737	10.6	53.0	22	6	AR007254	AR007254 Sequence
665	10.8	54.0	36	6	AR046549	Sequence	c 738	10.6	53.0	22	6	AR062458	AR062458 Sequence
666	10.8	54.0	36	6	AR046923	Sequence	c 739	10.6	53.0	22	6	AR131408	AR131408 Sequence
667	10.8	54.0	36	6	AR047091	Sequence	c 740	10.6	53.0	22	6	AR170040	AR170040 Sequence
668	10.8	54.0	36	6	AR057864	Sequence	c 741	10.6	53.0	22	6	AR170467	AR170467 Sequence
669	10.8	54.0	36	6	AR057921	Sequence	c 742	10.6	53.0	22	6	AR262567	AR262567 Sequence
670	10.8	54.0	36	6	AR115622	Sequence	c 743	10.6	53.0	22	6	AX420187	AX420187 Sequence
671	10.8	54.0	36	6	AR115679	Sequence	c 744	10.6	53.0	22	6	BD001814	BD001814 Immunogen
672	10.8	54.0	36	6	AX218456	Sequence	c 745	10.6	53.0	22	6	BD090827	BD090827 Mammalian
673	10.8	54.0	36	6	AX218463	Sequence	c 746	10.6	53.0	22	6	I27744	I27744 Sequence 32
674	10.8	54.0	36	6	AX218683	Sequence	c 747	10.6	53.0	23	6	AR083001	AR083001 Sequence
675	10.8	54.0	36	6	AX218786	Sequence	c 748	10.6	53.0	23	6	AR124357	AR124357 Sequence
676	10.8	54.0	36	6	AX219423	Sequence	c 749	10.6	53.0	23	6	AX427029	AX427029 Sequence
677	10.8	54.0	36	6	AX219904	Sequence	c 750	10.6	53.0	23	6	BD070470	BD070470 Methods f
678	10.8	54.0	36	6	AX222432	Sequence	751	10.6	53.0	23	6	BD172057	BD172057 Genetical
679	10.8	54.0	36	6	AX222482	Sequence	c 752	10.6	53.0	23	6	I27368	I27368 Sequence 4
680	10.8	54.0	36	6	AX228065	Sequence	c 753	10.6	53.0	24	6	A42514	A42514 Sequence 30
681	10.8	54.0	36	6	AX228293	Sequence	754	10.6	53.0	24	6	A88706	A88706 Sequence 85
682	10.8	54.0	36	6	AX228338	Sequence	c 755	10.6	53.0	24	6	AR037533	AR037533 Sequence
683	10.8	54.0	36	6	AX228472	Sequence	c 756	10.6	53.0	24	6	AR098433	AR098433 Sequence
684	10.8	54.0	36	6	AX273579	Sequence	c 757	10.6	53.0	24	6	AR109797	AR109797 Sequence
685	10.8	54.0	36	6	AX273808	Sequence	c 758	10.6	53.0	24	6	AX288715	AX288715 Sequence
686	10.8	54.0	36	6	AX273919	Sequence	c 759	10.6	53.0	24	6	AX453040	AX453040 Sequence
687	10.8	54.0	36	6	AX423940	Sequence	c 760	10.6	53.0	24	6	BD066219	BD066219 An antise
688	10.8	54.0	36	6	AX424127	Sequence	c 761	10.6	53.0	24	6	BD178299	BD178299 Mitochond
689	10.8	54.0	36	6	AX424152	Sequence	c 762	10.6	53.0	25	6	I16728	I16728 Sequence 5
690	10.8	54.0	36	6	AX424305	Sequence	c 763	10.6	53.0	25	6	I72377	I72377 Sequence 8
691	10.8	54.0	36	6	AX424790	Sequence	c 764	10.6	53.0	26	6	AX250037	AX250037 Sequence
692	10.8	54.0	36	6	AX424909	Sequence	c 765	10.6	53.0	26	8	ATH530957	ATH530957 Arabidops
693	10.8	54.0	36	6	AX580399	Sequence	c 766	10.6	53.0	27	6	AR2188	AR2188 Sequence 9
694	10.8	54.0	36	6	AX580439	Sequence	c 767	10.6	53.0	27	6	AR024295	AR024295 Sequence
695	10.8	54.0	36	6	AX581506	Sequence	c 768	10.6	53.0	27	6	AR045148	AR045148 Sequence
696	10.8	54.0	36	6	AX634923	Sequence	c 769	10.6	53.0	27	6	BD011372	BD011372 Chimeric
697	10.8	54.0	36	6	AX634980	Sequence	c 770	10.6	53.0	27	6	BD132636	BD132636 Methods a
698	10.8	54.0	36	6	E16907	Ribozyme wh	c 771	10.6	53.0	27	6	E43842	E43842 Chimeric an
699	10.8	54.0	36	6	I37730	Sequence 74	c 772	10.6	53.0	28	6	A48409	A48409 Sequence 32
700	10.8	54.0	36	6	I52578	Sequence 31	c 773	10.6	53.0	28	6	AR009049	AR009049 Sequence
701	10.8	54.0	36	6	I52834	Sequence 57	c 774	10.6	53.0	29	6	AR011238	AR011238 Sequence
702	10.8	54.0	36	6	I52916	Sequence 65	c 775	10.6	53.0	29	6	AR012703	AR012703 Sequence
703	10.8	54.0	36	6	I52926	Sequence 66	c 776	10.6	53.0	29	6	AR052703	AR052703 Sequence
704	10.8	54.0	36	6	I53601	Sequence 13	c 777	10.6	53.0	29	6	AR061003	AR061003 Sequence
705	10.8	54.0	36	6	I53975	Sequence 17	c 778	10.6	53.0	29	6	AR087734	AR087734 Sequence
706	10.8	54.0	36	6	I54143	Sequence 18	c 779	10.6	53.0	29	6	AR175137	AR175137 Sequence
c 707	10.8	54.0	36	6	I94580	Sequence 74	c 780	10.6	53.0	29	6	AR288016	AR288016 Sequence
708	10.8	54.0	36	11	ALU772535	Arabidops	c 781	10.6	53.0	29	6	AR309629	AR309629 Sequence
709	10.8	54.0	36	6	AB6948	Sequence 39	c 782	10.6	53.0	29	6	AX002790	AX002790 Sequence
710	10.8	54.0	36	6	AR048360	Sequence	c 783	10.6	53.0	29	6	AX149558	AX149558 Sequence
711	10.8	54.0	36	6	AR079251	Sequence	c 784	10.6	53.0	29	6	BD136160	BD136160 Vector. 9
712	10.8	54.0	36	6	AR079380	Sequence	c 785	10.6	53.0	29	6	I17876	I17876 Sequence 10
c 713	10.8	54.0	36	6	AR309682	Sequence	c 786	10.6	53.0	29	6	I74723	I74723 Sequence 63
714	10.8	54.0	36	6	AX598149	Sequence	c 787	10.6	53.0	30	6	A07223	A07223 Oligonucleo
c 715	10.8	54.0	40	6	A21272	Oligonucleo	c 788	10.6	53.0	30	6	A13535	A13535 oligonucleo
716	10.8	54.0	40	6	AX069264	Sequence	c 789	10.6	53.0	30	6	A13536	A13536 oligonucleo
c 717	10.8	54.0	40	6	AX255443	Sequence	c 790	10.6	53.0	30	6	A13564	A13564 oligonucleo
718	10.8	54.0	40	6	AX456273	Sequence	c 791	10.6	53.0	30	6	A13565	A13565 oligonucleo
719	10.8	54.0	40	6	I88195	Sequence 4	c 792	10.6	53.0	30	6	AX150219	AX150219 Sequence
720	10.6	53.0	17	6	AX579402	Sequence	c 793	10.6	53.0	30	6	AX431436	AX431436 Sequence
721	10.6	53.0	17	6	AX728644	Sequence	c 794	10.6	53.0	30	6	AX521576	AX521576 Sequence
c 722	10.6	53.0	18	6	BD067680	Enzymatic	c 795	10.6	53.0	31	6	E03817	E03817 DNA encodin
												AR206869	AR206869 Sequence

C 796	10.6	53.0	31	6	AX136898	Sequence	869	10.4	52.0	20	6	AR143118	Sequence
C 797	10.6	53.0	31	6	AX248581	Sequence	C 870	10.4	52.0	20	6	AR178796	Sequence
C 798	10.6	53.0	31	6	AX248849	Sequence	C 871	10.4	52.0	20	6	AR232341	Sequence
C 799	10.6	53.0	31	6	BD006824	N-Acetyl	C 872	10.4	52.0	20	6	AR287556	Sequence
C 800	10.6	53.0	32	6	AR016610	Sequence	C 873	10.4	52.0	20	6	AR287557	Sequence
C 801	10.6	53.0	32	6	AR016611	Sequence	C 874	10.4	52.0	20	6	AR298661	Sequence
C 802	10.6	53.0	32	6	AX058682	Sequence	C 875	10.4	52.0	20	6	AX107987	Sequence
C 803	10.6	53.0	32	6	AX069190	Sequence	C 876	10.4	52.0	20	6	BD012609	Human Cyt
C 804	10.6	53.0	32	6	AX093062	Sequence	C 877	10.4	52.0	20	6	BD142351	Plant hav
C 805	10.6	53.0	32	6	AX093062	Sequence	C 878	10.4	52.0	20	6	E05221	Primer for
C 806	10.6	53.0	32	6	AX167046	Sequence	C 879	10.4	52.0	20	6	E07344	Primer for
C 807	10.6	53.0	32	6	AX190631	Sequence	C 880	10.4	52.0	20	6	E16504	PCR primer
C 808	10.6	53.0	32	6	I15343	Sequence 24	C 881	10.4	52.0	20	6	E63764	Plant-deriv
C 809	10.6	53.0	32	6	I15344	Sequence 25	C 882	10.4	52.0	20	6	I73108	Sequence 4
C 810	10.6	53.0	33	6	AR265800	Sequence	C 883	10.4	52.0	21	6	A62903	Sequence 14
C 811	10.6	53.0	33	6	AX049958	Sequence	C 884	10.4	52.0	21	6	AR233393	Sequence
C 812	10.6	53.0	33	6	I16738	Sequence 15	C 885	10.4	52.0	21	6	AR299050	Sequence
C 813	10.6	53.0	33	6	I76337	Sequence 6	C 886	10.4	52.0	21	6	AX020691	Sequence
C 814	10.6	53.0	34	6	AR153230	Sequence	C 887	10.4	52.0	21	6	AX095041	Sequence
C 815	10.6	53.0	34	6	AR153232	Sequence	C 888	10.4	52.0	21	6	AX096615	Sequence
C 816	10.6	53.0	35	6	AX213688	Sequence	C 889	10.4	52.0	21	6	AX154270	Sequence
C 817	10.6	53.0	35	6	AX030077	Sequence	C 890	10.4	52.0	21	6	AX429394	Sequence
C 818	10.6	53.0	35	6	BD057747	Fusion pr	C 891	10.4	52.0	21	6	AX591053	Sequence
C 819	10.6	53.0	35	6	BD081577	BD081577	C 892	10.4	52.0	21	6	AX720485	Sequence
C 820	10.6	53.0	35	6	E49387	Process for	C 893	10.4	52.0	21	6	E13713	Probe for d
C 821	10.6	53.0	36	6	A42839	Sequence 16	C 894	10.4	52.0	21	6	E60298	Identificat
C 822	10.6	53.0	36	6	A42833	Sequence 16	C 895	10.4	52.0	22	6	A18257	oligonucleo
C 823	10.6	53.0	36	6	AX304642	Sequence	C 896	10.4	52.0	22	6	A18262	oligonucleo
C 824	10.6	53.0	36	6	E10194	Sequence	C 897	10.4	52.0	22	6	AR020537	Sequence
C 825	10.6	53.0	36	6	I87335	Sequence 16	C 898	10.4	52.0	22	6	AX355983	Sequence
C 826	10.6	53.0	36	6	I87339	Sequence 16	C 899	10.4	52.0	22	6	BD004675	Gene vect
C 827	10.6	53.0	38	6	AR020202	Sequence	C 900	10.4	52.0	22	6	I14924	Sequence 3
C 828	10.6	53.0	38	6	AR032154	Sequence	C 901	10.4	52.0	22	6	I14928	Sequence 7
C 829	10.6	53.0	38	6	AR043819	Sequence	C 902	10.4	52.0	23	6	AR301806	Sequence
C 830	10.6	53.0	38	6	AR072131	Sequence	C 903	10.4	52.0	24	6	AR059369	Sequence
C 831	10.6	53.0	38	6	AR095985	Sequence	C 904	10.4	52.0	24	6	AR071645	Sequence
C 832	10.6	53.0	38	6	AR136645	Sequence	C 905	10.4	52.0	24	6	AR090823	Sequence
C 833	10.6	53.0	38	6	AR157180	Sequence	C 906	10.4	52.0	24	6	AR197858	Sequence
C 834	10.6	53.0	38	6	AR164129	Sequence	C 907	10.4	52.0	24	6	AR260012	Sequence
C 835	10.6	53.0	38	6	AX038849	Sequence	C 908	10.4	52.0	24	6	AX445244	Sequence
C 836	10.6	53.0	38	6	AX127252	Sequence	C 909	10.4	52.0	24	6	AX445692	Sequence
C 837	10.6	53.0	38	6	AX665037	Sequence	C 910	10.4	52.0	24	6	AX445715	Sequence
C 838	10.6	53.0	38	6	I32815	Sequence 11	C 911	10.4	52.0	24	6	AX494006	Sequence
C 839	10.6	53.0	38	6	I59629	Sequence 11	C 912	10.4	52.0	24	6	I17089	Sequence 4
C 840	10.6	53.0	38	6	AR124556	Sequence	C 913	10.4	52.0	24	6	I63484	Sequence 4
C 841	10.4	52.0	17	6	AR046822	Sequence	C 914	10.4	52.0	25	6	AX316252	Sequence
C 842	10.4	52.0	17	6	AR192607	Sequence	C 915	10.4	52.0	25	6	AX533315	Sequence
C 843	10.4	52.0	17	6	AX722421	Sequence	C 916	10.4	52.0	25	6	AX533316	Sequence
C 844	10.4	52.0	17	6	AX726081	Sequence	C 917	10.4	52.0	25	6	AX533317	Sequence
C 845	10.4	52.0	17	6	I35436	Sequence 3	C 918	10.4	52.0	25	6	AX533318	Sequence
C 846	10.4	52.0	17	6	I53874	Sequence 16	C 919	10.4	52.0	25	6	AX533319	Sequence
C 847	10.4	52.0	17	6	I76170	Sequence 14	C 920	10.4	52.0	25	6	AX533320	Sequence
C 848	10.4	52.0	18	6	AR063182	Sequence	C 921	10.4	52.0	25	6	AX609542	Sequence
C 849	10.4	52.0	18	6	AR071378	Sequence	C 922	10.4	52.0	25	6	AX609630	Sequence
C 850	10.4	52.0	18	6	AR083943	Sequence	C 923	10.4	52.0	26	6	AR091018	Sequence
C 851	10.4	52.0	18	6	AR095829	Sequence	C 924	10.4	52.0	26	6	AR198053	Sequence
C 852	10.4	52.0	18	6	AR119364	Sequence	C 925	10.4	52.0	26	6	AR217187	Sequence
C 853	10.4	52.0	18	6	AR140626	Sequence	C 926	10.4	52.0	26	6	AR260207	Sequence
C 854	10.4	52.0	18	6	AR140627	Sequence	C 927	10.4	52.0	26	6	AX033455	Sequence
C 855	10.4	52.0	18	6	AR142942	Sequence	C 928	10.4	52.0	26	6	AX512392	Sequence
C 856	10.4	52.0	18	6	AR173913	Sequence	C 929	10.4	52.0	26	6	BD005397	Secreted
C 857	10.4	52.0	18	6	AR293769	Sequence	C 930	10.4	52.0	26	6	BD138850	Secreted
C 858	10.4	52.0	18	6	AX498020	Sequence	C 931	10.4	52.0	26	6	I89957	Sequence 37
C 859	10.4	52.0	18	6	AX498021	Sequence	C 932	10.4	52.0	27	6	AR109860	Sequence
C 860	10.4	52.0	18	6	BD087802	Sequence	C 933	10.4	52.0	27	6	AR182255	Sequence
C 861	10.4	52.0	18	12	AB068957	AB068957	C 934	10.4	52.0	27	6	AR189099	Sequence
C 862	10.4	52.0	19	6	AX129922	Sequence	C 935	10.4	52.0	27	6	AR189171	Sequence
C 863	10.4	52.0	19	6	AX130675	Sequence	C 936	10.4	52.0	27	6	AR207739	Sequence
C 864	10.4	52.0	19	6	AX131788	Sequence	C 937	10.4	52.0	27	6	AR225262	Sequence
C 865	10.4	52.0	20	6	A20337	oligonucleo	C 938	10.4	52.0	27	6	AR257876	Sequence
C 866	10.4	52.0	20	6	A30134	Probe P4. 7	C 939	10.4	52.0	27	6	BD068091	Enzymatic
C 867	10.4	52.0	20	6	A30135	Probe P4. (c	C 940	10.4	52.0	27	6	I15298	Sequence 6
C 868	10.4	52.0	20	6	AR099515	Sequence	C 941	10.4	52.0	27	6	I84646	Sequence 6

```

c 942 10.4 52.0 28 6 AR182244 Sequence
943 10.4 52.0 28 6 AX002953 Sequence
944 10.4 52.0 29 6 AR094438 Sequence
945 10.4 52.0 29 6 AR095758 Sequence
946 10.4 52.0 29 6 AX107825 Sequence
947 10.4 52.0 29 6 AX405126 Sequence
948 10.4 52.0 29 6 AX663718 Sequence
949 10.4 52.0 30 6 AX037662 Sequence
950 10.4 52.0 30 6 AX553587 Sequence
951 10.4 52.0 30 6 AX553588 Sequence
952 10.4 52.0 30 6 AX611435 Sequence
953 10.4 52.0 30 6 BD107119 Monoclonal
954 10.4 52.0 30 6 E32603 Novel nucle
955 10.4 52.0 31 6 AR099779 Sequence
956 10.4 52.0 31 6 AR195852 Sequence
957 10.4 52.0 31 6 AX582379 Sequence
958 10.4 52.0 31 6 BD002405 Gene comp
959 10.4 52.0 31 6 BD002861 Gene comp
960 10.4 52.0 33 4 OC021885 U21885 Oryctolagus
961 10.4 52.0 33 6 AR004367 Sequence
962 10.4 52.0 33 6 AR097158 Sequence
963 10.4 52.0 33 6 AR130656 Sequence
964 10.4 52.0 33 6 AR160114 Sequence
965 10.4 52.0 33 6 AR172005 Sequence
966 10.4 52.0 33 6 AX174930 Sequence
967 10.4 52.0 33 6 AX181203 Sequence
968 10.4 52.0 33 6 AX223934 Sequence
969 10.4 52.0 33 6 AX223943 Sequence
970 10.4 52.0 33 6 AX554247 Sequence
971 10.4 52.0 33 6 I65724 Sequence 84
972 10.4 52.0 33 6 I67956 Sequence 84
973 10.4 52.0 33 6 I82842 Sequence 21
974 10.4 52.0 35 6 AX686396 Sequence
975 10.4 52.0 36 6 AR057260 Sequence
976 10.4 52.0 36 6 AR094451 Sequence
977 10.4 52.0 36 6 AR115018 Sequence
978 10.4 52.0 36 6 AR132000 Sequence
979 10.4 52.0 36 6 AR133763 Sequence
980 10.4 52.0 36 6 AR262696 Sequence
981 10.4 52.0 36 6 AR287693 Sequence
982 10.4 52.0 36 6 AX634319 Sequence
983 10.4 52.0 36 6 AX636382 Sequence
984 10.4 52.0 36 6 AX636585 Sequence
985 10.4 52.0 36 6 I61976 Sequence 53
986 10.4 52.0 36 6 I62179 Sequence 73
987 10.4 52.0 37 6 AR140901 Sequence
988 10.4 52.0 37 6 AR140902 Sequence
989 10.4 52.0 37 6 AR140903 Sequence
990 10.4 52.0 37 6 AR140904 Sequence
991 10.4 52.0 37 6 AR140905 Sequence
992 10.4 52.0 37 6 AR140906 Sequence
993 10.4 52.0 37 6 AR140907 Sequence
994 10.4 52.0 37 6 AR150851 Sequence
995 10.4 52.0 37 6 AR150852 Sequence
996 10.4 52.0 37 6 AR150853 Sequence
997 10.4 52.0 37 6 AR150854 Sequence
998 10.4 52.0 37 6 AR150855 Sequence
999 10.4 52.0 37 6 AR150856 Sequence
1000 10.4 52.0 37 6 AR150857 Sequence

```

ALIGNMENTS

```

RESULT 1
LOCUS AS2133 20 bp
DEFINITION Sequence 6 from Patent WO9619240.
ACCESSION AS2133
VERSION AS2133.1 GI:2304738
KEYWORDS . unidentifed
SOURCE unidentifed
ORGANISM unidentifed

```

linear DNA

PAT 11-MAR-1997

```

unclassified.
1 (bases 1 to 20)
AUTHORS Haener,R. and Skobridis,K.
TITLE OLIGONUCLEOTIDE-DENDRIMER CONJUGATES
JOURNAL Patent: WO 9619240-A 6 27-JUN-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 4344696 960710.
FEATURES
source
location/Qualifiers
1..20
/organism="unidentifed"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
8 t
BASE COUNT 2 a 4 c 6 g
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGCTGGTGAGTTTCA 20
DB 1 GTTCTCGCTGGTGAGTTTCA 20
RESULT 2
AR003720 20 bp DNA linear PAT 04-DEC-1998
LOCUS AR003720
DEFINITION Sequence 1 from patent US 5744460.
ACCESSION AR003720
VERSION AR003720.1 GI:3964979
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Muller,M., Geiger,T., Altmann,K.-H., Fabbro,D., Dean,N.M., Monia,B.
and Bennett,C.Frank.
TITLE Combination for treatment of proliferative diseases
JOURNAL Patent: US 5744460-A 1 28-APR-1998;
FEATURES
location/Qualifiers
1..20
/organism="unknown"
8 t
BASE COUNT 2 a 4 c 6 g
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGCTGGTGAGTTTCA 20
DB 1 GTTCTCGCTGGTGAGTTTCA 20
RESULT 3
AR073302 20 bp DNA linear PAT 28-AUG-2000
LOCUS AR073302
DEFINITION Sequence 1 from patent US 5948898.
ACCESSION AR073302
VERSION AR073302.1 GI:10000065
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., Martin,P. and Altmann,K.-H.
TITLE Methoxyethoxy oligonucleotides for modulation of protein kinase C
expression
JOURNAL Patent: US 5948898-A 1 07-SEP-1999;
FEATURES
location/Qualifiers
1..20
/organism="unknown"
8 t
BASE COUNT 2 a 4 c 6 g

```

```

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 4
LOCUS AR076637 20 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 2 from patent US 5959096.
ACCESSION AR076637
VERSION AR076637.1 GI:10003383
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank, and Dean, N.
TITLE Antisense oligonucleotides against human protein kinase C
JOURNAL Patent: US 5959096-A 2 28-SEP-1999;
FEATURES Location/Qualifiers
          source
            1..20
            /organism="unknown"
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 5
LOCUS AR110486 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 4 from patent US 6114519.
ACCESSION AR110486
VERSION AR110486.1 GI:12826762
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Cole, D.L., Ravikumar, V.T. and Cheruvallath, Z.S.
TITLE Synthesis of sulfurylated oligonucleotides
JOURNAL Patent: US 6114519-A 4 05-SEP-2000;
FEATURES Location/Qualifiers
          source
            1..20
            /organism="unknown"
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 6
LOCUS AR120090 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6153599.

```

```

ACCESSION ARL20090
VERSION ARL20090.1 GI:14102789
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean, N.M., Martin, P. and Altmann, K.-H.
TITLE Methoxyethoxy oligonucleotides for modulation of protein kinase C
JOURNAL Patent: US 6153599-A 1 28-NOV-2000;
FEATURES Location/Qualifiers
          source
            1..20
            /organism="unknown"
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 7
LOCUS ARL21944 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 4 from patent US 6160152.
ACCESSION ARL21944
VERSION ARL21944.1 GI:14105520
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Capaldi, D.C. and Ravikumar, V.T.
TITLE Process for the synthesis of oligomeric compounds
JOURNAL Patent: US 6160152-A 4 12-DEC-2000;
FEATURES Location/Qualifiers
          source
            1..20
            /organism="unknown"
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
    |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 8
LOCUS ARL42474 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6175004.
ACCESSION ARL42474
VERSION ARL42474.1 GI:15102773
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Ross, B.S. and Manoharan, M.
TITLE Process for the synthesis of oligonucleotides incorporating
JOURNAL Patent: US 6175004-A 4 16-JAN-2001;
FEATURES Location/Qualifiers
          source
            1..20
            /organism="unknown"

```

RESULT 11
AR165322

```

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 14
LOCUS
DEFINITION Sequence 13 from patent US 6287591.
ACCESSION AR167447
VERSION AR167447.1 GI:17903227
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Sample, S.C., Klimuk, S.K., Harasym, T., Hope, M.J., Ansell, S.M.,
Cullis, P., Scherrer, P. and DeBeyer, D.
TITLE Charged therapeutic agents encapsulated in lipid particles
JOURNAL Patent: US 6287591-A 13 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 15
LOCUS
DEFINITION Sequence 4 from patent US 6310047.
ACCESSION AR176025
VERSION AR176025.1 GI:17917324
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Partell, N. and Kloster, M.
TITLE High affinity DNA binding compounds as adjuvants in antisense
technology
JOURNAL Patent: US 6310047-A 4 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 16
LOCUS
DEFINITION Sequence 4 from patent US 6379698.
ACCESSION AR207553
VERSION AR207553.1 GI:21507336
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Leamon, C. Paul.
TITLE Fusogenic lipids and vesicles

```

```

AR179699
LOCUS
DEFINITION Sequence 4 from patent US 6326478.
ACCESSION AR179699
VERSION AR179699.1 GI:20221254
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cheruvallath, Z.S., Ravikumar, V.T. and Cole, D.L.
TITLE Process for the synthesis of oligomeric compounds
JOURNAL Patent: US 6326478-A 4 04-DEC-2001;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 17
LOCUS
DEFINITION Sequence 2 from patent US 6339066.
ACCESSION AR182694
VERSION AR182694.1 GI:20225901
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank., Dean, N.M., Cook, P. Dan. and Hoke, G.
TITLE Antisense oligonucleotides which have phosphorothioate linkages of
high chiral purity and which modulate .beta.1, .beta.2, .gamma.,
.delta., .epsilon., .zeta. and .eta. isoforms of human protein
kinase C
JOURNAL Patent: US 6339066-A 2 15-JAN-2002;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN

Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 18
LOCUS
DEFINITION Sequence 4 from patent US 6379698.
ACCESSION AR207553
VERSION AR207553.1 GI:21507336
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Leamon, C. Paul.
TITLE Fusogenic lipids and vesicles

```

JOURNAL Patent: US 6379698-A 4 30-APR-2002;
 FEATURES Location/Qualifiers
 source 1..20 8 t
 BASE COUNT 2 a 4 c 6 g
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
 |||||||
 Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 19
 AR212317
 LOCUS 20 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 4 from patent US 6399756.
 ACCESSION AR212317
 VERSION AR212317.1 GI:21515859
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Cheruvallath,Z.S., Ravikumar,V.T. and Cole,D.L.
 TITLE Process for the synthesis of oligomeric compounds
 JOURNAL Patent: US 6399756-A 4 04-JUN-2002;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 2 a 4 c 6 g 8 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
 |||||||
 Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 20
 AR212511
 LOCUS 20 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 3 from patent US 6399765.
 ACCESSION AR212511
 VERSION AR212511.1 GI:21516106
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Krotz,A.H., McElroy,B.M. and Scorzari,A.N.
 TITLE Methods for removing dimethoxytrityl groups from oligonucleotides
 JOURNAL Patent: US 6399765-A 3 04-JUN-2002;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 2 a 4 c 6 g 8 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
 |||||||
 Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 21
 AR224789
 LOCUS 20 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 3 from patent US 6440943.
 ACCESSION AR224789
 VERSION AR224789.1 GI:23333699
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Cook,P.D. and Manoharan,M.
 TITLE Oligonucleotides having site specific chiral phosphorothioate internucleoside linkages
 JOURNAL Patent: US 6440943-A 3 27-AUG-2002;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 2 a 4 c 6 g 8 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
 |||||||
 Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 22
 AR231438
 LOCUS 20 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 30 from patent US 6451991.
 ACCESSION AR231438
 VERSION AR231438.1 GI:27272521
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Martin,P., Altmann,K.-H., Cook,P.D. and Monia,B.P.
 TITLE Sugar-modified gapped oligonucleotides
 JOURNAL Patent: US 6451991-A 30 17-SEP-2002;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 2 a 4 c 6 g 8 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
 |||||||
 Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 23
 AR237041
 LOCUS 20 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 2 from patent US 6465439.
 ACCESSION AR237041
 VERSION AR237041.1 GI:27281699
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Nicklin,P.L., Phillips,J.A., Love,W.G. and Hamilton,K.O.
 TITLE Pharmaceutical compositions

JOURNAL Patent: US 6465439-A 2 15-OCT-2002;
 FEATURES Location/Qualifiers
 source
 BASE COUNT 2 a 4 c 6 g 8 t
 ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 24
 LOCUS AR279796 20 bp DNA linear PAT 10-APR-2003
 DEFINITION Sequence 42 from patent US 6518017.
 ACCESSION AR279796
 VERSION AR279796.1 GI:29714941
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Riley, F.A., Brown, B.D. and Arnold, L.J.
 TITLE Combinatorial antisense library
 JOURNAL Patent: US 6518017-A 42 11-FEB-2003;
 FEATURES Location/Qualifiers
 source
 BASE COUNT 2 a 4 c 6 g 8 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 25
 LOCUS AR300774 20 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 2 from patent US 6537973.
 ACCESSION AR300774
 VERSION AR300774.1 GI:31688341
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Bennett, C.F., Dean, N.M., Holmlund, J.T. and Dorr, F.A.
 TITLE Oligonucleotide inhibition of protein kinase C
 JOURNAL Patent: US 6537973-A 2 25-MAR-2003;
 FEATURES Location/Qualifiers
 source
 BASE COUNT 2 a 4 c 6 g 8 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 26
 LOCUS AX081370 20 bp DNA linear PAT 27-FEB-2001
 DEFINITION Sequence 49 from Patent WO0108707.
 ACCESSION AX081370
 VERSION AX081370.1 GI:13170212
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Uhlmann, E., Greiner, B., Unger, E., Gothe, G. and Schwerdel, M.
 TITLE Conjugates and methods for the production thereof, and their use
 JOURNAL for transporting molecules via biological membranes
 Patent: WO 0108707-A 49 08-FEB-2001;
 Aventis Pharma Deutschland GmbH (DE)
 FEATURES Location/Qualifiers
 source
 BASE COUNT 2 a 4 c 6 g 8 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 27
 LOCUS AX224865 20 bp DNA linear PAT 10-SEP-2001
 DEFINITION Sequence 19 from Patent WO0161030.
 ACCESSION AX224865
 VERSION AX224865.1 GI:15554938
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Gray, D.M. and Bollon, A.P.
 TITLE Libraries of optimum subsequence regions of mrna and genomic dna
 JOURNAL for control of gene expression
 Patent: WO 0161030-A 19 23-AUG-2001;
 Cytoconal Pharmaceuticals, Inc. (US); University of Texas at
 Dallas, Dept. of Molecular and Cell Biology (US); Lab. of
 Experimental Carcinogenesis, National Cancer Institute/NIH (US)
 FEATURES Location/Qualifiers
 source
 BASE COUNT 8 a 6 c 4 g 2 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 20 GTTCTCGCTGGTGAGTTTCA 1

RESULT 28
 LOCUS AX224866

LOCUS AX224866 20 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 20 from Patent WO0161030.
ACCESSION AX224866
VERSION AX224866.1 GI:15554939
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Gray, D.M. and Bollon, A.P.
TITLE Libraries of optimum subsequence regions of mrna and genomic dna for control of gene expression
JOURNAL Patent: WO 0161030-A 20 23-AUG-2001;
Cytoclonal Pharmaceuticals, Inc. (US); University of Texas at Dallas, Dept. of Molecular and Cell Biology (US); Lab. of Experimental Carcinogenesis, National Cancer Institute/NIH (US)
FEATURES Location/Qualifiers
source
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20
RESULT 29
LOCUS AX226292 20 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 2 from Patent EP1126025.
ACCESSION AX226292
VERSION AX226292.1 GI:15555556
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 Bennet, C.F. and Dean, N.
AUTHORS Oligonucleotide modulation of protein kinase c
TITLE Patent: EP 1126025-A 2 22-AUG-2001;
JOURNAL ISIS PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Artificial"
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20
RESULT 30
LOCUS AX283200 20 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 38 from Patent WO0179216.
ACCESSION AX283200
VERSION AX283200.1 GI:17044081

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 Uhlmann, E., Breipohl, G. and Will, D.W.
AUTHORS Polyamide nucleic acid derivatives, agents and methods for producing them
TITLE Patent: WO 0179216-A 38 25-OCT-2001;
JOURNAL Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz: Oligonukleotide"
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20
RESULT 31
LOCUS AX283268 20 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 32 from Patent WO0179249.
ACCESSION AX283268
VERSION AX283268.1 GI:17044149
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 Uhlmann, E., Breipohl, G. and Will, D.W.
AUTHORS Polyamide nucleic acid derivatives, agents and methods for producing the same
TITLE Patent: WO 0179249-A 32 25-OCT-2001;
JOURNAL Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz: Oligonukleotide"
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20
RESULT 32
LOCUS AX556256 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 1 from Patent WO0242447.
ACCESSION AX556256
VERSION AX556256.1 GI:25899593
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Uhler,M.D.
TITLE Surface transfection and expression procedure
JOURNAL Patent: WO 0242447-A 1 30-MAY-2002;
THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)
FEATURES Location/Qualifiers
source 1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606" 8 t

BASE COUNT 2 a 4 c 6 g
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 33
BD014068
LOCUS 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide having phosphorothioate bond with high chiral purity.
ACCESSION BD014068
VERSION BD014068.1 GI:22554397
KEYWORDS JP 2001103987-A/8.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook,P.D. and Hawk,G.
TITLE Oligonucleotide having phosphorothioate bond with high chiral purity
JOURNAL Patent: JP 2001103987-A 8 17-APR-2001;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2001103987-A/8
PD 17-APR-2001
PF 31-AUG-2000 JP 2000262871
PR 06-JUN-1995 US 08/471967,06-JUN-1995 US 08/467597 PR
06-JUN-1995 US 08/468447,06-JUN-1995 US 08/468569 PR
06-JUN-1995 US 08/466692,06-JUN-1995 US 08/471966 PR
06-JUN-1995 US 08/469851,06-JUN-1995 US 08/470129 PI PHILIP
DAN COOK,GLENN HAWK
PC C12N15/09,A61K31/7125,A61K48/00,A61P27/02,A61P29/00,A61P31/12,
PC A61P31/18,
PC A61P35/00,C07H21/00,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Oligonucleotide having phosphorothioate bond with high chiral purity
FH Key Location/Qualifiers
FT source 1..20
FT /organism="Unidentified".

FEATURES source
Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644" 8 t

BASE COUNT 2 a 4 c 6 g
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 35
BD015993
LOCUS 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide modulation of protein kinase C-epsilon.
ACCESSION BD015993
VERSION BD015993.1 GI:22557131
KEYWORDS JP 2001224386-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,F.C., Boggs,R.T. and Dean,N.M.
TITLE Oligonucleotide modulation of protein kinase C-epsilon
JOURNAL Patent: JP 2001224386-A 2 21-AUG-2001;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001224386-A/2

Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 34
BD014107
LOCUS 20 bp DNA linear PAT 27-AUG-2002
DEFINITION High-chimeric purity phosphorothioate bond-containing oligonucleotide.
ACCESSION BD014107
VERSION BD014107.1 GI:22554436
KEYWORDS JP 2001114798-A/8.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook,P.D. and Hawk,G.
TITLE High-chimeric purity phosphorothioate bond-containing oligonucleotide.
JOURNAL Patent: JP 2001114798-A 8 24-APR-2001;
ISIS PHARMACEUTICALS INC
OS Unidentified
PN JP 2001114798-A/8
PD 24-APR-2001
PF 31-AUG-2000 JP 2000262865
PR 06-JUN-1995 US 08/471967,06-JUN-1995 US 08/467597 PR
06-JUN-1995 US 08/468447,06-JUN-1995 US 08/468569 PR
06-JUN-1995 US 08/466692,06-JUN-1995 US 08/471966 PR
06-JUN-1995 US 08/469851,06-JUN-1995 US 08/470129 PI PHILIP
DAN COOK,GLENN HAWK
PC C07H21/00,A61K31/7125,A61K48/00,A61P1/16,A61P27/02,A61P29/00,
PC A61P31/14,
PC A61P31/18,A61P35/00,C12N15/09,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC High-chimeric purity phosphorothioate bond-containing oligonucleotide
FH Key Location/Qualifiers
FT source 1..20
FT /organism="Unidentified".

FEATURES source
Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644" 8 t

BASE COUNT 2 a 4 c 6 g
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 35
BD015993
LOCUS 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide modulation of protein kinase C-epsilon.
ACCESSION BD015993
VERSION BD015993.1 GI:22557131
KEYWORDS JP 2001224386-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,F.C., Boggs,R.T. and Dean,N.M.
TITLE Oligonucleotide modulation of protein kinase C-epsilon
JOURNAL Patent: JP 2001224386-A 2 21-AUG-2001;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001224386-A/2

PD 21-AUG-2001
 PF 13-DEC-2000 JP 2000379218
 PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
 FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
 C12N15/09, A61K48/00, C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, PC
 G01N33/53, G01N33/56, G01N33/573//A61K31/711, A61K31/712, A61K31/7125, PC
 PC G01N33/566, G01N33/573//A61K31/711, A61K31/712, A61K31/7125, PC
 A61P35/00,
 PC A61P43/00, A61P43/00, C12N5/10, C12N15/00, C12N5/00 CC synthetic
 FT key Location/Qualifiers
 FT source 1..20
 FT /organism='Artificial Sequence'.
 FEATURES
 source
 1..20
 /organism='synthetic construct'
 /mol_type='genomic DNA'
 /db_xref='taxon:32630' 8 t
 BASE COUNT 2 a 4 c 6 g 8 t
 ORIGIN
 1 GTTCTCGCTGGTGAGTTTCA 20
 1 GTTCTCGCTGGTGAGTTTCA 20

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 DB 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 36
 BD016112
 LOCUS
 DEFINITION
 Oligonucleotide modulation of protein kinase C-zeta.
 ACCESSION
 BD016112
 VERSION
 BD016112.1 GI:22557250
 KEYWORDS
 JP 2001224387-A/2.
 SOURCE
 synthetic construct
 ORGANISM
 artificial sequences.
 1 (bases 1 to 20)
 REFERENCE
 1 Bennett, F.C., Boggs, R.T. and Dean, N.M.
 AUTHORS
 Oligonucleotide modulation of protein kinase C-zeta
 TITLE
 Patent: JP 2001224387-A 2 21-AUG-2001;
 JOURNAL
 ISIS PHARMACEUTICALS INC
 COMMENT
 OS Artificial Sequence
 PN JP 2001224387-A/2
 PD 21-AUG-2001
 PR 13-DEC-2000 JP 2000379249
 PF 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
 FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
 C12N15/09, A61K31/7088, A61K48/00, A61P29/00, A61P35/00, A61P43/00, PC
 C07H21/00,
 PC C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
 G01N33/573//
 PC C12N5/10, C12N15/00, C12N5/00
 CC synthetic
 FT key Location/Qualifiers
 FT source 1..20
 FT /organism='Artificial Sequence'.
 FEATURES
 source
 1..20
 /organism='synthetic construct'
 /mol_type='genomic DNA'
 /db_xref='taxon:32630' 8 t
 BASE COUNT 2 a 4 c 6 g 8 t
 ORIGIN
 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||

Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 37
 BD017264
 LOCUS
 DEFINITION
 Oligonucleotide modulation of protein kinase C-eta.
 ACCESSION
 BD017264
 VERSION
 BD017264.1 GI:22558440
 KEYWORDS
 JP 2001231579-A/2.
 SOURCE
 synthetic construct
 ORGANISM
 artificial sequences.
 1 (bases 1 to 20)
 REFERENCE
 1 Bennett, F.C., Boggs, R.T. and Dean, N.M.
 AUTHORS
 Oligonucleotide modulation of protein kinase C-eta
 TITLE
 Patent: JP 2001231579-A 2 28-AUG-2001;
 JOURNAL
 ISIS PHARMACEUTICALS INC
 COMMENT
 OS Artificial Sequence
 PN JP 2001231579-A/2
 PD 28-AUG-2001
 PF 13-DEC-2000 JP 2000379234
 PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
 FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
 C12N15/09, A61K31/711, A61K31/712, A61K31/7125, A61K48/00, A61P29/00,
 PC A61P35/00,
 PC A61P43/00, C07H21/00, C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, PC
 G01N33/50,
 PC G01N33/53, G01N33/566//C12N5/10, G01N33/68, C12N15/00, C12N5/00 CC
 synthetic
 FT key Location/Qualifiers
 FT source 1..20
 FT /organism='Artificial Sequence'.
 FEATURES
 source
 1..20
 /organism='synthetic construct'
 /mol_type='genomic DNA'
 /db_xref='taxon:32630' 8 t
 BASE COUNT 2 a 4 c 6 g 8 t
 ORIGIN
 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 1 GTTCTCGCTGGTGAGTTTCA 20

Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 DB 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 38
 BD076448
 LOCUS
 DEFINITION
 Combined antisense library.
 ACCESSION
 BD076448
 VERSION
 BD076448.1 GI:22622051
 KEYWORDS
 JP 2001519170-A/42.
 SOURCE
 synthetic construct
 ORGANISM
 artificial sequences.
 1 (bases 1 to 20)
 REFERENCE
 1 Riley, T.A., Brown, B.D. and Arnold, L.J.
 AUTHORS
 Combined antisense library
 TITLE
 Patent: JP 2001519170-A 42 23-OCT-2001;
 JOURNAL
 OASIS BIOSCIENCES INC
 COMMENT
 OS Artificial Sequence
 PN JP 2001519170-A/42
 PD 23-OCT-2001
 PF 28-SEP-1998 JP 2000515030
 PR 02-OCT-1997 US 68/060673,18-AUG-1998 US 09/136080 PI
 TIMOTHY A RILEY, BOB D BROWN, DYLE J ARNOLD
 PC C12Q1/68, C07H21/04, C12N15/09, C12P19/34, C12N15/00 CC
 synthetic oligonucleotide

```

FH Key Location/Qualifiers
FT source 1..20 /organism='Artificial Sequence'
FT Location/Qualifiers
FEATURES
source 1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGTGGTGAGTTTCA 20
|||||

RESULT 39
BD106496
LOCUS 20 bp DNA linear PAT 18-SEP-2002
DEFINITION High efficiency encapsulation of charged therapeutic agents in lipid vesicles.
ACCESSION BD106496
VERSION BD106496.1 GI:23201314
KEYWORDS JP 2002501511-A/13.
SOURCE Chlamydia sp.
ORGANISM Chlamydia sp.
REFERENCE 1 (bases 1 to 20)
AUTHORS Semple,S.C., Klimuk,S.K., Harasym,T., Hope,M.J., Ansel,S.M., Cullis,P., Scherrer,P. and Debeyer,D.S.
TITLE High efficiency encapsulation of charged therapeutic agents in lipid vesicles
JOURNAL Patent: JP 2002501511-A 13 15-JAN-2002; INEX PHARMACEUTICALS CORP
COMMENT FN JP 2002501511-A/13
PD 15-JAN-2002
PI 14-MAY-1998 JP 1998548646
PI SEAN C SEMPLE,SANDRA K KLIMUK,TROY HARASYM,MICHAEL J HOPE, PI STEVEN M ANSELL,
PI PIETER CULLIS,PETER SCHERRER,DAN SUITE DEBEYER PC A61K9/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FEATURES
source 1..20
/organism='Chlamydia sp.'
/mol_type='genomic DNA'
/db_xref='taxon:35827'
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGTGGTGAGTTTCA 20
|||||

RESULT 40
I29012
LOCUS 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 8 from patent US 5576302.
ACCESSION I29012
VERSION I29012.1 GI:1819803
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.

```

```

Unclassified
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook,P.D. and Hoke,G.
TITLE Oligonucleotides for modulating hepatitis C virus having phosphorothioate linkages of high chiral purity
JOURNAL Patent: US 5576302-A 8 19-NOV-1996;
FEATURES
source Location/Qualifiers
1..20
/organism='unknown'
BASE COUNT 2 a 4 c 6 g 8 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGTGGTGAGTTTCA 20
|||||

```

Search completed: January 24, 2004, 15:05:27
Job time : 1983 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 24, 2004, 13:24:16 ; Search time 215 Seconds
(without alignments)
251.111 Million cell updates/sec

Title: US-10-002-884A-5

Perfect score: 20
Sequence: 1 gttctgctggtgagtttca 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 2329600

Minimum DB seq length: 0
Maximum DB seq length: 40

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : N Geneseq 19Jun03.*
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	14	AAQ49658 PKC 3' UTR binding
2	20	100.0	20	14	AAQ49708 PKC-A gapped oligo
3	20	100.0	20	14	AAQ49709 PKC-A gapped oligo
4	20	100.0	20	14	AAQ49710 PKC-A gapped oligo
5	20	100.0	20	16	AAQ97875 PNA oligomer target
6	20	100.0	20	16	AAQ84160 PKC-alpha 3' untra
7	20	100.0	20	17	AAT33478 Oligomeric compound
8	20	100.0	20	17	AAT33479 Oligomeric compound

9	20	100.0	20	17	AAT31818 Oligonucleotide (O
10	20	100.0	20	18	AAQ36455 Chimeric 2'-O-meth
11	20	100.0	20	18	AAQ33997 Oligonucleotide an
12	20	100.0	20	18	AAV06043 Oligonucleotide wh
13	20	100.0	20	18	AAV06045 Oligonucleotide ta
14	20	100.0	20	18	AAT77191 Oligonucleotide fo
15	20	100.0	20	18	AAT49211 Phosphorothioate o
16	20	100.0	20	18	AAT51075 ISIS-3521, PKC- α p
17	20	100.0	20	19	AAV28183 Antisense oligonuc
18	20	100.0	20	19	AAV35502 Oligo OM2 targeted
19	20	100.0	20	19	AAV11168 ISIS 9606 oligonuc
20	20	100.0	20	20	AAZ27267 Human protein kina
21	20	100.0	20	20	AAZ11590 Fully modified pho
22	20	100.0	20	20	AAZ99885 Phosphorothioate o
23	20	100.0	20	20	AAZ78525 Human PKC- α - α l
24	20	100.0	20	20	AAZ83634 Human protein kina
25	20	100.0	20	20	AAZ33511 Antisense oligonuc
26	20	100.0	20	20	AAZ33399 Phosphorothioate 2
27	20	100.0	20	20	AAZ23697 Deletion sequence
28	20	100.0	20	20	AAZ22563 Human protein kina
29	20	100.0	20	20	AAZ19127 Human PKC- α - α n
30	20	100.0	20	20	AAZ18706 Target PKC- α - α n
31	20	100.0	20	20	AAZ99433 Antisense oligonuc
32	20	100.0	20	20	AAZ72642 Human protein kina
33	20	100.0	20	21	AAZ62739 Phosphorothioate o
34	20	100.0	20	21	AAZ65035 Protein kinase C α
35	20	100.0	20	21	AAZ9219 PKC-a target phosph
36	20	100.0	20	21	AAZ94542 Example biological
37	20	100.0	20	21	AAZ16139 Human PKC- α - α n
38	20	100.0	20	21	AAZ14474 Synthetic oligonuc
39	20	100.0	20	21	AAZ10248 2-aminoadenosine-c
40	20	100.0	20	21	AAZ92764 Human protein kina
41	20	100.0	20	21	AAZ96859 Human PKC- α - α h
42	20	100.0	20	21	AAZ90214 Phosphorothioate h
43	20	100.0	20	21	AAZ44412 Human protein kina
44	20	100.0	20	21	AAZ57152 Phosphorothioate 2
45	20	100.0	20	21	AAZ40365 Antisense inhibito
46	20	100.0	20	21	AAZ47920 PKC- α - α phosphor
47	20	100.0	20	21	AAZ48121 PKC- α - α phosphor
48	20	100.0	20	21	AAZ48641 PKC- α - α antisens
49	20	100.0	20	21	AAZ49384 PKC- α - α targette
50	20	100.0	20	21	AAZ49392 PKC- α - α targette
51	20	100.0	20	21	AAZ49393 PKC- α - α targette
52	20	100.0	20	22	AAZ21404 Human PKC- α - α n
53	20	100.0	20	22	AAZ21514 Human PKC- α - α n
54	20	100.0	20	22	AAZ21515 Human PKC- α - α n
55	20	100.0	20	22	AAZ20916 Phosphorothioate o
56	20	100.0	20	22	AAZ15521 Human protein kina
57	20	100.0	20	22	AAZ15522 Human protein kina
58	20	100.0	20	22	AAZ13421 Nucleotide sequenc
59	20	100.0	20	22	AAZ28500 Oligonucleotide #4
60	20	100.0	20	22	AAZ46454 PKC- α - α antisens
61	20	100.0	20	22	AAZ77811 Anti-PKC- α - α oli
62	20	100.0	20	22	AAZ60940 Oligonucleotide ta
63	20	100.0	20	22	AAZ31597 Oligo #6 used to p
64	20	100.0	20	22	AAZ23806 Modified phosphoro
65	20	100.0	20	22	AAZ38208 Synthetic phosphor
66	20	100.0	20	24	ABX10632 Oligomeric compound
67	20	100.0	20	24	ABK30762 Protein kinase C p
68	20	100.0	20	24	ABK31274 Human protein kina
69	20	100.0	20	24	ABL90855 PKC- α - α targeted
70	20	100.0	20	24	ABL01632 Human PKC- α - α n
71	20	100.0	20	24	AAZ22795 PKC- α - α targeted
72	20	100.0	20	24	ABA97486 HCMV gene targetin
73	20	100.0	20	25	ABZ75969 Oligonucleotide wi
74	20	100.0	20	25	ABX13931 Anti-PKCalpha 2'-O
75	20	100.0	21	16	AAQ85828 Modified oligonuc
76	19	95.0	19	18	AAV06233 Oligonucleotide co
77	19	95.0	19	19	AAV06822 PKC- α - α antisens
78	19	95.0	19	21	AAA06837 PKC-a targeting ph
79	19	95.0	19	21	AAZ57156 Anti-PKCalpha 2'-O
80	19	95.0	20	16	AAQ85820 PKC- α - α 3' untra
81	18	90.0	18	16	AAQ84179

82	18	90.0	18	18	AA336453	Chimeric 2'-O-meth	c 155	12.4	52.0	20	24	ABA83488
83	18	90.0	18	19	AA335552	Oligo ON52 targete	156	12.4	52.0	29	20	AAA18201
84	18	90.0	18	20	AAZ27317	Human protein kina	157	12.4	52.0	29	21	AAAF6451
85	18	90.0	18	20	AAZ10288	Oligonucleotide us	158	12.2	61.0	20	20	AAAF96191
86	18	90.0	18	20	AAZ78575	Human PKC-alpha 3'	159	12.2	61.0	20	22	AAAF56743
87	18	90.0	18	20	AAZ83684	Human protein kina	c 160	12.2	61.0	20	24	ABQ78106
88	18	90.0	18	20	AAZ22613	Human protein kina	c 161	12.2	61.0	20	24	ABQ78106
89	18	90.0	18	20	AAZ19178	Human PKC-alpha an	c 162	12.2	61.0	20	25	ABX15790
90	18	90.0	18	20	AAZ05460	Chimeric 2' O-prop	163	12.2	61.0	20	25	AAZ10700
91	18	90.0	18	20	AAZ15062	Human protein kina	164	12.2	61.0	22	22	AAZ30906
92	18	90.0	18	21	AAZ44414	Antisense oligonuc	165	12.2	61.0	23	19	AAV15771
93	18	90.0	18	21	AAZ44158	Human protein kina	166	12.2	61.0	23	19	AAV16283
94	18	90.0	18	22	AAZ21423	Human PKC-alpha an	167	12.2	61.0	23	24	AAV172880
95	18	90.0	18	22	AAZ21520	Human PKC-alpha an	168	12.2	61.0	23	25	AAZ20706
96	18	90.0	18	24	ABL90905	Human protein kina	169	12.2	61.0	23	25	AAZ49783
97	18	90.0	22	16	AAQ85832	Anti-PKCalpha alky	170	12.2	61.0	25	22	AAAF80472
98	17	85.0	17	16	AAQ84180	PKC-alpha 3' untra	c 171	12.2	61.0	25	24	AAAL49409
99	17	85.0	17	18	AAZ36454	Chimeric 2'-O-meth	c 172	12.2	61.0	25	24	AAAL49409
100	17	85.0	17	19	AAV35553	Oligo ON53 targete	c 173	12.2	61.0	27	22	AAAF84804
101	17	85.0	17	20	AAZ27318	Human protein kina	174	12.2	61.0	29	20	AAAF84804
102	17	85.0	17	20	AAZ10289	Oligonucleotide us	175	12.2	61.0	29	21	AAAF84804
103	17	85.0	17	20	AAZ78576	Human PKC-alpha 3'	176	12.2	61.0	30	14	AAQ54155
104	17	85.0	17	20	AAZ83685	Human protein kina	177	12.2	61.0	30	24	ABK54499
105	17	85.0	17	20	AAZ22614	Human protein kina	c 178	12.2	61.0	31	20	AAH06431
106	17	85.0	17	20	AAZ19179	Human PKC-alpha an	179	12.2	61.0	31	22	AAH91025
107	17	85.0	17	20	AAZ05461	Chimeric 2' O-prop	c 180	12.2	61.0	32	22	AAAF77254
108	17	85.0	17	20	AAZ15063	Antisense oligonuc	181	12.2	61.0	35	21	AAZ44418
109	17	85.0	17	21	AAZ44415	Human protein kina	182	12.2	61.0	18	21	AAAF65034
110	17	85.0	17	21	AAZ48159	PKC-alpha chimeric	c 183	12.2	61.0	18	24	ABK66022
111	17	85.0	17	22	AAZ21424	Human PKC-alpha an	184	12.2	61.0	19	24	AAAL47003
112	17	85.0	17	22	AAZ21513	Human PKC-alpha an	c 185	12.2	61.0	21	21	AAAF53106
113	17	85.0	17	24	ABL90906	Human protein kina	c 186	12.2	61.0	21	22	AAAF95577
114	16.2	81.0	19	20	AAH28505	PKC antisense olig	c 187	12.2	61.0	22	18	AAAF76671
115	16	80.0	17	22	AAZ44395	Nucleotide sequenc	c 188	12.2	61.0	22	19	AAAF65822
116	15	75.0	15	21	AAZ44420	Human protein kina	189	12.2	61.0	22	21	AAAF53901
117	15	75.0	15	21	AAZ44421	Human protein kina	190	12.2	61.0	22	21	AAAF53901
118	15	75.0	15	21	AAZ44422	Human protein kina	191	12.2	61.0	22	21	AAAF53901
119	15	75.0	15	21	AAZ44423	Human protein kina	192	12.2	61.0	22	21	AAAF53901
120	15	75.0	15	21	AAZ44424	Human protein kina	193	12.2	61.0	22	21	AAAF53901
121	15	75.0	15	21	AAZ44425	Human protein kina	194	12.2	61.0	22	21	AAAF53901
122	14.8	74.0	18	22	AAZ04179	Nested primer ZF-1	c 195	12.2	61.0	23	24	ABK66022
123	14	70.0	15	21	AAZ44419	Human protein kina	c 196	12.2	61.0	23	24	ABK66022
124	13.8	69.0	18	22	AAZ04178	Nested primer ZF-1	c 197	12.2	61.0	23	24	ABK66022
125	13.8	69.0	18	22	AAZ04180	Nested primer ZF-1	c 198	12.2	61.0	24	24	ABZ22198
126	13.8	69.0	20	22	AAZ10575	Human WWP2 chimeri	c 199	12.2	61.0	25	18	AAAF59974
127	13.8	69.0	20	22	AAZ56742	Canine wild-type H	c 200	12.2	61.0	25	18	AAAF59974
128	13.6	68.0	33	16	AAQ83646	Internal primer (e)	201	12.2	61.0	27	12	AAAF11326
129	13.6	68.0	33	16	AAQ83647	Internal primer (f)	202	12.2	61.0	27	12	AAAF11326
130	13.4	67.0	22	22	AAZ72361	PCR primer specifi	203	12.2	61.0	29	21	AAAF04246
131	13.4	67.0	22	25	ABX11029	Human XA5 specifi	c 204	12.2	61.0	30	21	AAAF04246
132	13.4	67.0	24	24	ABQ02192	Oligonucleotide ad	c 205	12.2	61.0	30	21	AAAF04246
133	13.4	67.0	24	24	ABQ08283	Oligonucleotide ad	c 206	12.2	61.0	30	24	ABT12734
134	13.4	67.0	24	24	ABQ08324	Oligonucleotide ad	c 207	12.2	61.0	30	24	ABT12734
135	13.4	67.0	29	21	AAQ06511	Hammerhead ribozym	208	12.2	61.0	39	12	AAQ11327
136	13.4	67.0	31	22	AAI31311	Human single nucle	c 209	12.2	61.0	39	17	AAAT34838
137	13.4	67.0	38	17	AAZ64151	Rabbit stromelysin	c 210	12.2	61.0	39	25	ABZ57823
138	13.2	66.0	21	16	AAZ00711	Human trkC recepto	c 211	11.8	59.0	17	18	AAAF69757
139	13.2	66.0	21	16	AAZ68861	Human trkC recepto	c 212	11.8	59.0	18	24	AAAF69757
140	13.2	66.0	23	24	ABQ78108	HuVH related mutat	c 213	11.8	59.0	18	24	AAAF69757
141	13.2	66.0	23	24	ABQ78110	HuVH related mutat	214	11.8	59.0	18	25	ABX77410
142	13.2	66.0	23	24	ABQ78112	HuVH related mutat	215	11.8	59.0	20	18	AAV03714
143	13.2	66.0	23	24	ABK15797	Mutation PCR prime	c 216	11.8	59.0	20	18	AAV03698
144	12.8	64.0	18	22	AAZ04178	Nested primer ZF-1	c 217	11.8	59.0	20	20	AAAF92380
145	12.8	64.0	20	25	ABQ77198	Human ABCG12 exon	c 218	11.8	59.0	20	21	AAAF92380
146	12.8	64.0	24	24	ABA83445	Human MP-1 PCR pri	219	11.8	59.0	20	21	AAAF92380
147	12.8	64.0	30	22	AAZ14205	Synthetic transcri	220	11.8	59.0	21	19	AAAF92380
148	12.6	63.0	27	17	AAZ42568	Primer #2 for chro	221	11.8	59.0	22	24	AAAF92380
149	12.6	63.0	27	20	AAZ06678	AML1 gene exon 5	c 222	11.8	59.0	23	20	AAZ37156
150	12.6	63.0	29	22	AAZ55886	Wild-type HPIV fra	c 223	11.8	59.0	24	20	AAZ34087
151	12.6	63.0	30	20	AAZ87377	Human GTPase cDNA	224	11.8	59.0	24	20	AAZ21375
152	12.6	63.0	33	24	AAZ76386	Human transcriptio	c 225	11.8	59.0	24	20	AAZ21375
153	12.6	63.0	33	24	ABL56683	PCR primer #4 for	c 226	11.8	59.0	24	21	AAAF78749
154	12.4	62.0	19	20	AAZ30241	GRK4 allele specifi	c 227	11.8	59.0	24	21	AAAF78749

Human MP-1 antisen
Human TIE-2 hammer
Hammerhead ribozym
PCR primer used to
Canine narcoleptic
HuVH related mutat
Mutation PCR prime
Humanising COL-1 V
Human MATER intron
Primer B #34 used
Candida albicans G
Upper primer U2492
AAVS1 human integr
Human AAVS1 upper
U2492 PCR primer u
U2492 PCR primer u
Probe used to dete
Human PTMAX coding
PCR primer used fo
PCR primer used fo
Human P32 PCR pri
Protein H gene fra
Norwalk virus dete
Human biallelic po
Human inflammatory
ALG3 specific 3' p
Human protein kina
Protein kinase C a
Universal fungi de
Candida 18S rRNA g
Phage DNA primer M
Human gene single
Target specific pr
Invasive oligonucle
Nucleotide sequenc
Pan-fungal rRNA/rD
Pan-fungal probe.
Pan-fungal probe u
Pan-fungal oligonu
Pan-fungal positiv
Positive control p
INVADER-directed c
Mouse LTPB-3 prime
Regulatory protein
Probe RDR480 for P
Soybean 240L17 reg
Probe 1417 specifi
RNA oligonucleotid
Polymorphic fragme
Oligonucleotide w
Interferon B relat
Interferon B relat
Probe 1418 specifi
Primer used for fr
Primer used for fr
GM soybean CP4 BPS
Human flt1 VRGF re
Nested primer ZF-1
RT-PCR primer used
Human lrb gene 5'
Primer SHR-8 for H
Primer SHF-10 for
PCR primer used to
Anti-human Fas ant
Anti-human Fas ant
Primer FhEx178 use
Ras gene PCR prime
Rx specific primer
Human PRO792 PCR r
Thermus thermophil
Thermus thermophil
Human PRO792 rever
Human PRO792 rever

c 228	11.8	59.0	24	21	AAA77637	Human PRO792 PCR p	301	11.6	58.0	22	20	AA75864	H. pylori OMP DNA
c 229	11.8	59.0	24	24	AB187794	Capture oligonucle	302	11.6	58.0	22	20	AA75842	H. pylori OMP DNA
c 230	11.8	59.0	24	24	AB187795	Capture oligonucle	c 303	11.6	58.0	22	23	ABA10178	Tail primer #171 f
c 231	11.8	59.0	24	25	AB189245	Human PRO DNA PCR	304	11.6	58.0	23	18	AA795708	DNA from HIV-1 inf
c 232	11.8	59.0	25	21	ABT32023	OSPH2 PCR primer S	305	11.6	58.0	23	19	AAV04923	Primer LTR-test us
c 233	11.8	59.0	27	21	AAZ62071	Hammerhead ribozym	306	11.6	58.0	23	19	AAV09864	Primer LTR-test us
c 234	11.8	59.0	28	24	ABT04880	Human G protein co	307	11.6	58.0	23	20	AA715221	PCR primer LTR-tes
c 235	11.8	59.0	28	24	ABK67067	Human gene specifi	308	11.6	58.0	23	21	AA790157	PCR primer LTR-tes
c 236	11.8	59.0	29	19	AAV36882	Nucleotide sequenc	309	11.6	58.0	23	24	AA72530	Nested PCR primer,
c 237	11.8	59.0	29	20	AAA16975	Aryl hydrocarbon n	310	11.6	58.0	23	25	ABX11223	HIV-1 PCR primer L
c 238	11.8	59.0	29	20	AAA19571	Integrin alpha 6 s	c 311	11.6	58.0	24	19	AAV45497	Neisseria meningit
c 239	11.8	59.0	29	20	AAA22178	Integrin subunit b	c 312	11.6	58.0	25	17	AA741428	PCR obese gene sen
c 240	11.8	59.0	29	21	AAF00345	Hammerhead ribozym	313	11.6	58.0	25	22	AA702137	PCR primer #1 used
c 241	11.8	59.0	29	21	AAF01035	Hammerhead ribozym	314	11.6	58.0	25	24	ABL58384	RF-kappaB binding
c 242	11.8	59.0	29	21	AAF01188	Hammerhead ribozym	c 315	11.6	58.0	25	24	ABL58385	RF-kappaB binding
c 243	11.8	59.0	29	21	AAF01192	Hammerhead ribozym	c 316	11.6	58.0	26	18	AA791830	Probe 2 used to is
c 244	11.8	59.0	29	21	AAF01463	Hammerhead ribozym	317	11.6	58.0	27	11	AAQ04699	HIV enhancer negat
c 245	11.8	59.0	29	21	AAF01485	Hammerhead ribozym	318	11.6	58.0	27	17	AA740192	HIV target sequenc
c 246	11.8	59.0	29	22	AAI68580	A. thaliana SUT4 p	319	11.6	58.0	27	17	AA730587	Target binding reg
c 247	11.8	59.0	29	22	AAI68802	ATCDPK1 and ATCDPK	320	11.6	58.0	27	17	AA730588	Target binding reg
c 248	11.8	59.0	30	24	ABL91083	Hominidae LDL rece	321	11.6	58.0	28	15	AAQ74525	Primer for the amp
c 249	11.8	59.0	33	24	ABQ78111	HuVH related mutat	322	11.6	58.0	28	15	AAQ74616	Primer for the amp
c 250	11.8	59.0	33	24	ABK15793	Mutation PCR prime	c 323	11.6	58.0	28	15	AAQ73477	NF KB transcriptio
c 251	11.8	59.0	33	25	ABX11305	Humanising COL-1 V	c 324	11.6	58.0	28	17	AA738840	Primer for dhat op
c 252	11.8	59.0	33	16	AA755401	Human reLA hammerh	c 325	11.6	58.0	28	19	AAV42035	Glycerol dehydrata
c 253	11.8	59.0	36	16	AA755212	Mouse reLA hammerh	c 326	11.6	58.0	28	19	AAV35756	Synthetic dhaB/dha
c 254	11.8	59.0	36	16	AA752973	Mouse ICM hammerh	327	11.6	58.0	29	20	AA759847	NF-kappaB specific
c 255	11.8	59.0	36	16	AA753079	Mouse ICM hammerh	328	11.6	58.0	29	20	AA756005	NF-kappaB specific
c 256	11.8	59.0	36	16	AA752617	Human ICM hammerh	329	11.6	58.0	29	20	AAV84353	Human NF kappa B o
c 257	11.8	59.0	36	17	AA766406	Mouse B7-2 hammerh	c 330	11.6	58.0	29	20	AAV72528	NF-kappaB-specific
c 258	11.8	59.0	36	17	AA766343	Mouse B7-2 hammerh	331	11.6	58.0	29	22	AA724297	NF-kappa-B EMSA pr
c 259	11.8	59.0	36	17	AA764917	Human B7-1 hammerh	332	11.6	58.0	29	22	AA784483	NF-kappa-B electro
c 260	11.8	59.0	36	17	AA750394	Rabbit CERP HH rib	333	11.6	58.0	29	24	ABX53576	32P-labelled oligo
c 261	11.8	59.0	36	17	AA749933	Human CERP HH ribo	334	11.6	58.0	29	24	ABX13180	Nucleotide sequenc
c 262	11.8	59.0	36	24	ABX02028	HCV hammerhead rib	335	11.6	58.0	29	25	ABX13180	Human Nuclear fact
c 263	11.8	59.0	37	20	AA751941	Porphyromonas ging	336	11.6	58.0	29	25	ABX15467	Necrosis factor ka
c 264	11.8	59.0	38	16	AA753875	Rat ICM hammerhea	337	11.6	58.0	29	25	ABX15467	32P-labelled NF-ka
c 265	11.8	59.0	38	16	AA753838	Rat ICM hammerhea	338	11.6	58.0	29	25	ABX15510	32P-labelled NF-ka
c 266	11.8	59.0	38	17	AA781873	Human c-myc hammer	339	11.6	58.0	29	25	ABX15843	Radiolabelled nucl
c 267	11.8	59.0	38	20	AAZ34421	Nucleic acid-based	340	11.6	58.0	30	22	AA7502612	PCR primer #1 used
c 268	11.8	59.0	38	21	ABN87027	HCV NS5B ribozyme	c 341	11.6	58.0	30	22	AA7502612	Nucleotide sequenc
c 269	11.8	59.0	38	21	AA796436	Human Chk1 ribozyme	c 342	11.6	58.0	30	22	AA7502612	Human Nuclear fact
c 270	11.8	59.0	38	23	ABK04599	Human NOGO Inozyme	c 343	11.6	58.0	30	24	AA749462	Mutation detection
c 271	11.8	59.0	38	23	ABK07926	Human CD20 Hammerh	344	11.6	58.0	32	17	AA732697	Vector fragment co
c 272	11.8	59.0	38	24	ABQ78109	HuVH related mutat	345	11.6	58.0	32	22	AA717455	Nuclear factor kap
c 273	11.8	59.0	38	24	ABK58935	Human CICAL gene e	c 346	11.6	58.0	32	22	AA717457	Human immunodefici
c 274	11.8	59.0	38	24	ABK58694	Human CICAL gene e	347	11.6	58.0	33	17	AA734849	Primer used for fir
c 275	11.8	59.0	38	24	ABK58729	Human CICAL gene e	348	11.6	58.0	33	20	AA734336	HIV probe correspon
c 276	11.8	59.0	38	24	ABK15792	Mutation PCR prime	c 349	11.6	58.0	33	24	ABX14190	Human ATP-dependen
c 277	11.8	59.0	38	24	ABK19556	Human ERG hammerhe	350	11.6	58.0	33	24	AA730686	Human SOS coding s
c 278	11.8	59.0	38	24	ABK19698	Human ERG hammerhe	351	11.6	58.0	34	10	AA730922	Part of the kappa
c 279	11.8	59.0	38	25	ABX11303	Humanising COL-1 V	352	11.6	58.0	34	18	AA744440	Haemopoietin recep
c 280	11.8	59.0	40	24	ABQ78107	HuVH related mutat	353	11.6	58.0	34	22	AA766959	Lymphoid cell nucl
c 281	11.8	59.0	40	24	ABQ78113	HuVH related mutat	c 354	11.6	58.0	34	22	AA765030	Hydroxymethyl glut
c 282	11.8	59.0	40	24	ABN88861	Human Mr-Ia Rz for	355	11.6	58.0	35	21	AA799615	NF-kB oligonucleot
c 283	11.8	59.0	40	24	ABN88863	Human Mr-Ia Rz for	c 356	11.6	58.0	35	21	AA799616	NF-kB oligonucleot
c 284	11.8	59.0	40	24	ABK15791	Human ERG hammerhe	357	11.6	58.0	35	21	AA761055	Electrophoretic mo
c 285	11.8	59.0	40	24	ABK15791	Mutation PCR prime	358	11.6	58.0	36	19	AA767098	HIV LTR #2. Human
c 286	11.8	59.0	40	24	ABX11301	Humanising COL-1 V	359	11.6	58.0	37	15	AAQ61543	HIV long terminal
c 287	11.8	59.0	40	25	ABX11307	Humanising COL-1 V	c 360	11.6	58.0	37	15	AAQ73476	NF KB transcriptio
c 288	11.6	58.0	40	25	AAZ70081	Human biallelic ma	361	11.6	58.0	37	19	AAV45402	Probe nucleic acid
c 289	11.6	58.0	40	26	AA700102	Hepatitis GB virus	362	11.6	58.0	37	19	AAV45402	HIV LTR binding si
c 290	11.6	58.0	20	21	AA755348	Hepatitis GB virus	363	11.6	58.0	38	21	AA732919	Kappa-B-pr sequenc
c 291	11.6	58.0	21	21	AA755348	Mouse R55 primer M	364	11.6	58.0	38	22	AA799023	Immunostimulatory
c 292	11.6	58.0	22	18	AA725153	Primer for H. pyl	365	11.6	58.0	38	24	ABX77664	Angiogenesis inhib
c 293	11.6	58.0	22	18	AA746873	5' primer amplifie	c 366	11.6	58.0	38	24	ABX39015	Immunostimulatory
c 294	11.6	58.0	22	18	AA746895	5' primer amplifie	c 367	11.6	58.0	39	15	AAQ58049	Oligonucleotide NF
c 295	11.6	58.0	22	18	AA77529	5' primer for H. p	c 368	11.6	58.0	39	15	AAQ58050	Oligonucleotide NF
c 296	11.6	58.0	22	18	AA77529	5' primer for H. p	c 369	11.6	58.0	39	16	AAQ75295	Oligo RV138 encodi
c 297	11.6	58.0	22	19	AA77529	Oligonucleotide pr	c 370	11.6	58.0	39	18	AA789779	Transcription fact.
c 298	11.6	58.0	22	19	AA77529	Oligonucleotide pr	c 371	11.6	58.0	39	18	AA789780	Transcription fact
c 299	11.6	58.0	22	19	AA77529	Oligonucleotide pr	c 372	11.6	58.0	39	18	AA788239	NF-kappaB transcri
c 300	11.6	58.0	22	19	AA77529	Oligonucleotide pr	c 373	11.6	58.0	39	18	AA788240	NF-kappaB transcri
c 301	11.6	58.0	22	19	AA77529	Oligonucleotide pr	c 374	11.6	58.0	39	18	AA788240	NF-kappa B binding

374	11.6	58.0	39	19	AAV56615	NF-kappaB binding	447	11.2	56.0	21	22	AAS11302	Human ANK gene SNP
C 375	11.6	58.0	39	19	AAV56616	NF-kappaB binding	448	11.2	56.0	21	22	AAH46135	Human CLCA1 sequen
C 376	11.6	58.0	39	20	AAV72977	Human Doc2-alpha p	449	11.2	56.0	21	22	AAD03957	Human checkpoint D
C 377	11.6	58.0	39	20	AAV72978	Human Doc2-alpha p	C 450	11.2	56.0	21	24	AAK55784	Human single nucle
C 378	11.6	58.0	39	24	AAV26647	NF-kB wild type bi	C 451	11.2	56.0	21	24	ABK27364	Mutant gamma-amino
C 379	11.6	58.0	39	24	AAD26648	NF-kB wild type bi	C 452	11.2	56.0	21	24	AAK18431	Degenerate PCR pri
C 380	11.6	58.0	40	17	AAZ70776	Stenotic carotid a	C 453	11.2	56.0	22	24	ABV72978	c-myb2 gene specif
C 381	11.6	58.0	40	17	AAZ96168	Polynucleotide seq	C 454	11.2	56.0	22	24	ABV72979	c-myb2 gene specif
C 382	11.4	57.0	14	15	AAQ78415	TGF-beta gene phos	455	11.2	56.0	22	24	ABL44387	Human chromosome 1
C 383	11.4	57.0	19	21	AAAB6323	PCBA HH ribozyme b	456	11.2	56.0	22	25	ABT23694	Stabilising reagen
C 384	11.4	57.0	19	22	AAAS4379	SPINK5 gene oligon	C 457	11.2	56.0	24	24	AAK87548	Mycobacterium bovi
C 385	11.4	57.0	19	22	AAAS44380	SPINK5 gene oligon	458	11.2	56.0	24	24	AAQ00528	Oligonucleotide ad
C 386	11.4	57.0	19	22	AAH61485	PCNA HH ribozyme b	C 459	11.2	56.0	25	16	AAQ00943	Almond N-glycosida
C 387	11.4	57.0	19	24	ABS98504	Human acetyl choli	460	11.2	56.0	25	21	AA449659	Human testis speci
C 388	11.4	57.0	20	18	AAV01355	Plasminogen activa	C 461	11.2	56.0	25	21	AAZ48824	PCR primer for Hum
C 389	11.4	57.0	20	19	AAV14142	Nucleotide sequenc	462	11.2	56.0	25	22	AAQ07332	Human testis-speci
C 390	11.4	57.0	20	21	AAAS18376	Non-B, non-C, non-	C 463	11.2	56.0	25	24	ABAC0346	Testis specific gl
C 391	11.4	57.0	20	21	AAAS36336	Primer RD052 for T	C 464	11.2	56.0	26	24	AAL43478	Gap insertion sequ
C 392	11.4	57.0	20	24	AAD331177	HMG-CoA reductase	C 465	11.2	56.0	26	24	AAAL49406	Human calcivirius
C 393	11.4	57.0	20	25	AAD52934	Human CYP3A5 gene	C 466	11.2	56.0	27	20	AAAX26286	Human PTMAX codin
C 394	11.4	57.0	21	25	ABK99823	PCR primer used to	C 467	11.2	56.0	27	24	AAAX26344	Trichloroethylene-
C 395	11.4	57.0	21	25	ABV77067	"Beta-amyrin synth	C 468	11.2	56.0	29	22	AAAC86783	Next extension seq
C 396	11.4	57.0	22	22	AAAS09788	PCR primer for L	C 471	11.2	56.0	30	22	AAAC86783	Human clone EC172
C 397	11.4	57.0	22	22	AAAS09789	Human glutamate tr	472	11.2	56.0	30	22	AAAC86783	Human cDNA clone A
C 398	11.4	57.0	23	20	AAAX84398	Oligonucleotide ad	C 473	11.2	56.0	32	25	ABX93251	PCR primer used to
C 399	11.4	57.0	24	20	AAZ28127	Oligonucleotide ad	474	11.2	56.0	33	24	ABA97892	Physcomitrella pat
C 400	11.4	57.0	24	24	ABQ005672	Oligonucleotide ad	C 475	11.2	56.0	34	25	ABA91088	DPPI0 PCR primer #
C 401	11.4	57.0	24	24	ABQ005306	Oligonucleotide ad	C 476	11.2	56.0	35	20	ABQ84486	Human single nucle
C 402	11.4	57.0	24	24	ABQ05347	Oligonucleotide ad	C 477	11.2	56.0	35	21	AAI30453	Human single nucle
C 403	11.4	57.0	24	24	ABQ11593	Oligonucleotide ad	C 478	11.2	56.0	37	25	ABZ76357	Quadruplex/duplex
C 404	11.4	57.0	24	24	ABQ11634	Oligonucleotide ad	C 479	11.2	56.0	38	18	AAV04406	Construct pC2-m9#5
C 405	11.4	57.0	25	22	AAD13162	Human MTSF1 protea	480	11.2	56.0	38	18	AAV	PCR primer #1 used
C 406	11.4	57.0	25	24	AAD36933	Human MTSF1 protea	481	11.2	56.0	38	18	AAV	T cell receptor al
C 407	11.4	57.0	25	24	ABQ13129	Oligonucleotide ad	482	11.2	56.0	38	18	AAV	Human ubiquitin C
C 408	11.4	57.0	25	24	ABQ13170	Oligonucleotide ad	483	11.2	56.0	38	18	AAV	Lambda primer 4
C 409	11.4	57.0	26	21	AAA63767	PCR primer used to	484	11.2	56.0	38	18	AAV	Minisequencing det
C 410	11.4	57.0	27	19	AAV96902	Potato citrate syn	485	11.2	56.0	38	22	AAV	Human SOS cDNA iso
C 411	11.4	57.0	27	20	AAK78400	Rat GAPDH primer 9	486	11.2	56.0	40	18	AAV	A. thaliana LMP cod
C 412	11.4	57.0	27	20	AAK25915	Interleukin 2 prob	C 487	11.2	56.0	40	18	AAV	Primer used in pre
C 413	11.4	57.0	28	18	AAI75157	Primer Pr-2 used i	C 488	11.2	56.0	40	18	AAV	Murine OPG mutagen
C 414	11.4	57.0	29	20	AAA21761	Integrin subunit b	C 489	11.2	56.0	40	18	AAV	EBV gene specific
C 415	11.4	57.0	29	20	AAV92926	Human B-raf hamme	C 490	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 416	11.4	57.0	29	20	AAV92077	Human A-Raf hamme	C 491	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 417	11.4	57.0	31	18	AAK62508	Granule bound star	C 492	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 418	11.4	57.0	33	17	AAK39335	Primer for amplif	C 493	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 419	11.4	57.0	33	18	AAI49011	Oct1 PCR primer 5'	C 494	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 420	11.4	57.0	33	19	AAV45049	Primer 5'NotochD	C 495	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 421	11.4	57.0	33	24	AAD24521	Oct1 homeodomain c	C 496	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 422	11.4	57.0	33	24	AAD24521	Oct1 homeodomain a	C 497	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 423	11.4	57.0	34	25	ABZ83586	Toxicologically re	C 498	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 424	11.4	57.0	36	19	AAV19386	Hemicola insolens	C 499	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 425	11.4	57.0	36	19	AAV13432	Primer MKA-05 for	C 500	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 426	11.4	57.0	36	20	AAK21722	Competitor Oligo A	C 501	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 427	11.4	57.0	38	24	ABK20480	Human ERG inozyme,	C 502	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 428	11.4	57.0	39	12	AAQ11466	Probe #8 complemen	C 503	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 429	11.2	56.0	15	21	AAK46259	Interphotoreceptor	C 504	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 430	11.2	56.0	17	22	AAH95029	Human Chk1 ribozym	C 505	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 431	11.2	56.0	17	22	AAH95855	Human Chk1 ribozym	C 506	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 432	11.2	56.0	17	22	AAH95856	Human Chk1 ribozym	C 507	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 433	11.2	56.0	18	24	ABK41025	Human obesity-asso	C 508	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 434	11.2	56.0	18	24	ABK41025	Human obesity-asso	C 509	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 435	11.2	56.0	19	20	AZ06665	Reverse primer use	C 510	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 436	11.2	56.0	19	21	AAZ71895	Human biallelic ma	C 511	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 437	11.2	56.0	20	14	AAQ39134	HCV sense primer X	C 512	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 438	11.2	56.0	20	18	AAV76684	Pyrococcus furiosu	C 513	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 439	11.2	56.0	20	19	AAV65839	Pyrococcus furiosu	C 514	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 440	11.2	56.0	20	19	AAV53950	Nucleotide sequenc	C 515	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 441	11.2	56.0	20	20	AZ031157	PCR primer used to	C 516	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 442	11.2	56.0	20	20	AAK34448	PCR primer used to	C 517	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 443	11.2	56.0	20	24	ABQ91343	Mouse CTLA4 gene P	C 518	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 444	11.2	56.0	20	24	ABQ93543	Human DISC1 gene e	C 519	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 445	11.2	56.0	20	25	AAV49029	Human WATER intron	C 520	11.2	56.0	40	18	AAV	Oligonucleotide SE
C 446	11.2	56.0	21	19	AAV52908	marx-lacZ fragment	C 521	11.2	56.0	40	18	AAV	Oligonucleotide SE

C 666	10.8	54.0	23	21	AAA30796	Mutant ribonucleas	739	10.8	54.0	29	20	AAA22206	Integrin subunit b
C 667	10.8	54.0	23	24	AAAD39086	Flea peritrophin 4	740	10.8	54.0	29	20	AAA22307	Integrin subunit b
C 668	10.8	54.0	23	25	ABX70744	Human RTQ-PCR prob	741	10.8	54.0	29	20	AAA22386	Human B-raf hammer
C 669	10.8	54.0	23	25	ABX70747	Human RTQ-PCR prob	742	10.8	54.0	29	20	AAV92946	Human B-raf hammer
C 670	10.8	54.0	24	18	AAAT70400	Primer for AlkBa f	743	10.8	54.0	29	20	AAV92953	Human A-Raf hammer
C 671	10.8	54.0	24	19	AAV08664	Primer AIL18FB fo	744	10.8	54.0	29	20	AAV92204	Human C-raf hammer
C 672	10.8	54.0	24	21	AAAC61292	Human ACE, AGT and	745	10.8	54.0	29	20	AAV91769	Human C-raf hammer
C 673	10.8	54.0	24	21	AAA338293	Human ATL exon 5 P	746	10.8	54.0	29	20	AAV91490	Hammerhead ribozym
C 674	10.8	54.0	24	21	AAAZ57621	Alpha glucosidase	747	10.8	54.0	29	21	AAAF00300	Hammerhead ribozym
C 675	10.8	54.0	24	21	AAZ48033	Human glycogen sto	748	10.8	54.0	29	21	AAAF01292	Hammerhead ribozym
C 676	10.8	54.0	24	22	AAAF80466	Probe used to dete	749	10.8	54.0	29	21	AAAF01322	Hammerhead ribozym
C 677	10.8	54.0	24	24	ABV76384	Human transcrip tio	750	10.8	54.0	29	21	AAAF01638	Hammerhead ribozym
C 678	10.8	54.0	24	24	ABZ30407	Candida albicans G	751	10.8	54.0	29	21	AAAF03435	Hammerhead ribozym
C 679	10.8	54.0	24	24	ABX09241	Arteriosclerosis-d	752	10.8	54.0	29	21	AAAF03483	Hammerhead ribozym
C 680	10.8	54.0	24	24	AAAL49403	Human PTMAX coding	753	10.8	54.0	29	21	AAAF03582	Hammerhead ribozym
C 681	10.8	54.0	24	24	AAAL49415	Human PTMAX coding	754	10.8	54.0	29	21	AAAF03883	Hammerhead ribozym
C 682	10.8	54.0	24	24	ABQ03631	Oligonucleotide ad	755	10.8	54.0	29	21	AAAF03931	Hammerhead ribozym
C 683	10.8	54.0	24	24	ABI84544	Capture oligonucle	756	10.8	54.0	29	21	AAAF04030	Hammerhead ribozym
C 684	10.8	54.0	24	24	ABI84545	Capture oligonucle	757	10.8	54.0	29	21	AAAF04124	Hammerhead ribozym
C 685	10.8	54.0	25	19	AAV55967	Chimeric E/NS1 jun	758	10.8	54.0	29	21	AAAF05248	Hammerhead ribozym
C 686	10.8	54.0	25	22	AAI61990	Soybean 240017 reg	759	10.8	54.0	29	21	AAAF06409	Hammerhead ribozym
C 687	10.8	54.0	25	22	AAAF83786	PCR primer derived	760	10.8	54.0	29	21	AAAF06447	Hammerhead ribozym
C 688	10.8	54.0	25	24	AAAF45008	Psammomys obesus A	761	10.8	54.0	29	21	AAAF06664	Hammerhead ribozym
C 689	10.8	54.0	25	24	ABN05256	Human GDMPL-1 25-m	762	10.8	54.0	29	21	AAAF06729	Hammerhead ribozym
C 690	10.8	54.0	25	24	ABN05257	Human GDMPL-1 25-m	763	10.8	54.0	29	21	AAAF06922	Hammerhead ribozym
C 691	10.8	54.0	25	24	ABN05258	Human GDMPL-1 25-m	764	10.8	54.0	29	21	AAAF06922	Hammerhead ribozym
C 692	10.8	54.0	25	24	ABN05259	Human GDMPL-1 25-m	765	10.8	54.0	29	21	AAAF06922	Hammerhead ribozym
C 693	10.8	54.0	25	24	ABN05260	Human GDMPL-1 25-m	766	10.8	54.0	29	21	AAAF06922	Hammerhead ribozym
C 694	10.8	54.0	25	24	ABN05261	Human GDMPL-1 25-m	767	10.8	54.0	29	21	AAAF06922	Hammerhead ribozym
C 695	10.8	54.0	25	24	ABN05262	Human GDMPL-1 25-m	768	10.8	54.0	29	21	AAAF06922	Hammerhead ribozym
C 696	10.8	54.0	25	24	ABN05263	Human GDMPL-1 25-m	769	10.8	54.0	29	21	AAAF06922	Hammerhead ribozym
C 697	10.8	54.0	25	24	ABN05264	Human GDMPL-1 25-m	770	10.8	54.0	29	21	AAAF06922	Hammerhead ribozym
C 698	10.8	54.0	25	24	ABN05265	Human GDMPL-1 25-m	771	10.8	54.0	29	21	AAAF06922	Hammerhead ribozym
C 699	10.8	54.0	25	24	ABN05266	Human GDMPL-1 25-m	772	10.8	54.0	29	21	AAAF06922	Hammerhead ribozym
C 700	10.8	54.0	25	24	ABN05267	Human GDMPL-1 25-m	773	10.8	54.0	29	21	AAAF06922	Hammerhead ribozym
C 701	10.8	54.0	26	17	AAAT69052	Primer for univ ers	774	10.8	54.0	30	20	AAAX38707	Human genomic DNA
C 702	10.8	54.0	26	19	AAV40674	Primer GOX3 for he	775	10.8	54.0	30	24	ABT12734	Interferon B relat
C 703	10.8	54.0	26	24	ABK32071	Novel secreted pro	776	10.8	54.0	30	24	ABT12735	Interferon B relat
C 704	10.8	54.0	27	18	AAAT73963	Mouse flt-1 VEGF r	777	10.8	54.0	30	24	ABQ96662	Human TTP-1 PDZ do
C 705	10.8	54.0	27	18	AAAT72035	Mouse flk-1 VEGF r	778	10.8	54.0	31	18	AAAX62440	Granule bound star
C 706	10.8	54.0	27	18	AAAT70982	Human KDR VEGF rec	779	10.8	54.0	31	18	AAAX62440	Flea peritrophin 4
C 707	10.8	54.0	27	18	AAAT70607	Human KDR VEGF rec	780	10.8	54.0	31	24	AAAD39087	K. aestuarii carbo
C 708	10.8	54.0	27	18	AAAT67809	Human KDR VEGF rec	781	10.8	54.0	32	21	AAAX38789	K. aestuarii carbo
C 709	10.8	54.0	27	18	AAAX63228	Delta-9 desaturase	782	10.8	54.0	32	21	AAAX38790	BCR oncogene exon
C 710	10.8	54.0	27	18	AAAX63175	Delta-9 desaturase	783	10.8	54.0	33	17	AAAT10496	Primer 6 related t
C 711	10.8	54.0	27	18	AAAX63093	Delta-9 desaturase	784	10.8	54.0	33	24	ABL40340	Ribozyme cleavage
C 712	10.8	54.0	27	19	AAV98340	Human EGF-R hammer	785	10.8	54.0	34	14	AAQ53038	Primer used for fr
C 713	10.8	54.0	27	19	AAV98216	Human EGF-R hammer	786	10.8	54.0	34	17	AAAT34844	Tumour necrosis fa
C 714	10.8	54.0	27	19	AAV98141	Human EGF-R hammer	787	10.8	54.0	34	18	AAAT59051	Anti-IT15-4 hammer
C 715	10.8	54.0	27	19	AAV94402	Canine IL-2 recept	788	10.8	54.0	34	21	AAAC88541	Tar mini-ribozyme
C 716	10.8	54.0	27	19	AAV96077	Solanidine glucosy	789	10.8	54.0	35	18	AAAT59072	Primer used to amp
C 717	10.8	54.0	27	19	AAV933934	Human IL-2 recepto	790	10.8	54.0	35	20	AAAX99689	R. etlii CNPAF512 r
C 718	10.8	54.0	27	21	AAZ62143	Hammerhead ribozym	791	10.8	54.0	35	24	ABSG67604	PCR primer, #45, u
C 719	10.8	54.0	27	21	AAZ622956	Hammerhead ribozym	792	10.8	54.0	36	16	AAAT56082	Human TNF-alpha ha
C 720	10.8	54.0	27	21	AAZ63481	Hammerhead ribozym	793	10.8	54.0	36	16	AAAT56082	Human ICAM hammerh
C 721	10.8	54.0	27	24	AAI69470	Human tumour-assoc	794	10.8	54.0	36	16	AAAT56717	Human CD40 hammerh
C 722	10.8	54.0	27	24	AAI69470	Human tumour-assoc	795	10.8	54.0	36	17	AAAX66914	Mouse CD40 hammerh
C 723	10.8	54.0	28	17	AAQ99271	Human tyrosine pho	796	10.8	54.0	36	17	AAAX66915	Mouse CD40 hammerh
C 724	10.8	54.0	28	18	AAAT67117	Helminth MIF antis	797	10.8	54.0	36	17	AAAX66915	Human B7-2 hammerh
C 725	10.8	54.0	29	20	AAAT17799	Human TIE-2 hammer	798	10.8	54.0	36	17	AAAX66915	Mouse B7-1 hammerh
C 726	10.8	54.0	29	20	AAAT17930	Human TIE-2 hammer	799	10.8	54.0	36	17	AAAX66915	Mouse B7-1 hammerh
C 727	10.8	54.0	29	20	AAAT18069	Human TIE-2 hammer	800	10.8	54.0	36	17	AAAX66915	Rabbit CETP HH rib
C 728	10.8	54.0	29	20	AAAT18180	Human TIE-2 hammer	801	10.8	54.0	36	17	AAAT50461	Rabbit CETP HH rib
C 729	10.8	54.0	29	20	AAAT18218	Human TIE-2 hammer	802	10.8	54.0	36	17	AAAT50493	Human CETP HH ribo
C 730	10.8	54.0	29	20	AAAT18310	Human TIE-2 hammer	803	10.8	54.0	36	20	AAAX05514	Synthetic Fn3 gene
C 731	10.8	54.0	29	20	AAAT18310	Human TIE-2 hammer	804	10.8	54.0	36	20	AAAX05514	HCV hammerhead rib
C 732	10.8	54.0	29	20	AAAT19530	Integrin alpha 6 s	805	10.8	54.0	36	24	ABX02100	HCV hammerhead rib
C 733	10.8	54.0	29	20	AAAT20086	Integrin alpha 6 s	806	10.8	54.0	36	24	ABX02406	HCV hammerhead rib
C 734	10.8	54.0	29	20	AAAT21702	Integrin subunit b	807	10.8	54.0	36	24	ABX02931	HCV hammerhead rib
C 735	10.8	54.0	29	20	AAAT21991	Integrin subunit b	808	10.8	54.0	36	24	ABX02944	Double amino acid
C 736	10.8	54.0	29	20	AAAT22130	Integrin subunit b	809	10.8	54.0	36	24	ABX02944	Double amino acid
C 737	10.8	54.0	29	20	AAAT22130	Integrin subunit b	810	10.8	54.0	36	24	ABX02944	Fibronectin 3 codi
C 738	10.8	54.0	29	20	AAAT22200	Integrin subunit b	811	10.8	54.0	38	16	AAAT53919	Rat ICAM hammerhea

XX
PN
WO9319203-A1.

RESULT 2
AAQ49708
ID AAQ49708 standard: DNA: 20 BP.

PKC-A gapped oligonucleotide 5357.

Antisense; oligonucleotide; inter-s-
phosphorothionate linkage; PKC; tra-
translation initiation site; 5' cap
diagnosis; therapeutics; prophylaxi-
Synthetic.

Key	Location/Qualifiers
1	
2	
3	
4	
5	

```

FT FT /*tag= e
FT FT /label= tm
FT FT 6
FT FT /*tag= f
FT FT /label= cm
FT FT 15
FT FT /*tag= g
FT FT /label= gm
FT FT 16
FT FT /*tag= h
FT FT /label= tm
FT FT 17
FT FT /*tag= i
FT FT /label= tm
FT FT 18
FT FT /*tag= j
FT FT /label= tm
FT FT 19
FT FT /*tag= k
FT FT /label= cm
FT FT 20
FT FT /*tag= l
FT FT /label= 2'-O-methyl adenosine
FT FT
XX WO9319203-A1.
XX
XX
XX
XX
XX 30-SEP-1993.
XX
XX 25-FEB-1993; 93WO-US02213.
XX
XX 16-MAR-1992; 92US-0852852.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dean N;
XX WPI; 1993-320768/40.
XX
XX Oligo-nucleotide(s) hybridise to nucleic acids encoding Protein
FT Kinase C - useful as diagnostics and therapeutics for disease
FT states associated with particular isozymes of PKC
XX
XX Example 11; Page 25; 64pp; English.
XX
XX The sequences given in AAQ49708-716 are chimeric phosphorothionate
CC oligonucleotides which have "deoxy gaps" of 4-8 deoxynucleotides in an
CC otherwise 2'-O-methyl oligonucleotides. These oligomers were tested
CC for their ability to decrease PKC-alpha mRNA levels. These oligomers
CC are based on the sequences given in AAQ49658, AAQ49659 and AAQ49660.
CC The 8-deoxy gapped oligomers were able to lower PKC-alpha mRNA levels by
CC at least 85%. Two of the 6-deoxy gapped oligomers (AAQ49709 and
CC AAQ49712) were able to lower PKC-alpha mRNA by >50% and one of the
CC 4-gapped oligomers was able to inhibit PKC-alpha mRNA by approx. 85%.
CC These oligonucleotides may be used in diagnostics, therapeutics,
CC prophylaxis and as research reagents.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence, 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGTGGTGAGTTTCA 20
Db 1 GTTCTCGTGGTGAGTTTCA 20
RESULT 3
AAQ49709
ID AAQ49709 standard; DNA; 20 BP.
XX
XX AAQ49709;
AC

```

25-MAR-2003 (updated)
25-APR-1994 (first entry)
PKC-A gapped oligonucleotide 5361.
Antisense; oligonucleotide; inter-sugar linkage; protein kinase C;
phosphorothionate linkage; PKC; transcription initiation site;
translation initiation site; 5' cap region; intron/exon boundary;
diagnosis; therapeutics; prophylaxis; deoxy gap; ss.
Synthetic.

Key	Location/Qualifiers
modified_base 1	/*tag= a /label= gm
modified_base 2	/*tag= b /label= tm
modified_base 3	/*tag= c /label= tm
modified_base 4	/*tag= d /label= cm
modified_base 5	/*tag= e /label= tm
modified_base 6	/*tag= f /label= cm
modified_base 7	/*tag= g /label= gm
modified_base 14	/*tag= h /label= 2'-O-methyl adenosine
modified_base 15	/*tag= i /label= gm
modified_base 16	/*tag= j /label= tm
modified_base 17	/*tag= k /label= tm
modified_base 18	/*tag= l /label= tm
modified_base 19	/*tag= m /label= cm
modified_base 20	/*tag= n /label= 2'-O-methyl adenosine

WO9319203-A1.
30-SEP-1993.
25-FEB-1993; 93WO-US02213.
16-MAR-1992; 92US-0852852.
(ISIS-) ISIS PHARM INC.
Bennett CF, Dean N;
WPI; 1993-320768/40.
Oligo-nucleotide(s) hybridise to nucleic acids encoding Protein Kinase C - useful as diagnostics and therapeutics for disease states associated with particular isozymes of PKC

Example 11; Page 25; 64pp; English.

The sequences given in AAQ49708-716 are chimeric phosphorothionate oligonucleotides which have "deoxy gaps" of 4-8 deoxynucleotides in an otherwise 2'-O-methyl oligonucleotides. These oligomers were tested for their ability to decrease PKC-alpha mRNA levels. These oligomers are based on the sequences given in AAQ49658, AAQ49659 and AAQ49660. The 8-deoxy gapped oligomers were able to lower PKC-alpha mRNA levels by at least 85%. Two of the 6-deoxy gapped oligomers (AAQ49709 and AAQ49712) were able to lower PKC-alpha mRNA by >50% and one of the 4-gapped oligomers was able to inhibit PKC-alpha mRNA by approx. 85%. These oligonucleotides may be used in diagnostics, therapeutics, prophylaxis and as research reagents. (Updated on 25-MAR-2003 to correct PN field.)

Sequence, 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 3
AAQ49709
ID AAQ49709 standard; DNA; 20 BP.
XX
XX AAQ49709;
AC

states associated with particular isozymes of PKC

Example 11; Page 25; 64pp; English.

The sequences given in AAQ49708-716 are chimeric phosphorothionate oligonucleotides which have "deoxy gaps" of 4-8 deoxynucleotides in an otherwise 2'-O-methyl oligonucleotides. These oligomers were tested for their ability to decrease PKC-alpha mRNA levels. These oligomers are based on the sequences given in AAQ49658, AAQ49659 and AAQ49660. The 8-deoxy gapped oligomers were able to lower PKC-alpha mRNA levels by at least 85%. Two of the 6-deoxy gapped oligomers (AAQ49709 and AAQ49712) were able to lower PKC-alpha mRNA by >50% and one of the 4-gapped oligomers was able to inhibit PKC-alpha mRNA by approx. 85%. These oligonucleotides may be used in diagnostics, therapeutics, prophylaxis and as research reagents.

(Updated on 25-MAR-2003 to correct PN field.)

Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 4
AAQ49710
ID AAQ49710 standard; DNA; 20 BP.
XX AC AAQ49710;
XX XX 25-MAR-2003 (updated)
DT 25-APR-1994 (first entry)
XX PKC-A gapped oligonucleotide 5360.
XX Antisense; oligonucleotide; inter-sugar linkage; protein kinase C;
KW phosphorothionate linkage; PKC; transcription initiation site;
KW translation initiation site; 5' cap region; intron/exon boundary;
KW diagnosis; therapeutics; prophylaxis; deoxy gap; ss.
XX Synthetic.

Key Location/Qualifiers

FT modified_base	1	/tag= a
FT modified_base	2	/label= gm
FT modified_base	3	/tag= b
FT modified_base	4	/label= tm
FT modified_base	5	/tag= c
FT modified_base	6	/label= tm
FT modified_base	7	/tag= d
FT modified_base	8	/label= cm
FT modified_base	9	/tag= e
FT modified_base	10	/label= tm
FT modified_base	11	/tag= f
FT modified_base	12	/label= cm
FT modified_base	13	/tag= g
FT modified_base	14	/label= gm
FT modified_base	15	/tag= g
FT modified_base	16	/label= gm
FT modified_base	17	/tag= g
FT modified_base	18	/label= cm
FT modified_base	19	/tag= g
FT modified_base	20	/label= cm

FT modified_base 14 /label= gm
FT modified_base 15 /tag= h
FT modified_base 16 /label= 2'-O-methyl adenosine
FT modified_base 17 /tag= i
FT modified_base 18 /label= gm
FT modified_base 19 /tag= j
FT modified_base 20 /label= tm
FT modified_base 21 /tag= k
FT modified_base 22 /label= tm
FT modified_base 23 /tag= l
FT modified_base 24 /label= tm
FT modified_base 25 /tag= m
FT modified_base 26 /label= cm
FT modified_base 27 /tag= n
FT modified_base 28 /label= 2'-O-methyl adenosine
XX WO9319203-A1.
XX 30-SEP-1993.
XX 25-FEB-1993; 93WO-US02213.
XX 16-MAR-1992; 92US-0852852.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dean N;
XX WPI; 1993-320768/40.
XX Oligo-nucleotide(s) hybridise to nucleic acids encoding Protein kinase C - useful as diagnostics and therapeutics for disease states associated with particular isozymes of PKC
XX Example 11; Page 25; 64pp; English.
XX The sequences given in AAQ49708-716 are chimeric phosphorothionate oligonucleotides which have "deoxy gaps" of 4-8 deoxynucleotides in an otherwise 2'-O-methyl oligonucleotides. These oligomers were tested for their ability to decrease PKC-alpha mRNA levels. These oligomers are based on the sequences given in AAQ49658, AAQ49659 and AAQ49660. The 8-deoxy gapped oligomers were able to lower PKC-alpha mRNA levels by at least 85%. Two of the 6-deoxy gapped oligomers (AAQ49709 and AAQ49712) were able to lower PKC-alpha mRNA by >50% and one of the 4-gapped oligomers was able to inhibit PKC-alpha mRNA by approx. 85%. These oligonucleotides may be used in diagnostics, therapeutics, prophylaxis and as research reagents.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
SQ Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 5
AAQ97875
ID AAQ97875 standard; DNA; 20 BP.
XX AC AAQ97875;
XX XX

DT 25-MAR-2003 (updated)
DT 17-OCT-1995 (first entry)
XX PNA oligomer targeting 3' UTR region of PKC-alpha.
XX
XX Peptide nucleic acid; PNA; PKC-alpha; protein kinase C; ss;
KW cell proliferation; cell differentiation; isozyme; antisense;
KW triple helix; cancer; psoriasis; inflammation.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT misc_feature 1..20
FT /*tag= a
FT /note= "at least one (and preferably all) of
FT the backbone subunits are composed of N-acetyl
FT N-(2-aminoethyl)glycine peptide residues, the
FT nucleobase being attached covalently to the
FT acetyl group and the peptide linkage being
FT formed by condensation of the glycine
FT carboxy group of one residue with the amino
FT group of the 2-aminoethyl moiety in the next
FT residue"
XX
XX WO9503833-A1.
XX
XX 09-FEB-1995.
XX
XX 28-JUL-1994; 94WO-US08465.
XX
XX 29-JUL-1993; 93US-0099098.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dean NM;
XX
XX WPI; 1995-082040/11.
XX
XX New peptide nucleic acid oligomers specific for protein kinase C
PT isozyme(s) - useful as anti-sense molecules for treating PKC
PT mediated disease, e.g. cancer, psoriasis and inflammation
XX
XX Claim 2; Page 257; 287pp; English.
XX
XX New peptide nucleic acid (PNA) oligomers are provided which (a) consist
CC of naturally occurring nucleobases covalently bound to a polyamide
CC backbone and (b) hybridise to the translation initiation AUG region,
CC coding region, 5' untranslated region (5' UTR) or 3' untranslated region
CC (3' UTR) of PKC-alpha or its isoforms. The PNAs can be used to target
CC RNA and single stranded DNA (ssDNA) to produce antisense-type gene
CC regulation moieties. They inhibit expression of PKC-alpha and its
CC isoforms (including beta, gamma, delta, epsilon, zeta and eta) and so
CC are useful for treating and diagnosing cell proliferation and
CC differentiation processes such as neoplastic, hyperproliferative
CC and inflammatory diseases.
CC PNA oligomers have high affinity for complementary single stranded DNA.
CC They are also able to form triple helices in which a first PNA strand
CC binds with RNA or ssDNA and a second PNA strand binds with the resulting
CC double helix or with the first PNA strand. The PNAs possess no
CC significant charge and are water soluble, which facilitates cellular
CC uptake. Further, since they contain amides of non-biological amino acids,
CC they are biostable and resistant to enzymatic degradation by proteases.
CC The present sequence targets the 3' UTR of PKC-alpha.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
SQ

Query Match 100.0%; Score 20; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GTTCTCGTGGTGAGTTTCA 20
|||||

Db 1 GTTCTCGTGGTGAGTTTCA 20
RESULT 6
AAQ84160
ID AAQ84160 standard; DNA; 20 BP.
XX
AC AAQ84160;
XX
DT 25-MAR-2003 (updated)
DT 20-SEP-1995 (first entry)
XX
XX PKC-alpha 3' untranslated region antisense oligo, ISIS #3521.
XX
XX Antisense; protein kinase C; alpha; PKC; beta; gamma; eta; epsilon;
KW zeta; modulation; expression; isozyme; hybridise; 5' UTR; human;
KW 3' untranslated region; translation initiation site; detection;
KW phosphorothioate linkage; 2'-O-methyl modification;
KW 2'-O-propyl modification; ss.
XX
OS Synthetic.
XX
XX WO9502069-A1.
XX
XX 19-JAN-1995.
XX
XX 08-JUL-1994; 94WO-US07770.
XX
XX 09-JUL-1993; 93US-0089996.
XX
XX 22-FEB-1994; 94US-0199779.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Boggs RT, Dean NM;
XX WPI; 1995-066911/09.
XX
XX Oligo:nucleotide(s) hybridisable with Protein Kinase C mRNA or
PT gene - also novel PKC-alpha 3'-UTR sequence, useful for
PT diagnosis and treatment of hyperproliferative disorders.
XX
XX Claim 11; Page 21; 125pp; English.
XX
XX The sequences given in AAQ84159-80 are oligos which are antisense to
CC the protein kinase C-alpha (PKC-alpha) cDNA. These antisense
CC molecules may be used in modulating the expression of this particular
CC isozyme of PKC. These oligos preferably hybridise with the 5'- or 3'-
CC untranslated regions of the PKC gene, or the translation initiation
CC site, or the coding region. These oligos may be used in the detection
CC of the human PKC-alpha gene and for treatment of animals which have
CC conditions associated with PKC-alpha. These oligos may contain at
CC least one phosphorothioate linkage and/or at least one of the
CC nucleotides comprises a modification on the 2' position of the sugar,
CC esp. a 2'-O-methyl or a 2'-O-propyl modification.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
SQ

Query Match 100.0%; Score 20; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GTTCTCGTGGTGAGTTTCA 20
|||||

RESULT 7
AAT33478
ID AAT33478 standard; DNA; 20 BP.
XX
AC AAT33478;
XX

Query Match 100.0%; Score 20; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GTTCTCGTGGTGAGTTTCA 20
|||||

DT 18-FEB-1997 (first entry)
 XX Oligomeric compound with 2'-O-substituted pyrimidine nucleoside.
 DE
 XX
 XX Oligomer; pyrimidine; inhibition; gene expression; gene therapy;
 KW research; diagnostic reagent; diagnosis; protein kinase C; PKC;
 KW ss.
 XX
 XX Synthetic.
 OS
 XX
 PN WO9627606-A1.
 XX
 PD 12-SEP-1996.
 XX
 XX 06-MAR-1996; 96WO-US03174.
 PF
 XX
 PR 07-JUN-1995; 95US-0475467.
 PR 06-MAR-1995; 95US-0398901.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 XX Cook PD, Griffey RH, Ross BS, Sanghvi YS, Sprankle KG;
 PI Springer RH;
 XX
 DR WPI; 1996-425375/42.
 XX
 XX New 2'-O-substituted pyrimidine monomeric nucleoside sub-unit(s) -
 PT used for the prepn. of oligomeric cpds. which can be used for gene
 PT therapy or as research or diagnostic reagents
 XX
 PS Disclosure; Page 20; 97pp; English.
 XX
 CC Oligomeric compounds containing 2'-O-substituted pyrimidine
 CC nucleoside subunits can be used for inhibiting specific gene
 CC expression in gene therapy and as research and diagnostic reagents.
 CC The oligomeric compounds exhibit high binding affinity to nucleic
 CC acids and high nuclease resistance. This sequence is a 20 mer
 CC deoxyphosphothioate and can be used to inhibit the synthesis of the
 CC protein kinase C-alpha protein and has a melting temperature of 52.1
 CC degrees Celsius. A similar sequence which is a fully modified
 CC phosphorothioate has a higher melting temperature and is described
 CC in AAT33479.
 XX
 SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
 Query Match 100.0%; Score 20; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 DB 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||

RESULT 8
 AAT33479
 ID AAT33479 standard; DNA; 20 BP.
 AC
 AC AAT33479;
 XX
 DT 18-FEB-1997 (first entry)
 XX
 XX Oligomeric compound with 2'-O-substituted pyrimidine nucleoside.
 DE
 XX
 XX Oligomer; pyrimidine; inhibition; gene expression; gene therapy;
 KW research; diagnostic reagent; diagnosis; protein kinase C; PKC;
 KW ss.
 XX
 XX Synthetic.
 OS
 OS
 XX
 PH Key Location/Qualifiers
 FT misc_feature 1
 FT /*tag= a

FT misc_feature /mod_base= 2'-flouro
 FT 2
 FT /*tag= b
 FT /mod_base= 2'-flouro
 FT 3
 FT misc_feature /mod_base= 2'-flouro
 FT 4
 FT /*tag= c
 FT /mod_base= 2'-flouro
 FT 5
 FT /*tag= d
 FT /mod_base= 2'-flouro
 FT 6
 FT /*tag= e
 FT /mod_base= 2'-flouro
 FT 7
 FT /*tag= f
 FT /mod_base= 2'-flouro
 FT 15
 FT /*tag= g
 FT /mod_base= 2'-flouro
 FT 16
 FT /*tag= h
 FT /mod_base= 2'-flouro
 FT 17
 FT /*tag= i
 FT /mod_base= 2'-flouro
 FT 18
 FT /*tag= j
 FT /mod_base= 2'-flouro
 FT 19
 FT /*tag= k
 FT /mod_base= 2'-flouro
 FT 20
 FT /*tag= l
 FT /mod_base= 2'-flouro
 FT
 FT WO9627606-A1.
 XX
 PD 12-SEP-1996.
 XX
 XX 06-MAR-1996; 96WO-US03174.
 XX
 XX 07-JUN-1995; 95US-0475467.
 XX 06-MAR-1995; 95US-0398901.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Cook PD, Griffey RH, Ross BS, Sanghvi YS, Sprankle KG;
 XX Springer RH;
 PI
 XX WPI; 1996-425375/42.
 DR
 XX New 2'-O-substituted pyrimidine monomeric nucleoside sub-unit(s) -
 FT used for the prepn. of oligomeric cpds. which can be used for gene
 FT therapy or as research or diagnostic reagents
 XX
 PS Disclosure; Page 20; 97pp; English.
 XX
 CC Oligomeric compounds containing 2'-O-substituted pyrimidine
 CC nucleoside subunits can be used for inhibiting specific gene
 CC expression in gene therapy and as research and diagnostic reagents.
 CC The oligomeric compounds exhibit high binding affinity to nucleic
 CC acids and high nuclease resistance. This sequence is a 20 mer
 CC phosphorothioate and can be used to inhibit the synthesis of the
 CC protein kinase C-alpha protein. It has a melting temperature of 54.9
 CC degrees Celsius. A similar sequence which is a deoxyphosphorothioate
 CC and has a lower melting temperature and is described in AAT33478.
 XX
 SQ Sequence 20 BP; 2 A; 4 C; 6 G; 2 T; 6 U; 0 other;
 Query Match 100.0%; Score 20; DB 17; Length 20;
 Best Local Similarity 70.0%; Pred. No. 1.4;
 Matches 14; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 GTTCTCGTGGTGAGTTTCA 20
Db 1 GUUCUCGCTGGTGAGUUUCA 20

RESULT 9
AAT31818
ID AAT31818 standard; DNA; 20 BP.
XX AC AAT31818;
XX DT 10-JAN-1997 (first entry)
XX DE Oligonucleotide (ON) from ON-dendrimer targeting conjugate.
XX KW Oligonucleotide-dendrimer conjugate; antisense; therapy; infection;
XX KW disease; anti-viral; anti-proliferative; tumour; diagnosis;
XX KW gene probe; detection; genetic disease; ss.
XX OS Synthetic.
XX PN W09619240-A1.
XX PD 27-JUN-1996.
XX PF 13-DEC-1995; 95WO-EP04933.
XX PR 09-JAN-1995; 95CH-0000047.
XX PR 21-DEC-1994; 94CH-0003854.
XX PA (CIBA ) CIBA GEIGY AG.
XX PI Haner R, Skobridis K, Haener R;
XX DR WPI; 1996-309315/31.
XX KW Oligo:nucleotide-dendrimer conjugates - useful in antisense therapy
PT for treating, e.g. viral infections or tumours and also for
PT diagnosis
XX PS Claim 65; Page 60; 65pp; English.
XX CC Oligonucleotide (ON)-dendrimer (DD) conjugates where the DD is
CC a monovalent residue of a DD of the 1st to the 10th generation and
CC is bonded to the ON directly or via a bridging group to an
CC internucleotide bridge, a nucleic acid base or a sugar of the ON and
CC the ON is complementary to a target nucleic acid, may be used in
CC antisense therapy for treating infection and disease. The ON_DD
CC conjugates can also have anti-viral and anti-proliferative
CC properties and can be used for e.g. decreasing tumour growth in vivo.
CC They are also useful as gene probes for detecting viral infections
CC or genetically determined diseases.
XX SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGTGGTGAGTTTCA 20
Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 10
AAX36455
ID AAX36455 standard; DNA; 20 BP.
XX AC AAX36455;
XX DT 06-JUL-1999 (first entry)
XX DE Chimeric 2'-O-methyl oligo for PKC-alpha inhibition.

XX RNaseH; RNA cleavage; DNA cleavage; hybridisation; protein kinase C gene;
XX gene expression modulation; ras; raf; therapy; AIDS; atherosclerosis;
XX infection; cell growth; ss.
XX OS Synthetic.
XX PN W09730067-A1.
XX PD 21-AUG-1997.
XX PF 07-FEB-1997; 97WO-JS02043.
XX PR 14-FEB-1996; 96US-0011620.
XX PA (ISIS-) ISIS PHARM INC.
XX PA (NOVS ) NOVARTIS AG.
XX PI Altmann K, Cook PD, Martin P, Monia B;
XX DR WPI; 1997-424969/39.
XX KW Oligo:nucleotide with RNaseH activity, which specifically hybridises
PT to DNA or RNA - comprises 1st and 2nd subsequence(s) having
PT 2'-O-CH2-CH2-O-CH3 and 2'-deoxy sugar moieties, useful for therapy
PT or diagnosis
XX PS Example 14; Page 39; 86pp; English.
XX CC This sequence is an example of an oligonucleotide of the invention, and
CC is an inhibitor of PKC-alpha expression.
CC The invention relates to oligonucleotides (A), which specifically
CC hybridises to RNA or DNA, comprises a linear sequence of nucleotide units
CC linked by phosphodiester or phosphorothioate linkages, comprising a first
CC subsequence having 2'-O-CH2-CH2-O-CH3 sugar moieties and a second
CC subsequence having 2'-deoxy sugar moieties. (A), which has RNaseH
CC activity for cleaving a complementary strand, can be used to modulate the
CC expression of ras, raf and protein kinase C genes, useful in the therapy
CC of AIDS, atherosclerosis, bacterial or other infections, or to control
CC aberrant cell growth in humans, animals or plants. (A) can also be used
CC diagnostically, particularly when labelled, to detect overexpression of
CC mRNA or expression of abnormal RNA, including imaging of tissue sections,
CC and as a research reagent. (A) has increased binding affinity for
CC complementary strands (attributable to the 2'-O-CH2-CH2-O-CH3 sugar
CC moiety, which overcomes the loss of affinity caused by altered intersugar
CC links), and increased resistance to nuclease (from the modified links and
CC the 2'-O-CH2-CH2-O-CH3 sugar moiety).
XX SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGTGGTGAGTTTCA 20
Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 11
AAX33997
ID AAX33997 standard; DNA; 20 BP.
XX AC AAX33997;
XX DT 06-JUL-1999 (first entry)
XX DE Oligonucleotide analogue for human PKC-alpha.
XX KW Oligonucleotide analogue; dinucleotide compound; antiviral agent;
XX KW antisense technology; diagnosis; gene probe; human PKC-alpha; ss.
XX OS Synthetic.

```



```

XX PN WO9732887-A1.
XX PD 12-SEP-1997.
XX PF 24-FEB-1997; 97WO-GB00499.
XX PR 05-MAR-1996; 96GB-0004669.
XX PA (NOVS ) NOVARTIS AG.
XX PI Baxter AD, Collingwood SP, Douglas ME, Taylor RJ;
XX PI WPI; 1997-457483/42.
XX DR New oligo-nucleotide containing one or more phosphinate links -
XX PT have good hybridisation properties, nuclease resistance, etc.,
XX PT useful for inhibiting gene expression in cancer or virus infection
XX PS Claim 25; Page 42; 52pp; English.
XX CC This sequence is an example of an oligonucleotide analogue of the
XX CC invention, and is specific for human PKC-alpha.
XX CC The oligonucleotide analogues of the invention contain 10-200 natural
XX CC and/or synthetic units each linked by internucleoside linkages at least
XX CC one of which has the formula -CH2-P(X)(R1)-O-(1), where CH2 is attached
XX CC to a 3' carbon, and the O is attached to a 5' carbon. In the formula,
XX CC R1 = H, OH, O-, SH, S-, NH2, Ra, ORa, SRA, NHRb or NRbRC;
XX CC Ra, Rb, RC = optionally substituted 1-10C alkyl, 2-10C alkenyl,
XX CC 3-8C cycloalkyl, 6-10C aryl or 7-13C aralkyl; or NRbRC = a 5-6 membered
XX CC heterocyclic ring; and X = O or S. The new oligonucleotide analogues and
XX CC dinucleotide compounds are useful as pharmaceuticals, especially as
XX CC antiviral agents. The oligonucleotide analogues may also be used in
XX CC antisense technology, as diagnostic agents and gene probes. The new
XX CC oligonucleotide analogues exhibit high stability to degradation by
XX CC nucleases and good hydrolytic stability. They also exhibit very good
XX CC pairing with complementary nucleic acid strands, especially of the RNA
XX CC type.
XX SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
DB 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 12
AAV06043
ID AAV06043 standard; DNA; 20 BP.
XX AC AAV06043;
XX XX
XX 25-MAR-2003 (updated)
XX 08-APR-1998 (first entry)
XX DE Oligonucleotide which targets nucleic acids encoding PKC.
XX XX
XX Antisense oligonucleotide; protein kinase C; PKC; tumour; mitomycin;
XX proliferative disease; chemotherapeutic agent; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /note= "Optionally, derivative may contain modified;
FT thymine, cytosine, adenine, guanine uracil,
FT 5-propynyluracil, 5-methylcytosine,

```

```

FT FT misc_feature 1..20
FT FT /*tag= b
FT FT 5-propynylcytosine or 2-aminoadenine bases"
FT FT "May contain e.g. amide, phosphoro(di)thioate
FT FT methylphosphonate, phosphoramidate, borano-
FT FT phosphate or phosphotriester bonds in place
FT FT of the phosphodiester bond. This oligonucleotide
FT FT may be shortened to 15 to 19 nucleotides on one
FT FT or both ends"
XX PN WO9732589-A1.
XX XX
XX PD 12-SEP-1997.
XX PF 24-FEB-1997; 97WO-EP00876.
XX PR 07-MAR-1996; 96US-0612775.
XX PA (NOVS ) NOVARTIS AG.
XX PI Mueller M, Geiger T, Altmann K, Fabbro D, Dean NM, Monia B;
XX PI Bennett CF;
XX XX WPI; 1997-457311/42.
XX DR Treatment of proliferative diseases such as tumours - by
XX PT administration of oligonucleotide targeted to nucleic acids
XX PT encoding protein kinase C, in combination with another
XX PT chemotherapeutic agent such as mitomycin
XX XX Claim 3; Page 85; 109pp; English.
XX CC This oligonucleotide (or derivative) targets nucleic acids encoding
XX CC protein kinase C (PKC) and is used in the treatment of proliferative
XX CC diseases. The method comprises administration of the oligonucleotide
XX CC which is capable of modulating PKC expression, and at least one other
XX CC chemotherapeutic agent except for an antisense oligonucleotide (or its
XX CC derivative) targeted to raf-kinase. Any component can also be present in
XX CC the form of a salt, if at least one salt-forming group is present.
XX CC The process/composition may be used in treatment of e.g. cancers,
XX CC tumours, hyperplasia, fibrosis, angiogenesis, psoriasis, atherosclerosis
XX CC or smooth muscle cell proliferation in the blood vessels, such as
XX CC stenosis or restenosis following angioplasty. The components act
XX CC synergistically.
XX CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
DB 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 13
AAV06045
ID AAV06045 standard; DNA; 20 BP.
XX AC AAV06045;
XX XX
XX 25-MAR-2003 (updated)
XX 08-APR-1998 (first entry)
XX DE Oligonucleotide targeted to nucleic acids encoding PKC.
XX XX
XX Antisense oligonucleotide; raf; protein kinase C; PKC; tumour; mitomycin;
XX proliferative disease; chemotherapeutic agent; ss.
XX OS Synthetic.
XX OS Homo sapiens.

```

XX PH Key Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /note= "Optionally, derivative may contain modified;
FT thymine, cytosine, adenine, guanine uracil,
FT 5-propynyluracil, 5-methylcytosine,
FT 5-propynylcytosine or 2-aminoadenine bases"
FT misc_feature 1..20
FT /*tag= b
FT /note= "May contain e.g. amide, phospho(di)thioate
FT methylphosphonate, phosphoramidate, borano-
FT phosphate or phosphotriester bonds in place
FT of the phosphodiester bond. This oligonucleotide
FT may be shortened to 15 to 19 nucleotides on one
FT or both ends"
XX PN WO9732604-A1.
XX
XX PD 12-SEP-1997.
XX PF 24-FEB-1997; 97WO-EP00875.
XX PR 07-MAR-1996; 96US-0612787.
XX (NOVS) NOVARTIS AG.
XX FA Mueller M, Geiger T, Altmann K, Fabbro D, Monia B;
XX PI WPI; 1997-457319/42.
XX DR
XX Treatment of proliferative diseases such as tumours or psoriasis -
FT by administration of an oligonucleotide targeted to nucleic acids
FT encoding raf, in combination with another chemotherapeutic agent
FT such as cisplatin
XX
XX PS Disclosure; Page 34; 119pp; English.
XX
CC This oligonucleotide (or derivative) targets nucleic acids encoding
CC protein kinase C (PKC) and is used in the treatment of proliferative
CC diseases. The invention relates to the administration of an
CC oligonucleotide which targets raf and is capable of modulating raf
CC expression, and at least one other chemotherapeutic agent, e.g.
CC the present oligonucleotide which targets PKC. Any component can also be
CC present in the form of a salt, if at least one salt-forming group is
CC present. The process/composition may be used in treatment of e.g.
CC cancers, tumours, hyperplasia, fibrosis, angiogenesis, psoriasis,
CC atherosclerosis or smooth muscle cell proliferation in the blood vessels,
CC such as stenosis or restenosis following angioplasty. The components act
CC synergistically.
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
Query Match 100.0%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20
RESULT 14
AAT77191
XX ID AAT77191 standard; DNA; 20 BP.
XX AC AAT77191;
XX
XX DT 03-NOV-1997 (first entry)
XX DE Oligonucleotide for modulation of protein kinase C expression.

KW Methoxyethoxy oligonucleotide; protein kinase C; inflammation;
KW antiinflammatory; hyperproliferation; antiproliferative; psoriasis;
XX antipsoriasis; cancer; therapy; diagnosis; purification; ss.
XX Synthetic.
XX OS
XX Key Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /note= "(opt.) phosphothioate and/or
FT phosphodiester linkages"
FT misc_feature 1..20
FT /*tag= b
FT /note= "(opt.) methoxyethoxy modification at
FT the 2' position of the sugar moiety"
XX PN WO9729780-A1.
XX
XX PD 21-AUG-1997.
XX PF 13-FEB-1997; 97WO-US02003.
XX PR 14-FEB-1996; 96US-0601269.
XX (ISIS-) ISIS PHARM INC.
XX FA (NOVS) NOVARTIS AG.
XX PI Altmann K, Dean NM, Martin P;
XX WPI; 1997-424765/39.
XX
XX New methoxyethoxy modified antisense oligonucleotide(s) - used
FT for inhibiting protein kinase C expression for treating inflammatory
FT or hyper-proliferative disorders e.g. cancer or psoriasis
XX
XX PS Claim 1; Page 30; 42pp; English.
XX
CC This sequence comprises an antisense oligonucleotide (ON) in which
CC at least one nucleotide has a 2'-O-CH₂CH₂OCH₃ modification of its
CC sugar moiety and in which the intersugar linkages are phosphothioate
CC or phosphodiester linkages, or a mixture of these linkages. The ON
CC is specifically hybridisable with a nucleic acid that encodes
CC protein kinase C (PKC)-alpha and is capable of inhibiting PKC-alpha
CC expression. It can be used in a claimed method for inhibiting PKC
CC expression in cells, esp. cancer cells. It can be used for
CC treating a condition associated with expression of PKC e.g. an
CC inflammatory or hyperproliferative disorders such as cancer or
CC psoriasis (claimed). The ON can also be used for diagnosis,
CC detection and purifications. It is more potent than previously
CC tested ONs for inhibiting PKC expression. The modification of the
CC ON increases both its affinity for its target and its nuclease
CC resistance.
XX
SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
Query Match 100.0%; Score 20; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20
RESULT 15
AAT49211
XX ID AAT49211 standard; DNA; 20 BP.
XX AC AAT49211;
XX
XX DT 02-JUL-2002 (updated)
XX DE 03-SEP-1997 (first entry)

DE Phosphorothioate oligonucleotide ISIS-3521.
 XX phosphorothioate; therapeutic; RNase H activity; ras; antisense;
 KW inhibit translation; treating; hepatitis; inflammatory disease;
 KW intercellular cell adhesion factor; ICAM-1; cytomegalovirus retinitis;
 KW cancer; protein kinase C alpha; c-ras; Ha-ras; Ki-ras; AIDS; chiral;
 KW thermodynamic stability; hepatitis C virus; ss.
 XX Synthetic.
 OS
 XX
 XX
 FE Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /note= "phosphorothioate 3' to 5' linkages"
 PN W09639154-A1.
 XX
 XX 12-DEC-1996.
 PD
 XX
 XX 05-JUN-1996; 96WO-US08757.
 XX
 XX 06-JUN-1995; 95US-0471967.
 PR 06-JUN-1995; 95US-0466692.
 PR 06-JUN-1995; 95US-0467597.
 PR 06-JUN-1995; 95US-0468447.
 PR 06-JUN-1995; 95US-0468569.
 PR 06-JUN-1995; 95US-0469851.
 PR 06-JUN-1995; 95US-0470129.
 PR 06-JUN-1995; 95US-0471966.
 PR 15-OCT-1991; 91US-0777670.
 PR 16-OCT-1991; 91US-0777007.
 PR 29-AUG-1994; 94US-0297703.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA Cook PD, Hoke G;
 PI WPI; 1997-042838/04.
 XX
 XX Sequence-specific oligo:nucleotide(s) useful in anti-sense therapy -
 PT contain phosphorothioate linkages of high chiral purity, also used
 PT to induce RNase H activity
 XX
 XX Claim 1; Page 22; 49pp; English.
 PS
 XX AAT49204-14 are oligonucleotides where at least 75 % of the nucleoside
 CC units are joined together by Sp or Rp phosphorothioate 3' to 5',
 CC linkages. The oligonucleotides are useful therapeutically, e.g. by
 CC eliciting RNase H activity ras antisense molecules to inhibit
 CC translation. Uses of the oligos include treating hepatitis, inflammatory
 CC diseases mediated by intercellular cell adhesion factor ICAM-1 and
 CC cytomegalovirus retinitis, as well as treatment of cancers mediated by
 CC protein kinase C alpha, c-ras, Ha-ras or Ki-ras and treating AIDS.
 CC The sequence-specific phosphorothioate oligonucleotides have
 CC substantially chiral pure intersugar linkages which increase the
 CC thermodynamic stability of heteroduplexes with target RNA and DNA. The
 CC present sequence is used in the treatment of cancer mediated by protein
 CC kinase C alpha.
 CC (Updated on 02-JUN-2002 to add missing PA field.)
 XX
 XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCTCGCTGGTGGAGTTTCA 20
 Db 1 GTTCTCGCTGGTGGAGTTTCA 20
 RESULT 16
 AAT51075

ID AAT51075 standard; DNA; 20 BP.
 XX
 XX AAT51075;
 AC
 XX 25-MAR-2003 (updated)
 DT 13-MAR-1997 (first entry)
 XX
 XX ISIS-3521, PKC-alpha mediated cancer inhibitor.
 DE
 XX RNA transcription inhibitor; hepatitis C virus; HCV; inflammation; AIDS;
 KW phosphorothioate oligonucleotide; primer; nuclease; RNaseH; therapy;
 KW thermodynamic stability; cytomegalovirus infection; cancer; ss.
 XX Synthetic.
 OS
 XX US5576302-A.
 PN
 XX 19-NOV-1996.
 PD
 XX
 XX 06-JUN-1995; 95US-0468447.
 PF
 XX 06-JUN-1995; 95US-0468447.
 PR 15-OCT-1991; 91US-0777670.
 PR 16-OCT-1991; 91US-0777007.
 PR 05-MAY-1993; 93US-0058023.
 PR 29-AUG-1994; 94US-0297703.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA Cook PD, Hoke G;
 PI WPI; 1997-011289/01.
 XX
 XX New oligo:nucleotide(s) for inhibiting transcription of hepatitis C
 PT virus RNA - contain diastereomerically pure phosphorothioate links
 PT for formation of more stable complexes with target nucleic acid
 XX
 XX Example 13; Column 19; 18pp; English.
 PS
 XX AAT51073-751079 represent inhibitors of the invention. This sequence
 CC can be used in the treatment of PKC-alpha mediated cancer. 75-100 % of
 CC the nucleotides in these sequences are preferably joined by either Sp or
 CC Rp phosphorothioate 3' to 5' links. To create these sequences,
 CC 2'-deoxyribonucleoside-5'-O-(1-thiophosphate) (dNTPalphas) is prepared
 CC as a racemic mixture, and the pure Sp and Rp diastereomers are isolated
 CC (such as by reverse-phase HPLC on ODS HyperSil). The chiral products
 CC are then used to make these sequences enzymatically in the presence of a
 CC template, primer, and nuclease. Alternatively these sequences can be
 CC chemically synthesized. Oligonucleotides with chirally pure intersugar
 CC links form heteroduplexes with target RNA or DNA of greater
 CC thermodynamic stability (compared with racemic mixtures), and elicit
 CC RNaseH activity. Chirally pure oligonucleotides also have a better
 CC resistance to nuclease digestion. As these sequences inhibit HCV RNA
 CC transcription, they can be used as therapeutic, diagnostic, and research
 CC agents. More generally, chirally pure phosphorothioate oligonucleotides
 CC can be used as therapeutic agents in the same way as racemic (or
 CC non-sulphur substituted) compounds, such as to treat AIDS, inflammation,
 CC cytomegalovirus infection, and various cancers.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCTCGCTGGTGGAGTTTCA 20
 Db 1 GTTCTCGCTGGTGGAGTTTCA 20
 RESULT 17
 AAT28183

ID XX AAV28183 standard; DNA; 20 BP.
 AC XX AAV28183;
 DT XX 08-OCT-1998 (first entry)
 DE XX Antisense oligonucleotide to protein kinase C gene.
 KW Purification; oligonucleotide; matrix; affinity unit;
 KW affinity purification; antisense; protein kinase C; ss.
 XX OS Synthetic.
 XX XX WO9827425-A1.
 XX XX 25-JUN-1998.
 XX XX 18-DEC-1997; 97WO-US23284.
 XX XX 19-DEC-1996; 96US-0769951.
 XX XX (ISIS-) ISIS PHARM INC.
 XX XX Chen D, Cole DL, Srivatsa GS;
 XX XX WPI; 1998-362922/31.
 XX XX Matrix for selective separation of oligonucleotide - useful for,
 PT e.g. large scale purification of anti-sense agents from their
 PT deletion derivatives formed during synthesis
 XX XX
 PS Disclosure; Page 87; 183pp; English.
 XX XX AAV28155-268 represent oligonucleotides which can be purified using the
 CC method of the invention. The specification describes a matrix that
 CC comprises a support and an affinity unit that specifically and
 CC reversibly binds a target oligonucleotide, and comprises a sequence of
 CC bases having the reverse complement of a hybridising portion of the
 CC target oligonucleotide. The matrix is used for affinity purification of
 CC synthetic oligonucleotides, specifically antisense agents, for treatment
 CC of hyperproliferative diseases, for treating a non-pathogen,
 CC non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
 CC expression of cell surface proteins, and to inhibit a eukaryotic
 CC pathogen, retrovirus or other viruses.
 XX XX
 SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGTGGTGAGTTTCA 20
 |||||

RESULT 18
 AAV35502
 ID AAV35502 standard; DNA; 20 BP.
 AC XX AAV35502;
 XX XX
 DT 01-SEP-1998 (first entry)
 DE Oligo ON2 targeted to human protein kinase C (PKC)-alpha isozyme.
 XX Protein kinase C; PKC; target; hybridisation; human; liposome;
 KW sterically stabilised; neoplastic disorder; inflammatory disorder;
 KW hyperproliferative disorder; cancer; psoriasis; PKC-alpha; ss.
 XX OS Synthetic.
 OS Homo sapiens.
 XX XX

PN WO9809633-A2.
 XX 12-MAR-1998.
 XX 03-SEP-1997; 97WO-EP04796.
 XX 04-SEP-1996; 96GB-0018376.
 XX (NOVS) NOVARTIS AG.
 XX Hamilton KO, Love WG, Nicklin PL, Phillips JA;
 XX WPI; 1998-260955/23.
 XX Oligo:nucleotide compositions for protein kinase C disorders -
 PT comprising sequence hybridisable to protein kinase C gene entrapped
 PT in sterically stabilised liposomes
 XX
 PS Claim 22; Page 5; 25pp; English.
 XX This represents an oligonucleotide sequence that is specifically
 CC hybridisable with DNA or RNA derived from a protein kinase C (PKC) gene,
 CC entrapped in sterically stabilised liposomes. Compositions comprising
 CC such oligonucleotides can be used in the treatment of PKC disorders and
 CC for modulating the expression of PKC in cells. They can be used in the
 CC diagnosis and treatment of disorders associated with PKC, particularly
 CC neoplastic, inflammatory and hyperproliferative disorders such as cancer
 CC or psoriasis. The compositions retain high activity after prolonged
 CC circulation in the bloodstream and exhibit reduced accumulation of
 CC oligonucleotides in non-target organs such as the liver and kidney.
 XX XX
 SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGTGGTGAGTTTCA 20
 |||||

RESULT 19
 AAV11168
 ID AAV11168 standard; DNA; 20 BP.
 AC XX AAV11168;
 XX XX
 DT 14-JUL-1998 (first entry)
 DE ISIS 9606 oligonucleotide for human PKC-alpha targeting.
 XX Protein kinase C alpha; treatment; prevention; restenosis; inhibitor;
 KW re-vascularisation; smooth muscle cell; SMC; proliferation; lesion;
 KW balloon angioplasty; apoptosis; matrix deposition;
 KW cellular proliferation; phosphorothioate linkage; ss.
 XX OS Synthetic.
 OS XX
 FH Key Location/Qualifiers
 FT misc_difference 1..6
 FT /*tag= a
 FT /note= "modified by the presence of 2'-O-methoxyethyl"
 FT modified_base 1..20
 FT /*tag= b
 FT /note= "bases linked by phosphorothioate bonds"
 FT misc_difference 15..19
 FT /*tag= c
 FT /note= "modified by the presence of 2'-O-methoxyethyl"
 XX
 PN WO9807415-A2.
 XX 26-FEB-1998.

XX 18-AUG-1997; 97WO-EP04503.
XX 30-AUG-1996; 96US-0025072.
XX 20-AUG-1996; 96US-0024219.
XX (NOVS) NOVARTIS AG.
XX Prescott MF;
XX WPI; 1998-168878/15.
XX Treating or preventing restenosis by administration of inhibitor of
PT protein kinase C - also for treatment of other proliferative
PT diseases, especially cancer, particularly applied topically in
PT hydrogel
XX Claim 24; Page 8; 26pp; English.
XX This sequence is a chimeric phosphorothioate oligonucleotide which
CC targets the 3' untranslated region of human protein kinase C-alpha
CC (PKC-alpha) and is used in a novel method for the treatment and
CC prevention of restenosis after re-vascularisation. The method involves
CC administering an inhibitor of protein kinase C (PKC) to prevent or
CC alleviate smooth muscle cell (SMC) proliferation. This method can be used
CC after balloon angioplasty of, e.g. a coronary artery. Not only is
CC proliferation of SMC prevented, but also apoptosis is stimulated, matrix
CC deposition inhibited and late lesions (those developing 3-9 months after
CC injury) are prevented. Treatment with this inhibitor is used generally to
CC treat diseases involving cellular proliferation and/or decreased
CC apoptosis, specifically cancer, especially when administered locally.
CC Localised delivery of the inhibitor ensures high concentration at the
CC target site and minimises systemic concentrations and thus potential
CC toxicity on other proliferating tissues.
XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
SQ Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20
RESULT 20
AAZ27267
ID AAZ27267 standard; DNA; 20 BP.
XX AAZ27267;
XX 01-DEC-1999 (first entry)
XX Human protein kinase C alpha antisense oligonucleotide #2.
XX Human; protein kinase C; PKC; diagnosis; antisense oligonucleotide;
XX phosphorothioate; hybridisation; isozyme; target; inflammation;
XX hyperproliferative disorder; psoriasis; tumour; cancer; glioblastoma; ss.
XX Synthetic.
OS Homo sapiens.
XX US5959096-A.
XX 28-SEP-1999.
XX 07-JUN-1995; 95US-0481066.
XX 16-MAR-1992; 92US-0852852.
XX 09-JUL-1993; 93US-0089996.
XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dean N;
XX WPI; 1999-561076/47.
XX Antisense oligonucleotides useful for treatment of hyperproliferative
PT and inflammatory conditions including psoriasis, tumours and cancer -
XX Example 1; Column 12; 56pp; English.
XX The present invention describes antisense oligonucleotides up to 50
CC nucleotides in length which specifically bind mRNA encoding human
CC protein kinase C (PKC). AAZ27266 to AAZ27386 represent human PKC
CC antisense oligonucleotides used in the exemplification of the present
CC invention. The antisense oligonucleotides are useful for the treatment of
CC diseases associated with PKC expression, such as hyperproliferative and
CC inflammatory conditions including psoriasis, tumours and cancer
CC (glioblastoma, bladder, breast, colon and lung cancer).
XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
SQ Query Match 100.0%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20
RESULT 21
AAZ11590
ID AAZ11590 standard; DNA; 20 BP.
XX AAZ11590;
XX 16-NOV-1999 (first entry)
XX Fully modified phosphorothioate oligo seq ID No: 4.
XX Phosphorus-linked oligomer; deprotection; protic acid; ether solvent;
KW hybridization probe; amplification primer; forensic; paleontology;
KW antisense agent; ss.
XX Synthetic.
XX OS
XX WO9943694-A1.
XX 02-SEP-1999.
XX 26-FEB-1999; 99WO-US04213.
XX 26-FEB-1999; 98US-0032972.
XX (ISIS-) ISIS PHARM INC.
XX Krotz AH, Ravikumar VT;
XX WPI; 1999-540559/45.
XX Use of aromatic solvents during deprotection of 5'-hydroxy groups in
PT solid phase synthesis of oligonucleotides -
XX Example 6; Page 28; 42pp; English.
XX The invention provides improved methods for synthesis of phosphorus-
CC linked oligomers. The method comprises deprotecting a 5'-hydroxy using a
CC protic acid in an aromatic, alkylaromatic, haloaromatic, halo-
CC alkylaromatic or aromatic ether solvent. The phosphorus-linked oligomers
CC particularly oligonucleotides, are useful as diagnostic or research
CC reagents, e.g. hybridization probes or amplification primers, useful in
CC forensics, paleontology, evolutionary studies, for screening expression
CC libraries, sequencing etc., or as therapeutic (antisense) agents for

CC inhibiting expression of genes or activity of transcription factors. The
 CC aromatic solvents are less expensive to use than hazardous halogenated
 CC alkanes since they do not require large investments in recycling
 CC equipment to meet environmental standards for disposal. They are thus
 CC better suited for large scale operations. Sequences AAZ11587-594
 CC represent phosphorothioate oligomers synthesized using the new method of
 CC the invention.

XX SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 22

AAK99985

ID AAK99985 standard; DNA; 20 BP.

XX AC

XX AAX99985;

XX DT 19-OCT-1999 (first entry)

XX DE

XX Phosphorothioate oligonucleotide #4.

XX KW

XX Phosphorothioate oligonucleotide; benzyl(thio)phosphite residue; primer;
 KW benzyl(thio)phosphoramidite; probe production; linker; adapter;
 KW gene fragment; ss.

XX OS

XX Synthetic.

XX FH

XX Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /note= "phosphorothioate backbone"

XX WO9940101-A1.

XX 12-AUG-1999.

XX PF

XX 09-FEB-1999; 99WO-US02474.

XX PR

XX 10-FEB-1998; 98US-0021277.

XX PA

XX (ISIS-) ISIS PHARM INC.

XX PI

XX Capaldi DC, Ravikumar VT;

XX DR

XX WPI; 1999-508484/42.

XX PT

XX Oligonucleotide synthesis using substituted benzyl phosphoramidite

XX for reaction with synthon having free 5'-hydroxy

XX PS

XX Example 13; Page 47; 72pp; English.

XX CC

XX This sequence represents a phosphorothioate oligonucleotide synthesised
 CC using the method of the invention. The method is for the preparation of
 CC oligonucleotides containing a substituted benzyl(thio)phosphite residue
 CC comprises reacting an oligonucleotide with a 3' substituted

CC benzyl(thio)phosphoramidite with an (oligo)nucleotide having a free
 CC 5'-hydroxy, with one of the reactants, optionally immobilised on a solid
 CC phase. The method is used to prepare oligonucleotides, or analogues, for

CC use as probes, primers, linkers, adapters or gene fragments, for
 CC diagnostic or therapeutic use, or as research reagents. The specified
 CC substituted benzyl group can be eliminated without release of toxic

CC acrylonitrile (contrast conventional 2-cyanoethoxy protecting groups).

XX SQ

XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 23

AAK78525

ID AAX78525 standard; DNA; 20 BP.

XX AC

XX AAX78525;

XX DT

XX 03-SEP-1999 (first entry)

XX DE

XX Human PKC-alpha oligonucleotide primer ISIS # 3521.

XX KW

XX PKC; human; PKC-alpha; primer; protein kinase C; expression modulator;
 KW PKC-beta type I; PKC-beta type II; PKC-gamma; PKC-eta; PKC-delta;
 KW PKC-epsilon; PKC-zeta; anti-inflammatory; cytostatic; antisense targeting;
 KW isozyme; growth control; hyperproliferative disease; colon cancer;
 KW glioblastoma; bladder cancer; inflammatory condition; psoriasis; ss.

XX OS

XX Synthetic.

XX OS

XX Homo sapiens.

XX PN

XX US5922686-A.

XX PD

XX 13-JUL-1999.

XX XX

XX 14-JUN-1996; 96US-0664336.

XX PR

XX 14-JUN-1996; 96US-0664336.

XX PR

XX 16-MAR-1992; 92US-0852852.

XX PR

XX 09-JUL-1993; 93US-0089996.

XX XX

XX (ISIS-) ISIS PHARM INC.

XX PI

XX Bennett CF, Dean N;

XX XX

XX WPI; 1999-404471/34.

XX DR

XX Oligonucleotides targeted against nucleic acids encoding protein

XX PT

XX kinase C

XX PS

XX Claim 1; Column 31-32; 56pp; English.

XX CC

XX This invention describes novel oligonucleotides (AAK78524-X78644) having
 CC up to 50 nucleotides hybridisable with, and able to modulate the
 CC expression of, a nucleic acid encoding protein kinase C and its isozymes
 CC alpha, beta type I, beta type II, gamma, eta, delta, epsilon and zeta.

CC The oligonucleotides of the invention have anti-inflammatory and
 CC cytostatic activity and are used for antisense targeting to modulate the
 CC expression of PKC or of a particular PKC isozyme or set of isozymes in
 CC cells or tissues. The products of the invention also hybridise with
 CC nucleic acids involved in the modulation of PKC expression, which is

CC known to be involved growth control in hyperproliferative diseases e.g.
 CC colon cancer, glioblastoma and bladder cancer as well as in inflammatory
 CC conditions e.g. psoriasis. Due to their specificity the oligonucleotides

CC are able to overcome the problems of toxicity associated with previous
 CC agents designed to modulate PKC expression.

XX SQ

XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 24
 AAX83634
 ID AAX83634 standard; DNA; 20 BP.
 AC AAX83634;
 XX
 XX 27-AUG-1999 (first entry)
 XX
 XX Human protein kinase C alpha antisense oligonucleotide SEQ ID NO:2.
 XX
 XX Human, protein kinase C; PKC; antisense oligonucleotide; diagnosis; ss;
 KW hybridisation; cancer; psoriasis; hyperproliferative disease; tumour.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX US5916807-A.
 XX
 XX 29-JUN-1999.
 XX
 XX 07-JUN-1995; 95US-0481072.
 XX
 XX 07-JUN-1995; 95US-0481072.
 PR 16-MAR-1992; 92US-082852.
 PR 09-JUL-1993; 93US-0089996.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Dean N;
 PI WPI; 1999-403817/34.
 XX
 XX New antisense oligonucleotides specific for human protein kinase C
 PT useful for diagnosis and treatment of cancer and psoriasis
 PT
 XX Claim 1; Column 12; 54pp; English.
 XX
 XX The present invention describes a method of inhibiting the expression of
 CC human protein kinase C (PKC) in cells. The method comprises contacting
 CC the cells with an antisense oligonucleotide which has up to 50
 CC nucleotide units. AAX83633 to AAX83720 represent specifically claimed
 CC antisense oligonucleotides for use in the method of the invention.
 CC The antisense oligonucleotides modulate hybridize to messenger RNA from
 CC the PKC gene which results in modulation of expression of the PKC gene.
 CC This means they can be used for diagnosis, therapeutic or prophylactic
 CC treatment of PKC associated diseases such as cancer and psoriasis, and
 CC as research agents. Abnormal proliferative states in tissue from
 CC patients suspected of having a hyperproliferative disease e.g. cancer,
 CC psoriasis can be diagnosed. Tumours associated with PKC can be
 CC distinguished from tumours which are not PKC associated to allow an
 CC efficacious treatment regime to be used. The antisense oligonucleotides
 CC have specific activity so are able to modulate PKC activity without
 CC producing side effects and with greater effectiveness than observed
 CC from administration of current agents. AAX83721 to AAX83753 represent
 CC other oligonucleotides used in examples from the present invention.
 XX
 XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
 SQ
 Query Match 100.0%; Score 20; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCTCGTGGTGAGTTTCA 20
 Db 1 GTTCTCGTGGTGAGTTTCA 20
 RESULT 25
 AAX33511
 ID AAX33511 standard; DNA; 20 BP.
 XX

AAX33511;
 XX
 XX 07-JUL-1999 (first entry)
 XX
 XX Antisense oligonucleotide SEQ ID NO:42.
 XX
 XX Combinatorial antisense library; oligonucleotide analogue; RNase;
 KW ribozyme; cleavage; anchor; binding; target RNA; ss.
 XX
 OS Synthetic.
 XX
 XX WO9918238-A1.
 XX
 XX 15-APR-1999.
 XX
 XX 28-SEP-1998; 98WO-US20361.
 XX
 XX 18-AUG-1998; 98US-0136080.
 PR 02-OCT-1997; 97US-0060673.
 XX
 XX (OASI-) OASIS BIOSCIENCES INC.
 XX
 XX Arnold LJ, Brown BD, Riley TA;
 PI WPI; 1999-264039/22.
 XX
 XX Oligonucleotide analog compositions capable of coupling to form
 PT antisense molecules
 PT
 XX Example 8; Page 42; 71pp; English.
 XX
 XX The present invention describes a composition comprising two
 CC oligonucleotide analogues, each having a binding domain and a coupling
 CC moiety, where the binding domains are capable of hybridizing to a target
 CC polynucleotide and the coupling moieties are capable of coupling to each
 CC other in the absence of a target molecule. The composition/compound is
 CC used to cleave an RNA target. The compositions can be used to determine
 CC an optimal antisense site for a given mRNA or an optimal ribozyme
 CC cleavage site for a target RNA. By separating the antisense molecules
 CC into two or more pieces, a comprehensive antisense library can be
 CC prepared in advance, rather than synthesizing a plurality of candidate
 CC antisense molecules as needed. A complete library of every possible
 CC 17-mer oligonucleotide, using the four natural bases, would consist of
 CC 417 (or about 1.7 x 10¹⁰) molecules. By providing the antisense molecules
 CC in at least two components, e.g. a library of 8-mers and a library of
 CC 9-mers, assembled quickly as needed, the library size is reduced to 48 +
 CC 49, or 327 650 molecules. The complexity of the library can be further
 CC reduced by substituting one or more universal or degenerate bases for
 CC some of the natural bases. The present sequence represents an
 CC oligonucleotide, which is used in an example from the present invention.
 XX
 XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
 SQ
 Query Match 100.0%; Score 20; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCTCGTGGTGAGTTTCA 20
 Db 1 GTTCTCGTGGTGAGTTTCA 20
 RESULT 26
 AAX33399
 ID AAX33399 standard; DNA; 20 BP.
 XX
 XX AAX33399;
 XX
 XX 29-JUN-1999 (first entry)
 XX
 XX Phosphorothioate 20-mer oligonucleotide #4.
 DE Phosphorothioate; sulphurised oligonucleotide; ss.
 KW

```

XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /*tag= a
XX FT /note= "phosphorothioate linkages"
XX PN WO9919340-A1.
XX PD 22-APR-1999.
XX PF 13-OCT-1998; 98WO-US21502.
XX PR 15-OCT-1997; 97US-0950779.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Cheruvallath ZS, Cole DL, Ravikumar VT;
XX DR WPI; 1999-287949/24.
XX PT Preparation of Phosphorothioate oligonucleotides applicable
XX PT throughout nucleic acid chemistry
XX PS Example 3; Page 9; 17pp; English.
XX CC The present invention describes a method for preparing phosphorothioate
XX CC oligonucleotides by phosphorylating the 5'-hydroxyl of a nucleic acid
XX CC moiety in an acetonitrile containing solvent mixture to form a phosphite
XX CC intermediate (II) and oxidizing (II) with an acetyl disulfide in an
XX CC acetonitrile containing solvent mixture to effect conversion of the
XX CC intermediate to phosphorothioate (III). The present sequence represents a
XX CC phosphorothioate oligonucleotide from an example of the present
XX CC invention. The method can be used to sulphurise oligonucleotides of 8-50
XX CC nucleotides. The method is widely applicable throughout nucleic acid
XX CC chemistry. The process allows formation of phosphorothioate linkages in
XX CC the oligonucleotides or derivatives, without the need for complex
XX CC solvent mixtures and repeated washing or solvent changes. The process
XX CC uses a simplified solvent system and produces oligonucleotides having
XX CC phosphorothioate groups with efficiency and improved yields.
XX SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGCTGAGTTTCA 20
Db 1 GTTCTCGCTGCTGAGTTTCA 20

RESULT 27
AAX23697
ID AAX23697 standard; DNA; 20 BP.
XX AC AAX23697;
XX DT 18-JUN-1999 (first entry)
XX DE Deletion sequence oligonucleotide 150.
XX KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
XX KW probe; cellular adhesion modulator; cellular proliferation modulator;
XX KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
XX KW HIV; primer; ss.
XX OS Synthetic.
XX PN WO9911820-A1.
XX PD 11-MAR-1999.

```

```

XX PF 01-SEP-1998; 98WO-US18084.
XX PR 02-SEP-1997; 97US-0923771.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Chen D, Srivatsa GS;
XX DR WPI; 1999-205198/17.
XX PT New compositions comprising sensor arrays made up of unique probe
XX PT oligonucleotides - useful for characterizing a sample of target
XX PT deletion oligonucleotides
XX PS Example 9; Page 155; 163pp; English.
XX CC This invention describes a novel composition comprising a number of
XX CC sensor arrays, where each array comprises a unique probe
XX CC oligonucleotide, which is the reverse complement of part of a unique
XX CC target oligonucleotide present in a mixture of target deletion sequence
XX CC oligonucleotides. The compositions form a method for characterizing a
XX CC sample of target deletion oligonucleotides which are labelled and
XX CC hybridize with the probe oligonucleotides of the sensor arrays. Such
XX CC oligonucleotides and their targets are represented in AAX23548-X23709.
XX CC Oligonucleotides characterized by the method form pharmaceutical
XX CC compositions that are useful for modulating cellular adhesion or
XX CC proliferation, and being active against a eukaryotic pathogen, a human
XX CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
XX CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
XX CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
XX CC characterization of deletion sequence oligonucleotides having related,
XX CC but different nucleobase sequences, and quantification of different
XX CC species of deletion sequence ("target") oligonucleotides in a mixture.
XX CC Also, if the specificity of the oligonucleotide's nucleobase sequence
XX CC for its reverse complement is not modified, the method may be performed
XX CC using oligodeoxynucleotides.
XX SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGCTGAGTTTCA 20
Db 1 GTTCTCGCTGCTGAGTTTCA 20

RESULT 28
AAX22563
ID AAX22563 standard; DNA; 20 BP.
XX AC AAX22563;
XX DT 27-MAY-1999 (first entry)
XX DE Human protein kinase C antisense oligonucleotide #2.
XX KW Protein kinase C; PKC; human; antisense; primer; inhibitor; treatment;
XX KW hyperproliferative condition; cancer; colorectal; breast; lung;
XX KW brain; glioblastoma multiforme; skin; psoriasis; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN US5885970-A.
XX PD 23-MAR-1999.
XX PF 07-JUN-1995; 95US-0488177.
XX PR 07-JUN-1995; 95US-0488177.

```


PR 16-MAR-1992; 92US-0852852.
 PR 09-JUL-1993; 93US-0089996.
 PA (ISIS-) ISIS PHARM INC.
 PI Bennett CF, Dean N;
 XX WPI; 1999-228583/19.
 XX
 XX New human protein kinase C antisense oligonucleotides - useful for
 PT treating PKC-related hyperproliferative conditions e.g. cancer and
 PT psoriasis
 XX
 XX Example 1; Column 12; 55pp; English.
 XX
 XX This invention describes antisense oligonucleotides that specifically
 CC bind to human protein kinase C (PKC) mRNA. These oligonucleotides can be
 CC used to inhibit PKC mRNA and therefore be used to treat PKC-related
 CC hyperproliferative conditions, e.g. cancer, especially colorectal cancer,
 CC breast cancer, bladder cancer, lung cancer, or brain cancer (preferably
 CC glioblastoma multiforme). The products of the invention may also be used
 CC to treat skin cancer and psoriasis.
 XX
 XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
 SQ
 Query Match 100.0%; Score 20; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCTCGCTGGTGAGTTTCA 20
 DB 1 GTTCTCGCTGGTGAGTTTCA 20
 RESULT 29
 AAX19127
 ID AAX19127 standard; DNA; 20 BP.
 XX
 XX AAX19127;
 AC
 XX
 XX 20-MAR-2003 (updated)
 DT 14-MAY-1999 (first entry)
 XX
 XX Human PKC-alpha antisense oligonucleotide SEQ ID NO:2.
 DE
 XX Human; PKC; protein kinase C; diagnosis; antisense oligonucleotide;
 KW phosphorothioate linkage; hyperproliferative disease; cancer;
 KW psoriasis; tumour; inhibition; ss.
 XX
 XX Synthetic.
 OS
 OS Homo sapiens.
 XX
 XX US5882927-A.
 PN
 XX 16-MAR-1999.
 PD
 XX 07-JUN-1995; 95US-0478178.
 PF
 XX 07-JUN-1995; 95US-0478178.
 PR 16-MAR-1992; 92US-0852852.
 PR 09-JUL-1993; 93US-0089996.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett CF, Dean N;
 PI WPI; 1999-214073/18.
 XX
 XX New synthetic oligonucleotides inhibiting expression of protein
 PT kinase C (PKC)-alpha - useful for treating and diagnosing conditions
 PT associated with abnormal PKC expression
 XX
 XX Claim 1; Column 12; 56pp; English.
 PS

XX The present invention specifically describes antisense oligonucleotides
 CC of up to 50 nucleotides in length which specifically bind human protein
 CC kinase C-alpha (PKC-alpha) mRNA. AAX19127 to AAX19247 represent
 CC antisense oligonucleotides from the present invention which bind human
 CC PKC-alpha, -beta, -gamma, -delta, -epsilon, -zeta and -eta. The
 CC antisense oligonucleotides modulate the expression of the PKC gene (i.e.
 CC inhibit the PKC gene). The antisense oligonucleotides can be used to
 CC diagnose abnormal proliferative states in tissue or other samples from
 CC patients suspected of having a hyperproliferative disease e.g. cancer or
 CC psoriasis. The antisense oligonucleotides can be used to distinguish
 CC PKC-associated tumours and to detect and diagnose PKC expression (through
 CC the use of 32P labeled antisense oligonucleotides). Radiolabeled
 CC antisense oligonucleotides can also be used to perform autoradiography of
 CC tissues to determine the localization, distribution and quantitation of
 CC PKC expression for research, diagnostic and therapeutic purposes. The use
 CC of the antisense oligonucleotides eliminates the side effects associated
 CC with prior art methods because it modulates the amount of PKC protein
 CC made from the gene rather than inhibiting the enzyme itself.
 CC (Updated on 20-MAR-2003 to correct PF field.)
 XX
 XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
 SQ
 Query Match 100.0%; Score 20; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCTCGCTGGTGAGTTTCA 20
 DB 1 GTTCTCGCTGGTGAGTTTCA 20
 RESULT 30
 AAX18706
 ID AAX18706 standard; DNA; 20 BP.
 XX
 XX AAX18706;
 AC
 XX
 XX 10-MAY-1999 (first entry)
 DT
 XX
 XX Target PKC-zeta antisense oligonucleotide.
 DE
 XX Cellular adhesion protein; proliferation; antisense oligonucleotide;
 KW alimentary canal; transport; gastrointestinal mucosa; cancer;
 KW Alzheimer's disease; beta-thalassemia; malaria; viral infection;
 KW HIV; inflammation; ss.
 XX
 XX Synthetic.
 OS
 XX WO9901579-A1.
 PN
 XX 14-JAN-1999.
 PD
 XX 01-JUL-1999; 98WO-US13574.
 PF
 XX 01-JUL-1997; 97US-0886829.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Hardee G, Teng C;
 PI WPI; 1999-106077/09.
 DR
 XX Composition comprising nucleic acid and penetration enhancer - used
 PT particularly for delivering therapeutic antisense oligonucleotides
 PT across the gastrointestinal mucosa, provides high bioavailability
 XX
 XX Example 2; Page 88; 115pp; English.
 PS
 XX A pharmaceutical composition has been developed which comprises a
 CC nucleic acid and at least one penetration enhancer. The compositions are
 CC used: (i) to treat or prevent any disease or disorder that can be
 CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
 CC

CC beta-thalassemia, malaria, viral infections (including human immune
 CC deficiency virus (HIV)), inflammation, in human or animal medicine;
 CC (ii) to investigate the role of a gene or gene product in non-human
 CC animals; and (iii) to modulate gene expression in cells, tissues or
 CC organs. The compositions provide bioavailability of at least 15,
 CC preferably 17-35,%. The penetration enhancer improves: (i) transport of
 CC the nucleic acid across the mucosa of the alimentary canal and into
 CC cells; and (ii) increases stability of the nucleic acid. Oral
 CC administration avoids the complications and expense of intravenous or
 CC other methods of administration. AAX18669 to AAX18799 and AAX18801
 CC represent antisense oligonucleotides which can be used as the nucleic
 CC acid in the method of the invention.

XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
 SQ Query Match 100.0%; Score 20; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGTGGTGAGTTTCA 20
 Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 31
 AAV99433
 ID AAV99433 standard; DNA; 20 BP.
 XX AC AAV99433;
 XX DT 22-MAR-1999 (first entry)
 XX DE Antisense oligonucleotide directed against human phosphokinase C gene.
 XX KW Antisense oligonucleotide; human phosphokinase C gene;
 KW phosphorothioate; phosphodiester; lipid-encapsulation; tumour;
 KW aberrant gene expression; treatment; inflammation; infection; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /note= "phosphorothioate or phosphodiester bonds"
 XX WO9851278-A2.
 XX 19-NOV-1998.
 XX 14-MAY-1998; 98WO-CAC00485.
 XX 14-MAY-1997; 97US-0856374.
 XX (INEX-) INEX PHARM CORP.
 XX Ansell SM, Cullis P, Debever D, Harasym T, Hope MJ;
 PI Klimuk SK, Scherrer P, Sample SC;
 XX WPI; 1999-045179/04.
 XX Composition containing lipid-encapsulated therapeutic agent -
 PT useful, e.g. for delivering antisense molecules or ribozymes or
 PT treating diseases associated with aberrant gene expression
 XX Disclosure; Page 23; 98pp; English.
 XX The present sequence represents an antisense oligonucleotide directed
 CC against the human phosphokinase C gene. The oligonucleotide can have
 CC either phosphorothioate or phosphodiester bonds. The oligonucleotide
 CC is lipid-encapsulated using the method of the invention. A composition
 CC comprising lipid-encapsulated particles of a therapeutic agent,
 CC e.g. antisense oligonucleotides, is prepared by mixing at least 2 lipids

CC with buffered aqueous solution of charged therapeutic agent to form an
 CC intermediate mixture of lipid-encapsulated particles, and changing the
 CC pH of the mixture to neutralise at least some of the external surface
 CC charges on the particles. One lipid has a (de)protonatable group with
 CC Ka such that the lipid is charged at a first pH but neutral at a second
 CC pH (particularly near physiological pH) and the buffer maintains this
 CC lipid in the charged form (i.e. cationic when the therapeutic agent is
 CC anionic in the buffer, or vice versa). The second lipid prevents particle
 CC aggregation during formation of the lipid-therapeutic agent particles.
 CC The composition is used to introduce therapeutic agents into cells,
 CC in vivo or in vitro, particularly to treat or prevent diseases associated
 CC with aberrant gene expression in mammals, specifically tumours,
 CC inflammation or infection.

XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
 SQ Query Match 100.0%; Score 20; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGTGGTGAGTTTCA 20
 Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 32
 AAV72642
 ID AAV72642 standard; DNA; 20 BP.
 XX AC AAV72642;
 XX DT 11-FEB-1999 (first entry)
 XX DE Human protein kinase C-alpha antisense oligonucleotide.
 XX KW Mouse; protein kinase C-alpha; PKC-alpha; antisense oligonucleotide;
 KW phosphorothioate; enhanced bioavailability; oral delivery; diagnosis;
 KW heteroatomic backbone modification; 2'-modified sugar; tumour;
 KW autoimmune disease; inflammation; graft vs. host disease; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.

XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /note= "phosphorothioate linkages"
 XX WO9849348-A1.
 XX 05-NOV-1998.
 XX 30-APR-1998; 98WO-US08798.
 XX 30-APR-1997; 97US-0847151.
 XX (ISIS-) ISIS PHARM INC.
 XX Anderson KP, Baker BF, Bennett CF, Dean NM, Draper K;
 PI Ecker DJ, Monia BP;
 XX WPI; 1999-009446/01.
 XX Modified antisense oligonucleotide with increased bioavailability
 PT after oral delivery - has heteroatomic backbone modification or
 PT 2'-modified sugar, useful for diagnosis and therapy, e.g. of tumours
 XX Example 1; Page 37; 54pp; English.
 XX The present invention describes oligonucleotides having: (a) at least
 CC one heteroatomic backbone modification or at least one 2'-sugar
 CC modification; and (b) during or after administration to the alimentary
 CC canal, greater bioavailability than the corresponding phosphorothioate

CC oligodeoxynucleotide. Also described are compositions containing the
CC oligonucleotides having at least one 2'-alkoxyalkoxy sugar modification
CC and at least one 5-methylcytidine (5MeC) residue. The oligonucleotides
CC are antisense oligonucleotides for modulating expression of target genes
CC for diagnostic or therapeutic purposes, e.g. in cases of tumours,
CC autoimmune disease and inflammation, including graft vs. host disease.
CC The specified modifications increase bioavailability from the digestive
CC tract, eliminating the need for intravenous or other routes of
CC administration. The present sequence represents an antisense
CC oligonucleotide which is used in example to examine the effect of 2'
CC modifications on bioavailability after gastrointestinal administration
CC in mice.
XX
XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
SQ

Query Match 100.0%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 33
AAC62739
ID AAC62739 standard; DNA; 20 BP.
XX
AC AAC62739;
XX
DT 05-FEB-2001 (first entry)
XX
DE Phosphorothioate oligonucleotide ISIS-3521.
XX
XX Phosphorothioate; lipid; liposome; drug deliver; ss.
XX
XX Unidentified.
XX
XX WO200059474-A1.
XX
XX 12-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US09473.
XX
XX 06-APR-1999; 99US-0287175.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Leamon CP;
XX
XX WPI; 2000-679320/66.
XX
XX New pro-cationic lipid compounds useful as components of liposomes used
XX as vehicles for delivering pharmaceutical agents into cells -
XX
XX Disclosure; Page 31; 65pp; English.

CC The present oligonucleotide is given in a specification disclosing a new
CC lipid compound and its salts, solvates and hydrates. The compound
CC comprises a hydrophobic tail part covalently linked to a hydrophilic
CC head part. A region proximal to the hydrophobic tail part has a net
CC positive charge at physiological pH and a region distal to the
CC hydrophobic tail part has a net negative charge at physiological pH. A
CC disulphide bond connects the regions. The lipid compound is useful for
CC the construction of liposomes used as vehicles for delivering
CC pharmaceutical agents into cells. The lipids and liposomes are fusogenic
CC with membranes and deliver pharmaceutical agents to tissues or cells
CC without inherent aggregation, which reduces toxicity.
XX
XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
SQ

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;

QY 1 GTTCTCGTGGTGAGTTTCA 20
Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 34
AAC65035
ID AAC65035 standard; DNA; 20 BP.
XX
AC AAC65035;
XX
DT 12-FEB-2001 (first entry)
XX
DE Protein kinase C alpha antisense sequence SEQ ID NO: 18.
XX
KW Antisense oligonucleotide; RNA molecule cleavage; immune activation;
KW bcl; protein kinase C; PKC; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200061810-A1.
XX
XX 19-OCT-2000.
XX
XX 07-APR-2000; 2000WO-US09293.
XX
XX 08-APR-1999; 99US-0128377.
XX
XX (OASI-) OASIS BIOSCIENCES INC.
XX
XX Brown BD, Riley TA;
XX
XX WPI; 2000-679502/66.
XX
XX Antisense oligonucleotides containing degenerate and/or universal
XX bases, and modified backbone linkages is useful to target therapeutic
XX genes, preferably anti-apoptosis or chemoresistance genes -
XX
XX Example 3; Page 10; 32pp; English.

CC The present invention is concerned with antisense oligonucleotides
CC containing a number of degenerate bases and with a modified backbone
CC which can be used to direct cleavage of target RNA molecules. The use of
CC degenerate bases reduces the risk of immune activation following
CC injection into animals, which causes deleterious side effects associated
CC with many therapeutic antisense oligonucleotides. Sequences
CC AAC65029-C65077 are antisense oligonucleotides and PCR primers used in
CC assays to demonstrate the effects of the sequences of the invention.
XX
XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
SQ

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 35
AAA99219
ID AAA99219 standard; DNA; 20 BP.
XX
AC AAA99219;
XX
DT 23-JAN-2001 (first entry)
XX
DE PKC-a target phosphorothioate antisense oligonucleotide SEQ ID NO:3.
XX
KW Phosphorothioate; antisense oligonucleotide; target; purification;

KW dimethoxytrityl group removal; synthesis; deprotection; ss.

OS Synthetic.

EH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /note= "phosphorothioate linkages"

XX WO200055170-A1.

XX 21-SEP-2000.

XX 17-MAR-2000; 2000WO-US07003.

XX 17-MAR-1999; 99US-0271220.

XX (ISIS-) ISIS PHARM INC.

XX Krotz AH, McElroy B, Scozzari AN;

XX WPI; 2000-647063/62.

XX Improving deprotection of acid labile 5'-hydroxy protecting
PT group-containing oligonucleotides for large scale synthesis of
PT oligonucleotides, involves determining the half life of protecting
PT groups in acid solution -

PS Example 1; Page 14; 25pp; English.

XX The present invention describes a method for improving deprotection of
CC an acid labile 5'-hydroxy protecting group-containing oligonucleotides
CC (I). The method involves determining the half life for (I) in an acid
CC solution capable of removing the 5'-hydroxy protecting group from
CC oligonucleotide, and reacting (I) in acid solution for approximately
CC 5-20 half lives. The method is useful for synthesizing and purifying
CC oligonucleotides in large scale. The method allows the user to determine
CC an optical reaction time for removal of the 5'-hydroxy protecting group
CC so that a fine balance between detritylation and depurination is
CC maintained. The present sequence represents a phosphorothioate antisense
CC oligonucleotide targeted to PKC-a, which is used in an example from
CC the present invention.

XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20

Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 36

AAA94542

ID AAA94542 standard; DNA; 20 BP.

XX AAA94542;

XX 10-JAN-2001 (first entry)

XX Example biologically active oligonucleotide #4.

XX Oligonucleotide; non-parenteral; multi-particulate;
KW phosphorothioate; ss.

XX Synthetic.

EH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

/note= "Phosphorothioate internucleotide linkage"

XX WO200050050-A1.

XX 31-AUG-2000.

XX 23-FEB-2000; 2000WO-US04662.

XX 23-FEB-1999; 99US-0256515.

XX (ISIS-) ISIS PHARM INC.

XX Hardee GE, Tillman LG, Mehta RC, Teng C;

XX WPI; 2000-572032/53.

XX Non-parenteral multi-particulate formulations comprise biologically
PT active substances bound to carrier particles for delivery across
PT mucosal membranes -

PS Claim 4; Page 8; 38pp; English.

XX The present invention relates to non-parenteral multi-particulate
CC formulations for transporting agents (for example therapeutic) across
CC mucosal membranes. The formulations comprise carrier particles bound
CC with a biologically active agent and a penetration enhancer. The
CC formulations associate with buccal, nasal, pulmonary, gastrointestinal
CC and vaginal mucosal membranes to transport the biologically active
CC agents to the lymph system, blood system or epithelial tissue of the
CC subject. The formulation is administered orally which is preferred by
CC patients. The present sequence is an example oligonucleotide that may
CC be used in the formulation.

XX Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20

Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 37

AAA91619

ID AAA91619 standard; DNA; 20 BP.

XX AAA91619;

XX 20-DEC-2000 (first entry)

XX Human PKC-alpha antisense oligonucleotide.

XX Human; PKC-alpha antisense oligonucleotide; ribonucleotide reductase;
KW R1 protein; R2 protein; tumour cell proliferation inhibition; cancer;
KW cytostatic; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200047733-A1.

XX 17-AUG-2000.

XX 09-FEB-2000; 2000WO-CA00120.

XX 11-FEB-1999; 99US-0249730.

XX (GENE-) GENESENSE TECHNOLOGIES INC.

XX Wright JA, Young AH;

```

DR WPI; 2000-558216/51.
XX
PT New antisense oligonucleotide, AS-I-618-20, is useful for inhibiting
PT tumor cell growth -
XX
XX
PS Example 13; Page 105; 137pp; English.
XX
CC The present sequence is an antisense oligonucleotide directed against
CC PKC-alpha. Antisense oligonucleotides directed against a number of
CC tumour-associated genes were administered to mice injected with human
CC colon carcinoma cells, human melanoma cells or human lung cancer cells.
CC The tumour was removed 14 days after treatment and its weight was
CC measured. This was performed as an example of a method for modulating
CC cell proliferation. Antisense oligonucleotides were also made that were
CC directed against the R1 or R2 component of mammalian ribonucleotide
CC reductase. Ribonucleotide reductase catalyses the conversion of
CC ribonucleotides to their corresponding deoxyribonucleotides and thus
CC plays an important role in DNA synthesis and cell proliferation.
CC Regulation of ribonucleotide reductase is altered in cultured malignant
CC cells and increased levels of R2 protein and R2 mRNA have been found in
CC pre-malignant and malignant tissues as compared to normal control tissue
CC samples. Antisense sequence are therefore useful for inhibiting
CC tumorigenicity of neoplastic cells and inhibiting metastasis of tumour
CC cells. They are also useful for increasing sensitivity of neoplastic
CC cells to chemotherapeutic drugs, thus allowing chemotherapeutic
CC treatments to be used in patients who have become resistant or less
CC sensitive to chemotherapy.
XX
SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTCA 20
DB 1 GTTCTCGCTGGTGAGTTCA 20

RESULT 38
AA14474
ID AA14474 standard; DNA; 20 BP.
AC AA14474;
DT 21-AUG-2000 (first entry)
DE Synthetic oligonucleotide #4.
KW Solid phase DNA synthesis; phosphoramidate nucleoside;
KW acetonitrile; water content; synthetic oligonucleotide; ss.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /*note= "Phosphorothioate linkages"
FT
FT modified_base 4
FT /*tag= b
FT /*mod_base= m5c
FT modified_base 6
FT /*tag= c
FT /*mod_base= m5c
FT modified_base 8
FT /*tag= d
FT /*mod_base= m5c
FT modified_base 14
FT /*tag= e
FT /*mod_base= OTHER
FT /*note= "OTHER = 2-aminoadenosine"
FT modified_base 19
FT /*tag= f
FT /*mod_base= m5c
FT modified_base 20
FT /*tag= g
FT /*mod_base= OTHER
FT /*note= "OTHER = 2-aminoadenosine"
XX WO2000020431-A1.
XX
PD 13-APR-2000.
XX
PF 01-OCT-1999; 99WO-US22892.
XX
PR 06-OCT-1998; 98US-0167165.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Scozzari A;
XX
XX WPI; 2000-303729/26.
XX

```

```

PT Coupling of a phosphoramidite nucleoside to a solid support-bound
PT nucleoside, useful for the synthesis of oligonucleotides for use in
PT diagnostic, research or therapeutic applications -
XX
XX
PS Example 11; Page 21; 30pp; English.
XX
CC The invention relates to the use of acetonitrile having a water content
CC of 30-1250 ppm in the linking of a phosphoramidite nucleoside to a
CC solid support-bound nucleoside, and to the use of this process in the
CC synthesis of oligonucleotides. The method is used for the coupling of a
CC phosphoramidite nucleoside to a solid support-bound nucleoside,
CC particularly in the large-scale synthesis of oligonucleotides using the
CC phosphoramidite method. The oligonucleotides can be used in diagnostic,
CC research and therapeutic applications, e.g., as probes, primers,
CC linkers, adapters and antisense oligonucleotides. The use of acetonitrile
CC having a water content of 30-1250 ppm as compared to conventional methods
CC using lower water content acetonitrile (at most 30 ppm) provides more
CC economical synthesis without reduced efficiency of oligonucleotide
CC synthesis. Sequences AA14471-AA1474 represent oligonucleotides
CC synthesised using the process of the invention.
XX
SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;
Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTCA 20
DB 1 GTTCTCGCTGGTGAGTTCA 20

RESULT 39
AA10248
ID AA10248 standard; DNA; 20 BP.
AC AA10248;
DT 03-JUL-2000 (first entry)
DE 2-aminoadenosine-containing oligonucleotide #24683, SEQ ID NO:4.
KW 2-aminoadenosine; oligonucleotide; hybridisation; antisense therapy;
KW diagnosis; ss.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /*note= "Phosphorothioate linkages"
FT
FT modified_base 4
FT /*tag= b
FT /*mod_base= m5c
FT modified_base 6
FT /*tag= c
FT /*mod_base= m5c
FT modified_base 8
FT /*tag= d
FT /*mod_base= m5c
FT modified_base 14
FT /*tag= e
FT /*mod_base= OTHER
FT /*note= "OTHER = 2-aminoadenosine"
FT modified_base 19
FT /*tag= f
FT /*mod_base= m5c
FT modified_base 20
FT /*tag= g
FT /*mod_base= OTHER
FT /*note= "OTHER = 2-aminoadenosine"
XX WO200012563-A1.
XX

```

```

XX PD 09-MAR-2000.
XX PF 31-AUG-1999; 99WO-US19907.
XX PR 01-SEP-1998; 98US-0144883.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ross BS, Manoharan M;
XX DR WPI; 2000-246728/21.
XX PT Preparation of an oligonucleotide incorporating 2-aminoadenosine, with
XX PT stronger hybridization to its target sequence and useful in diagnosis
XX PT and therapy -
XX PS Example 23; Page 42; 48pp; English.
XX CC The invention relates to a novel method for the preparation of
XX CC oligonucleotides incorporating 2-aminoadenosine. A halogenated adenosine
XX CC is incorporated into an oligonucleotide using standard synthesis
XX CC methods, which is then reacted with an amine to produce 2-aminoadenosine.
XX CC The incorporation of 2-aminoadenosine and similar moieties into
XX CC oligonucleotides in place of adenosine provides an additional site for
XX CC hydrogen bonding to uridine or thymidine. This modification has been
XX CC shown to increase the binding affinity of oligonucleotides to their
XX CC target RNA sequences and, to a lesser extent, DNA sequences.
XX CC Oligonucleotides incorporating 2-aminoadenosine are useful as probes and
XX CC primers (e.g., for diagnostic use), linkers, adapters, and as antisense
XX CC therapeutics. Oligonucleotides incorporating 2-aminoadenosine exhibit
XX CC stronger hybridisation with their target sequences. Sequences AAA10245-
XX CC AAA10252 represent 2-aminoadenosine-containing oligonucleotides
XX CC synthesised in an exemplification of the present invention.
XX SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGCTGAGTTTCA 20
Db 1 GTTCTCGCTGCTGAGTTTCA 20

RESULT 40
AAZ92764
ID AAZ92764 standard; DNA; 20 BP.
XX AC AAZ92764;
XX DT 03-JUL-2000 (first entry)
XX DE Human protein kinase C (PKC)-alpha antisense oligonucleotide, ISIS 3521.
XX KW Protein kinase C-alpha; PKC; fluorescent label; cellular distribution;
XX KW differential labelling; lipid carrier; antisense; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT modified_base 1 /*tag= a
XX FT /*note= "Conjugated to an aminolinker which is optionally
XX FT linked to rhodamine"
XX FT modified_base 1..15 /*tag= b
XX FT /*note= "Phosphorothioate linkages"
XX PN WO200011955-A1.
XX PD 09-MAR-2000.

```

```

XX PF 01-SEP-1999; 99WO-US19982.
XX PR 02-SEP-1998; 98US-0145897.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Manoharan M, Herbert N, Bhat B;
XX DR WPI; 2000-237724/20.
XX PT Methods and compounds for tracking the biodistribution of
XX PT macromolecule-carrier complexes -
XX PS Example 8; Page 19; 31pp; English.
XX CC The invention relates to a novel method for tracking the biodistribution
XX CC of macromolecule-carrier complexes in cells. The method comprises using a
XX CC differentially fluorescently labelled oligonucleotide and lipid carrier
XX CC which are coadministered to the cells. The method of the invention is
XX CC used for tracking the distribution of macromolecules and carrier lipids
XX CC in cells. The method can be utilised to determine cellular pathways for
XX CC oligonucleotide uptake and to ascertain biodistribution of macromolecules
XX CC and carriers. Fully understanding the mechanism by which oligonucleotides
XX CC are taken up by cells and released from endosomes will aid in the design
XX CC of delivery vehicles to improve both the in vitro and in vivo efficacy of
XX CC the oligonucleotides. Such improved designs are important in the
XX CC investigation of the therapeutic utility of antisense oligonucleotides
XX CC and to improve the dosing regimens for antisense therapeutics. The
XX CC present sequence represents an antisense oligonucleotide targeted to
XX CC human protein kinase C-alpha (PKC-alpha) mRNA which was synthesised in
XX CC an exemplification of the invention. When fluorescently labelled, this
XX CC sequence may be used according to the method of the invention.
XX SQ Sequence 20 BP; 2 A; 4 C; 6 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGCTGAGTTTCA 20
Db 1 GTTCTCGCTGCTGAGTTTCA 20

Search completed: January 24, 2004, 14:32:21
Job time : 233 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 24, 2004, 14:22:02 ; Search time 52 Seconds
(without alignments)
169.763 Million cell updates/sec.

Title: US-10-002-884A-5

Perfect score: 20

Sequence: 1 gttctgctgggtgagtttca 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 679948

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
 - 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
 - 3: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
 - 4: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
 - 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
 - 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	US-08-468-447-8
2	20	100.0	20	1	US-08-469-851A-8
3	20	100.0	20	1	US-08-467-597A-8
4	20	100.0	20	1	US-08-468-569A-8
5	20	100.0	20	1	US-08-466-692A-8
6	20	100.0	20	1	US-08-471-966A-8
7	20	100.0	20	1	US-08-089-996-2
8	20	100.0	20	1	US-08-612-775-1
9	20	100.0	20	2	US-08-478-178A-2
10	20	100.0	20	2	US-08-488-177-2
11	20	100.0	20	2	US-08-481-072A-2
12	20	100.0	20	2	US-08-664-336-2
13	20	100.0	20	2	US-08-601-269-1
14	20	100.0	20	2	US-08-481-066A-2
15	20	100.0	20	3	US-08-578-615A-2
16	20	100.0	20	3	US-08-578-615A-121
17	20	100.0	20	3	US-08-950-779-4
18	20	100.0	20	3	US-09-094-714A-29
19	20	100.0	20	3	US-09-249-730-217
20	20	100.0	20	3	US-09-117-901-1
21	20	100.0	20	3	US-09-414-145-4
22	20	100.0	20	3	US-08-398-901-1
23	20	100.0	20	3	US-08-398-901-2
24	20	100.0	20	3	US-08-398-901-3
25	20	100.0	20	3	US-09-144-883C-4
26	20	100.0	20	3	US-08-894-899-27
27	20	100.0	20	3	US-08-894-899-28
28	20	100.0	20	3	US-08-894-899-29
29	20	100.0	20	3	US-09-177-953-4
30	20	100.0	20	3	US-09-177-953-13
31	20	100.0	20	3	US-09-177-953-27
32	20	100.0	20	3	US-09-177-953-35
33	20	100.0	20	3	US-09-177-953-42
34	20	100.0	20	3	US-09-078-954-13
35	20	100.0	20	4	US-09-225-749-2
36	20	100.0	20	4	US-09-379-718-4
37	20	100.0	20	4	US-09-111-678-4
38	20	100.0	20	4	US-08-829-637A-2
39	20	100.0	20	4	US-09-287-175-4
40	20	100.0	20	4	US-09-349-659-4
41	20	100.0	20	4	US-09-271-220-3
42	20	100.0	20	4	US-09-352-058A-3
43	20	100.0	20	4	US-08-802-331-30
44	20	100.0	20	4	US-09-254-322-2
45	20	100.0	20	4	US-09-136-080E-42
46	20	100.0	20	4	US-10-025-139-2
47	20	100.0	20	4	US-09-142-212A-2
48	20	100.0	20	4	US-09-495-398-5
49	20	100.0	20	4	US-09-495-398-6
50	20	100.0	20	5	PCT-US93-02213-2
51	20	100.0	20	5	PCT-US94-07770-2
52	20	100.0	20	5	PCT-US96-08757A-8
53	19	95.0	19	3	US-09-130-973-49
54	19	95.0	19	3	US-09-130-973-51
55	19	95.0	19	3	US-09-130-973-53
56	19	95.0	19	3	US-09-130-973-55
57	19	95.0	19	3	US-09-177-953-19
58	19	95.0	19	3	US-09-177-953-21
59	19	95.0	19	4	US-09-202-294-6
60	19	95.0	19	4	US-09-142-212A-12
61	18	90.0	18	1	US-08-089-996-52
62	18	90.0	18	2	US-08-468-037A-5
63	18	90.0	18	2	US-08-471-973A-5
64	18	90.0	18	2	US-08-478-178A-52
65	18	90.0	18	2	US-08-488-177-52
66	18	90.0	18	2	US-08-481-072A-52
67	18	90.0	18	2	US-08-664-336-52
68	18	90.0	18	2	US-08-465-880-5
69	18	90.0	18	2	US-08-481-066A-52
70	18	90.0	18	3	US-09-035-357-5
71	18	90.0	18	3	US-08-578-615A-52
72	18	90.0	18	3	US-09-094-714A-31
73	18	90.0	18	4	US-09-225-749-21
74	18	90.0	18	4	US-08-829-637A-52
75	18	90.0	18	4	US-09-135-202-5
76	18	90.0	18	4	US-08-802-331-5
77	18	90.0	18	4	US-09-254-322-52
78	18	90.0	18	4	US-09-389-283-5
79	18	90.0	18	4	US-10-025-139-52
80	18	90.0	18	5	PCT-US94-07770-52
81	17	85.0	17	1	US-08-089-996-53
82	17	85.0	17	2	US-08-468-037A-6
83	17	85.0	17	2	US-08-471-973A-6
84	17	85.0	17	2	US-08-478-178A-53
85	17	85.0	17	2	US-08-488-177-53
86	17	85.0	17	2	US-08-481-072A-53
87	17	85.0	17	2	US-08-664-336-53
88	17	85.0	17	2	US-08-465-880-6
89	17	85.0	17	2	US-08-481-066A-53
90	17	85.0	17	3	US-09-035-357-6
91	17	85.0	17	3	US-08-578-615A-53
92	17	85.0	17	3	US-09-094-714A-32
93	17	85.0	17	4	US-09-225-749-22
94	17	85.0	17	4	US-08-829-637A-53
95	17	85.0	17	4	US-09-135-202-6
96	17	85.0	17	4	US-08-802-331-6
97	17	85.0	17	4	US-09-254-322-53
98	17	85.0	17	4	US-09-389-283-6
99	17	85.0	17	4	US-10-025-139-53
100	17	85.0	17	5	PCT-US94-07770-53

101	16	80.0	27	4	US-09-136-080E-38	Sequence 38, Appl						1	US-08-379-078-57	Sequence 57, Appl
102	15	75.0	15	3	US-09-094-714A-12	Sequence 12, Appl	c 174	12	60.0	18	1	US-08-379-078-57	Sequence 58, Appl	
103	15	75.0	15	3	US-09-094-714A-37	Sequence 37, Appl	c 175	12	60.0	18	1	US-08-379-078-58	Sequence 59, Appl	
104	15	75.0	15	3	US-09-094-714A-38	Sequence 38, Appl	c 176	12	60.0	18	1	US-08-379-078-59	Sequence 60, Appl	
105	15	75.0	15	3	US-09-094-714A-39	Sequence 39, Appl	c 177	12	60.0	18	1	US-08-379-078-60	Sequence 61, Appl	
106	15	75.0	15	3	US-09-094-714A-40	Sequence 40, Appl	c 178	12	60.0	21	4	US-09-427-834A-30	Sequence 30, Appl	
107	15	75.0	15	3	US-08-199-779-5	Sequence 5, Appl	c 179	12	60.0	22	2	US-08-756-386-61	Sequence 61, Appl	
108	15	75.0	37	1	US-08-578-615A-108	Sequence 108, Appl	c 180	12	60.0	22	2	US-08-823-516-50	Sequence 50, Appl	
109	15	75.0	37	5	PCT-US94-07770-108	Sequence 108, Appl	c 181	12	60.0	22	3	US-08-882-853A-61	Sequence 61, Appl	
110	14.8	74.0	18	3	US-08-154-364-39	Sequence 39, Appl	c 182	12	60.0	22	3	US-08-759-038-61	Sequence 61, Appl	
111	14	70.0	15	3	US-09-094-714A-36	Sequence 36, Appl	c 183	12	60.0	22	3	US-08-758-314-61	Sequence 61, Appl	
112	13.8	69.0	18	3	US-08-154-364-38	Sequence 38, Appl	c 184	12	60.0	22	3	US-09-565-596-7	Sequence 7, Appl	
113	13.8	69.0	18	3	US-08-154-364-40	Sequence 40, Appl	c 185	12	60.0	22	4	US-09-565-156A-7	Sequence 7, Appl	
114	13.8	69.0	20	3	US-09-657-481A-74	Sequence 74, Appl	c 186	12	60.0	22	4	US-09-350-309-61	Sequence 61, Appl	
115	13.6	68.0	33	5	PCT-US94-09653A-5	Sequence 5, Appl	c 187	12	60.0	22	4	US-09-565-241-7	Sequence 7, Appl	
116	13.6	68.0	33	5	PCT-US94-09653A-6	Sequence 6, Appl	c 188	12	60.0	22	4	US-09-847-842-8	Sequence 8, Appl	
117	13.4	67.0	22	4	US-09-487-792-45	Sequence 45, Appl	c 189	12	60.0	22	4	US-09-684-938-61	Sequence 61, Appl	
118	13.4	67.0	22	4	US-09-908-594-45	Sequence 45, Appl	c 190	12	60.0	22	4	US-09-308-825A-61	Sequence 61, Appl	
119	13.4	67.0	38	1	US-08-390-850-783	Sequence 783, Appl	c 191	12	60.0	24	2	US-08-316-650-4	Sequence 4, Appl	
120	13.4	67.0	38	1	US-08-435-634-783	Sequence 783, Appl	c 192	12	60.0	24	2	PCT-US95-02251-4	Sequence 29, Appl	
121	13.2	66.0	21	2	US-08-359-705B-28	Sequence 28, Appl	c 193	12	60.0	25	1	US-08-448-204-29	Sequence 29, Appl	
122	13.2	66.0	21	2	US-08-286-848A-28	Sequence 28, Appl	c 194	12	60.0	27	1	US-07-780-800A-1	Sequence 1, Appl	
123	13.2	66.0	21	2	US-08-458-880A-28	Sequence 28, Appl	c 195	12	60.0	29	4	US-09-304-232-446	Sequence 446, Appl	
124	13.2	66.0	21	3	US-08-444-622A-28	Sequence 28, Appl	c 196	12	60.0	39	1	US-07-780-800A-2	Sequence 2, Appl	
125	13.2	66.0	21	3	US-08-942-562-28	Sequence 28, Appl	c 197	11.8	59.0	17	4	US-08-584-040-2507	Sequence 2507, Appl	
126	13.2	66.0	21	3	US-09-156-923-28	Sequence 28, Appl	c 198	11.8	59.0	17	4	US-09-371-772B-1031	Sequence 1031, Appl	
127	12.8	64.0	18	3	US-09-156-923-28	Sequence 28, Appl	c 199	11.8	59.0	18	3	US-08-154-364-36	Sequence 36, Appl	
128	12.8	64.0	18	3	US-08-154-364-37	Sequence 37, Appl	c 200	11.8	59.0	18	4	US-09-733-444-21	Sequence 21, Appl	
129	12.6	63.0	24	4	US-09-721-822A-4	Sequence 4, Appl	c 201	11.8	59.0	20	4	US-09-198-452A-1681	Sequence 1681, Appl	
130	12.6	63.0	27	1	US-08-230-002-2	Sequence 2, Appl	c 202	11.8	59.0	21	4	US-08-318-428B-11	Sequence 11, Appl	
131	12.6	63.0	27	2	US-08-678-854-2	Sequence 2, Appl	c 203	11.8	59.0	28	2	US-08-859-998-1155	Sequence 1155, Appl	
132	12.4	62.0	20	4	US-09-721-822A-47	Sequence 47, Appl	c 204	11.8	59.0	28	4	US-09-225-928-1155	Sequence 1155, Appl	
133	12.2	61.0	17	4	US-09-371-772B-5390	Sequence 47, Appl	c 205	11.8	59.0	28	4	US-09-225-201B-1155	Sequence 1155, Appl	
134	12.2	61.0	20	4	US-09-672-609-44	Sequence 44, Appl	c 206	11.8	59.0	33	4	US-09-672-609-47	Sequence 47, Appl	
135	12.2	61.0	20	4	US-09-025-403A-44	Sequence 44, Appl	c 207	11.8	59.0	33	4	US-09-025-403A-47	Sequence 47, Appl	
136	12.2	61.0	20	4	US-09-198-452A-5517	Sequence 44, Appl	c 208	11.8	59.0	36	1	US-08-291-932A-421	Sequence 421, Appl	
137	12	60.0	15	3	US-09-094-714A-35	Sequence 35, Appl	c 209	11.8	59.0	36	1	US-08-291-932A-610	Sequence 610, Appl	
138	12	60.0	18	1	US-08-379-081B-41	Sequence 41, Appl	c 210	11.8	59.0	36	1	US-08-305-699-3	Sequence 3, Appl	
139	12	60.0	18	1	US-08-379-081B-42	Sequence 42, Appl	c 211	11.8	59.0	36	1	US-08-305-699-4	Sequence 4, Appl	
140	12	60.0	18	1	US-08-379-081B-43	Sequence 43, Appl	c 212	11.8	59.0	36	1	US-08-363-240A-311	Sequence 311, Appl	
141	12	60.0	18	1	US-08-379-081B-44	Sequence 44, Appl	c 213	11.8	59.0	36	1	US-08-363-240A-823	Sequence 823, Appl	
142	12	60.0	18	1	US-08-379-081B-45	Sequence 45, Appl	c 214	11.8	59.0	36	2	US-08-292-620A-823	Sequence 823, Appl	
143	12	60.0	18	1	US-08-379-081B-46	Sequence 46, Appl	c 215	11.8	59.0	36	2	US-08-292-620A-1179	Sequence 1179, Appl	
144	12	60.0	18	1	US-08-379-081B-47	Sequence 47, Appl	c 216	11.8	59.0	36	2	US-08-292-620A-1285	Sequence 1285, Appl	
145	12	60.0	18	1	US-08-379-081B-48	Sequence 48, Appl	c 217	11.8	59.0	36	2	US-08-585-684B-411	Sequence 411, Appl	
146	12	60.0	18	1	US-08-379-081B-49	Sequence 49, Appl	c 218	11.8	59.0	36	2	US-08-585-684B-1837	Sequence 1837, Appl	
147	12	60.0	18	1	US-08-379-081B-50	Sequence 50, Appl	c 219	11.8	59.0	36	2	US-08-585-684B-1900	Sequence 1900, Appl	
148	12	60.0	18	1	US-08-379-081B-51	Sequence 51, Appl	c 220	11.8	59.0	36	3	US-09-071-845-823	Sequence 823, Appl	
149	12	60.0	18	1	US-08-379-081B-52	Sequence 52, Appl	c 221	11.8	59.0	36	3	US-09-071-845-1179	Sequence 1179, Appl	
150	12	60.0	18	1	US-08-379-081B-53	Sequence 53, Appl	c 222	11.8	59.0	36	3	US-09-071-845-1285	Sequence 1285, Appl	
151	12	60.0	18	1	US-08-379-081B-54	Sequence 54, Appl	c 223	11.8	59.0	36	3	US-09-038-073-411	Sequence 411, Appl	
152	12	60.0	18	1	US-08-379-081B-55	Sequence 55, Appl	c 224	11.8	59.0	36	3	US-09-038-073-1837	Sequence 1837, Appl	
153	12	60.0	18	1	US-08-379-081B-56	Sequence 56, Appl	c 225	11.8	59.0	36	3	US-09-038-073-1900	Sequence 1900, Appl	
154	12	60.0	18	1	US-08-379-081B-57	Sequence 57, Appl	c 226	11.8	59.0	38	1	US-08-373-124A-533	Sequence 533, Appl	
155	12	60.0	18	1	US-08-379-081B-58	Sequence 58, Appl	c 227	11.8	59.0	38	1	US-08-373-124A-1700	Sequence 1700, Appl	
156	12	60.0	18	1	US-08-379-081B-59	Sequence 59, Appl	c 228	11.8	59.0	38	1	US-08-373-124A-2420	Sequence 2420, Appl	
157	12	60.0	18	1	US-08-379-081B-60	Sequence 60, Appl	c 229	11.8	59.0	38	1	US-08-373-124A-2576	Sequence 2576, Appl	
158	12	60.0	18	1	US-08-379-078-41	Sequence 41, Appl	c 230	11.8	59.0	38	1	US-08-435-628-533	Sequence 533, Appl	
159	12	60.0	18	1	US-08-379-078-42	Sequence 42, Appl	c 231	11.8	59.0	38	1	US-08-435-628-1700	Sequence 1700, Appl	
160	12	60.0	18	1	US-08-379-078-43	Sequence 43, Appl	c 232	11.8	59.0	38	1	US-08-435-628-2420	Sequence 2420, Appl	
161	12	60.0	18	1	US-08-379-078-44	Sequence 44, Appl	c 233	11.8	59.0	38	1	US-08-435-628-2576	Sequence 2576, Appl	
162	12	60.0	18	1	US-08-379-078-45	Sequence 45, Appl	c 234	11.8	59.0	38	2	US-08-292-620A-2044	Sequence 2044, Appl	
163	12	60.0	18	1	US-08-379-078-46	Sequence 46, Appl	c 235	11.8	59.0	38	2	US-08-292-620A-2081	Sequence 2081, Appl	
164	12	60.0	18	1	US-08-379-078-47	Sequence 47, Appl	c 236	11.8	59.0	38	3	US-08-292-620A-2081	Sequence 2081, Appl	
165	12	60.0	18	1	US-08-379-078-48	Sequence 48, Appl	c 237	11.8	59.0	38	3	US-09-071-845-2044	Sequence 2044, Appl	
166	12	60.0	18	1	US-08-379-078-49	Sequence 49, Appl	c 238	11.8	59.0	38	4	US-09-071-845-2081	Sequence 2081, Appl	
167	12	60.0	18	1	US-08-379-078-50	Sequence 50, Appl	c 239	11.8	59.0	38	4	US-09-672-609-46	Sequence 46, Appl	
168	12	60.0	18	1	US-08-379-078-51	Sequence 51, Appl	c 240	11.8	59.0	38	4	US-09-270-140A-74	Sequence 74, Appl	
169	12	60.0	18	1	US-08-379-078-52	Sequence 52, Appl	c 241	11.8	59.0	38	4	US-09-025-403A-46	Sequence 46, Appl	
170	12	60.0	18	1	US-08-379-078-53	Sequence 53, Appl	c 242	11.8	59.0	38	4	US-09-371-772B-7677	Sequence 7677, Appl	
171	12	60.0	18	1	US-08-379-078-54	Sequence 54, Appl	c 243	11.8	59.0	38	4	US-09-371-772B-8926	Sequence 8926, Appl	
172	12	60.0	18	1	US-08-379-078-55	Sequence 55, Appl	c 244	11.8	59.0	38	4	US-09-371-772B-9301	Sequence 9301, Appl	
173	12	60.0	18	1	US-08-379-078-56	Sequence 56, Appl	c 245	11.8	59.0	38	4	US-09-371-772B-9626	Sequence 9626, Appl	
174	12	60.0	18	1	US-08-379-078-55	Sequence 55, Appl	c 246	11.8	59.0	40	4	US-09-371-772B-10576	Sequence 10576, Appl	

247	11.8	59.0	40	4	US-09-672-609-48	Sequence 48, Appl	320	11.2	56.0	20	1	US-08-231-368-1	Sequence 1, Appli
248	11.8	59.0	40	4	US-09-025-403A-45	Sequence 45, Appl	321	11.2	56.0	20	1	US-08-440-210-1	Sequence 1, Appli
249	11.8	59.0	40	4	US-09-025-403A-48	Sequence 48, Appl	322	11.2	56.0	20	2	US-08-757-653-174	Sequence 174, Appl
250	11.6	58.0	18	4	US-09-422-978-4437	Sequence 4437, Ap	323	11.2	56.0	20	2	US-08-823-516-77	Sequence 77, Appl
251	11.6	58.0	20	4	US-08-469-260A-136	Sequence 136, App	324	11.2	56.0	20	3	US-08-759-038-113	Sequence 113, App
252	11.6	58.0	20	4	US-08-488-446-136	Sequence 136, App	325	11.2	56.0	20	3	US-08-758-314-113	Sequence 113, App
253	11.6	58.0	20	4	US-08-467-344A-136	Sequence 136, App	326	11.2	56.0	20	4	US-09-046-604-1	Sequence 1, Appli
254	11.6	58.0	21	3	US-08-255-889-13	Sequence 13, Appl	327	11.2	56.0	20	4	US-09-684-938-113	Sequence 113, App
255	11.6	58.0	21	3	US-08-876-078-3	Sequence 3, Appli	328	11.2	56.0	20	4	US-09-198-452A-3774	Sequence 3774, Ap
256	11.6	58.0	23	4	US-08-831-823-3	Sequence 3, Appli	329	11.2	56.0	20	4	US-09-308-825A-113	Sequence 113, App
257	11.6	58.0	24	4	US-08-936-107A-49	Sequence 49, Appl	330	11.2	56.0	21	3	US-09-027-130-9	Sequence 9, Appli
258	11.6	58.0	26	4	US-09-138-277C-13	Sequence 13, Appl	331	11.2	56.0	21	3	US-08-924-183-5	Sequence 5, Appli
259	11.6	58.0	26	4	US-09-538-709-457	Sequence 457, App	332	11.2	56.0	21	4	US-09-488-364-5	Sequence 5, Appli
260	11.6	58.0	26	1	US-08-479-852-44	Sequence 44, Appl	333	11.2	56.0	21	4	US-09-596-390-9	Sequence 9, Appli
261	11.6	58.0	27	1	US-08-479-852-124	Sequence 124, App	334	11.2	56.0	22	6	5225537-11	Patent No. 5225537
262	11.6	58.0	27	2	US-08-462-646-44	Sequence 44, Appl	335	11.2	56.0	25	3	US-09-441-346A-10	Sequence 10, Appl
263	11.6	58.0	27	2	US-08-462-646-124	Sequence 124, App	336	11.2	56.0	25	3	US-09-789-453A-10	Sequence 10, Appl
264	11.6	58.0	27	2	US-08-333-476-7	Sequence 7, Appli	337	11.2	56.0	25	4	US-08-993-228-31	Sequence 31, Appl
265	11.6	58.0	27	2	US-08-353-476-8	Sequence 8, Appli	338	11.2	56.0	32	5	PCT-US95-1198A-26	Sequence 26, Appl
266	11.6	58.0	27	3	US-09-013-406-44	Sequence 44, Appl	339	11.2	56.0	33	5	PCT-US95-15696-4	Sequence 4, Appli
267	11.6	58.0	27	3	US-09-013-406-124	Sequence 124, App	340	11.2	56.0	40	2	US-08-628-422-44	Sequence 44, Appl
268	11.6	58.0	28	3	US-08-968-563-40	Sequence 40, Appl	341	11.2	56.0	14	3	US-09-094-714A-67	Sequence 67, Appl
269	11.6	58.0	28	3	US-08-969-683A-40	Sequence 40, Appl	342	11.2	56.0	19	1	US-08-379-081B-127	Sequence 127, App
270	11.6	58.0	29	4	US-09-078-029-4	Sequence 4, Appli	343	11.2	56.0	19	1	US-08-379-081B-128	Sequence 128, App
271	11.6	58.0	29	4	US-08-928-069-14	Sequence 14, Appl	344	11.2	56.0	19	1	US-08-379-081B-135	Sequence 135, App
272	11.6	58.0	29	4	US-08-828-683A-10	Sequence 10, Appl	345	11.2	56.0	19	1	US-08-379-081B-139	Sequence 139, App
273	11.6	58.0	30	2	US-08-860-882A-30	Sequence 30, Appl	346	11.2	56.0	19	1	US-08-379-081B-144	Sequence 144, App
274	11.6	58.0	30	2	US-08-860-882A-32	Sequence 32, Appl	347	11.2	56.0	19	1	US-08-379-078-127	Sequence 127, App
275	11.6	58.0	33	2	US-08-484-397A-25	Sequence 25, Appl	348	11.2	56.0	19	1	US-08-379-078-128	Sequence 128, App
276	11.6	58.0	33	2	US-08-484-397A-26	Sequence 26, Appl	349	11.2	56.0	19	1	US-08-379-078-135	Sequence 135, App
277	11.6	58.0	34	4	US-08-483-816E-1C	Sequence 1C, Appl	350	11.2	56.0	19	1	US-08-379-078-139	Sequence 139, App
278	11.6	58.0	36	1	US-08-465-590-142	Sequence 142, App	351	11.2	56.0	19	1	US-08-379-078-144	Sequence 144, App
279	11.6	58.0	36	3	US-08-711-417C-142	Sequence 142, App	352	11.2	56.0	20	2	US-08-478-178A-116	Sequence 116, App
280	11.6	58.0	36	5	PCT-US93-08743-142	Sequence 142, App	353	11.2	56.0	20	2	US-08-488-177-116	Sequence 116, App
281	11.6	58.0	37	2	US-08-353-476-38	Sequence 38, Appl	354	11.2	56.0	20	2	US-08-481-072A-116	Sequence 116, App
282	11.6	58.0	38	2	US-08-607-519-2	Sequence 2, Appli	355	11.2	56.0	20	2	US-08-664-336-116	Sequence 116, App
283	11.6	58.0	39	1	US-08-450-257-43	Sequence 43, Appl	356	11.2	56.0	20	2	US-08-481-066A-116	Sequence 116, App
284	11.6	58.0	39	1	US-08-450-257-44	Sequence 44, Appl	357	11.2	56.0	20	2	US-08-578-615A-78	Sequence 78, Appl
285	11.6	58.0	39	1	US-08-450-246-43	Sequence 43, Appl	358	11.2	56.0	20	3	US-08-629-637A-116	Sequence 116, App
286	11.6	58.0	39	1	US-08-450-246-44	Sequence 44, Appl	359	11.2	56.0	20	4	US-10-025-139-116	Sequence 116, App
287	11.6	58.0	39	1	US-08-450-098-43	Sequence 43, Appl	360	11.2	56.0	20	5	PCT-US94-07770-78	Sequence 78, Appl
288	11.6	58.0	39	1	US-08-450-098-44	Sequence 44, Appl	361	11.2	56.0	23	3	US-09-012-198-1	Sequence 1, Appli
289	11.6	58.0	39	1	US-08-451-233-43	Sequence 43, Appl	362	11.2	56.0	23	4	US-09-187-289-7	Sequence 7, Appli
290	11.6	58.0	39	1	US-08-451-233-44	Sequence 44, Appl	363	11.2	56.0	23	4	US-09-187-289-8	Sequence 8, Appli
291	11.6	58.0	39	1	US-08-450-236-43	Sequence 43, Appl	364	11.2	56.0	24	4	US-09-297-269-6	Sequence 6, Appli
292	11.6	58.0	39	1	US-08-450-236-44	Sequence 44, Appl	365	11.2	56.0	24	4	US-09-297-269-7	Sequence 7, Appli
293	11.6	58.0	39	2	US-08-533-298-7	Sequence 7, Appli	366	11.2	56.0	25	4	US-09-538-709-353	Sequence 353, App
294	11.6	58.0	39	2	US-08-533-298-9	Sequence 9, Appli	367	11.2	56.0	25	4	US-08-073-103A-7	Sequence 7, Appli
295	11.6	58.0	39	4	US-08-235-403-43	Sequence 43, Appl	368	11.2	56.0	27	1	US-08-112-817C-3	Sequence 3, Appli
296	11.6	58.0	39	4	US-08-235-403-44	Sequence 44, Appl	369	11.2	56.0	27	1	US-08-443-341-7	Sequence 7, Appli
297	11.4	57.0	13	4	US-09-216-584-35	Sequence 35, Appl	370	11.2	56.0	27	3	US-08-354-679C-7	Sequence 7, Appli
298	11.4	57.0	14	4	US-08-535-249-64	Sequence 64, Appl	371	11.2	56.0	27	3	US-08-393-273E-7	Sequence 7, Appli
299	11.4	57.0	20	1	US-08-789-047-17	Sequence 17, Appl	372	11.2	56.0	27	4	US-08-584-040-71	Sequence 71, Appl
300	11.4	57.0	20	3	US-08-924-870A-17	Sequence 17, Appl	373	11.2	56.0	27	4	US-09-518-386B-20	Sequence 20, Appl
301	11.4	57.0	20	3	US-09-245-248B-35	Sequence 35, Appl	374	11.2	56.0	27	4	US-08-443-580F-7	Sequence 7, Appli
302	11.4	57.0	22	1	US-08-469-802B-46	Sequence 46, Appl	375	11.2	56.0	27	4	US-08-571-263-7	Sequence 7, Appli
303	11.4	57.0	22	2	US-08-267-803B-64	Sequence 64, Appl	376	11.2	56.0	27	5	PCT-US93-08157-7	Sequence 8, Appli
304	11.4	57.0	26	4	US-08-976-063E-43	Sequence 43, Appl	377	11.2	56.0	27	5	PCT-US95-04094-8	Sequence 8, Appli
305	11.4	57.0	28	4	US-09-101-272G-4	Sequence 4, Appli	378	11.2	56.0	28	3	US-09-309-317-16	Sequence 16, Appl
306	11.4	57.0	31	4	US-08-679-645-393	Sequence 393, App	379	11.2	56.0	28	3	US-08-274-608-6	Sequence 6, Appli
307	11.4	57.0	33	4	US-08-672-213-8	Sequence 8, Appli	380	11.2	56.0	29	4	US-08-771-190-6	Sequence 6, Appli
308	11.4	57.0	33	4	US-08-672-213-49	Sequence 49, Appl	381	11.2	56.0	29	5	PCT-US94-07955-6	Sequence 6, Appli
309	11.4	57.0	33	4	US-08-973-131-38	Sequence 38, Appl	382	11.2	56.0	30	1	US-08-384-708A-31	Sequence 31, Appl
310	11.4	57.0	33	4	US-09-481-620A-6	Sequence 6, Appli	383	11.2	56.0	30	1	US-08-384-708A-68	Sequence 68, Appl
311	11.4	57.0	36	2	US-08-17A-672D-34	Sequence 34, Appl	384	11.2	56.0	30	3	US-08-687-421-31	Sequence 31, Appl
312	11.4	57.0	36	3	US-09-230-222-22	Sequence 22, Appl	385	11.2	56.0	30	3	US-08-687-421-68	Sequence 68, Appl
313	11.4	57.0	36	4	US-09-230-225B-29	Sequence 29, Appl	386	11.2	56.0	30	3	US-09-142-334-8	Sequence 8, Appli
314	11.4	57.0	38	4	US-09-371-772B-9439	Sequence 9439, Ap	387	11.2	56.0	30	4	US-09-624-390-4	Sequence 4, Appli
315	11.4	57.0	38	4	US-09-371-772B-11432	Sequence 11432, A	388	11.2	56.0	30	4	US-09-648-569A-33	Sequence 33, Appl
316	11.4	57.0	39	6	5256648-34	Patent No. 5256648	389	11.2	56.0	30	4	US-09-648-569A-35	Sequence 35, Appl
317	11.2	56.0	19	4	US-09-422-978-6251	Sequence 6251, Ap	390	11.2	56.0	31	4	US-09-431-705-31	Sequence 31, Appl
318	11.2	56.0	20	1	US-08-440-103-1	Sequence 1, Appli	391	11.2	56.0	31	4	US-08-233-030-61	Sequence 61, Appl
319	11.2	56.0	20	1	US-08-440-542-1	Sequence 1, Appli	392	11.2	56.0	32	1		

C 393	11	55.0	33	2	US-08-917-456-5	Sequence 5, Appli	C 466	10.8	54.0	32	4	US-09-940-019-11	Sequence 11, Appli
C 394	11	55.0	33	3	US-09-229-804-5	Sequence 5, Appli	467	10.8	54.0	32	4	US-09-940-037A-10	Sequence 10, Appli
C 395	11	55.0	35	1	US-07-869-380B-15	Sequence 15, Appl	C 468	10.8	54.0	32	4	US-09-940-037A-11	Sequence 11, Appli
C 396	11	55.0	35	4	US-09-475-460A-12	Sequence 12, Appl	469	10.8	54.0	33	3	US-08-793-038-10	Sequence 10, Appli
C 397	11	55.0	35	4	US-09-748-061A-12	Sequence 12, Appl	470	10.8	54.0	33	3	US-09-139-762A-10	Sequence 10, Appli
C 398	11	55.0	36	1	US-08-225-22A-29	Sequence 29, Appl	471	10.8	54.0	34	3	US-08-574-396-19	Sequence 19, Appli
C 399	11	55.0	36	3	US-08-722-25B-29	Sequence 29, Appl	472	10.8	54.0	34	3	US-08-488-181-17	Sequence 17, Appli
C 400	11	55.0	36	5	PCT-US95-04468-29	Sequence 29, Appl	473	10.8	54.0	34	3	US-08-973-568-19	Sequence 19, Appli
C 401	11	55.0	37	1	US-08-468-700-17	Sequence 17, Appl	474	10.8	54.0	35	3	US-08-574-396-41	Sequence 41, Appli
C 402	11	55.0	37	2	US-08-704-706A-17	Sequence 17, Appl	475	10.8	54.0	35	3	US-08-973-568-41	Sequence 41, Appli
C 403	11	55.0	37	2	US-09-028-361A-17	Sequence 17, Appl	476	10.8	54.0	35	4	US-09-582-379-7	Sequence 7, Appli
C 404	11	55.0	37	3	US-08-985-659-17	Sequence 17, Appl	477	10.8	54.0	36	1	US-08-319-492B-558	Sequence 558, App
C 405	11	55.0	38	1	US-07-863-380B-16	Sequence 16, Appl	478	10.8	54.0	36	1	US-08-363-240A-371	Sequence 371, App
C 406	11	55.0	38	1	US-08-108-216-3	Sequence 3, Appli	479	10.8	54.0	36	1	US-08-363-240A-923	Sequence 923, App
C 407	11	55.0	38	3	US-09-109-063-16	Sequence 16, Appl	480	10.8	54.0	36	1	US-08-363-240A-962	Sequence 962, App
C 408	11	55.0	38	4	US-09-448-310-16	Sequence 16, Appl	481	10.8	54.0	36	1	US-08-311-486C-475	Sequence 475, App
C 409	11	55.0	38	4	US-09-371-772B-7189	Sequence 7189, Ap	482	10.8	54.0	36	2	US-08-292-620A-880	Sequence 880, App
C 410	11	55.0	40	2	US-08-425-684-38	Sequence 38, Appl	483	10.8	54.0	36	2	US-08-585-684B-1094	Sequence 1094, Ap
C 411	11	55.0	40	2	US-08-675-502-38	Sequence 38, Appl	484	10.8	54.0	36	2	US-08-585-684B-1095	Sequence 1095, Ap
C 412	11	55.0	40	3	US-08-448-446B-17	Sequence 17, Appl	485	10.8	54.0	36	2	US-08-585-684B-1548	Sequence 1548, Ap
C 413	11	55.0	40	4	US-09-245-802-38	Sequence 38, Appl	486	10.8	54.0	36	2	US-08-585-684B-2211	Sequence 2211, Ap
C 414	10.8	54.0	14	3	US-09-234-163-9	Sequence 9, Appli	487	10.8	54.0	36	2	US-08-585-684B-2408	Sequence 2408, Ap
C 415	10.8	54.0	14	3	US-08-901-379-9	Sequence 381, App	488	10.8	54.0	36	2	US-09-071-845-880	Sequence 880, App
C 416	10.8	54.0	15	1	US-08-313-492B-381	Sequence 382, App	489	10.8	54.0	36	3	US-09-038-073-1094	Sequence 1094, Ap
C 417	10.8	54.0	15	1	US-08-313-492B-382	Sequence 382, App	490	10.8	54.0	36	3	US-09-038-073-1095	Sequence 1095, Ap
C 418	10.8	54.0	15	1	US-08-313-492B-383	Sequence 10, Appl	491	10.8	54.0	36	3	US-09-038-073-1548	Sequence 1548, Ap
C 419	10.8	54.0	18	3	US-08-927-722-10	Sequence 10, Appl	492	10.8	54.0	36	3	US-09-038-073-2211	Sequence 2211, Ap
C 420	10.8	54.0	18	3	US-08-835-728D-50	Sequence 50, Appl	493	10.8	54.0	36	3	US-09-038-073-2408	Sequence 2408, Ap
C 421	10.8	54.0	18	3	US-08-154-364-35	Sequence 35, Appl	494	10.8	54.0	36	3	US-09-038-073-2409	Sequence 2409, Ap
C 422	10.8	54.0	18	3	US-09-490-558-50	Sequence 50, Appl	495	10.8	54.0	36	3	US-09-638-202A-26	Sequence 26, Appli
C 423	10.8	54.0	18	4	US-09-268-544B-28	Sequence 28, Appl	496	10.8	54.0	36	4	US-08-390-850-743	Sequence 743, App
C 424	10.8	54.0	18	4	US-09-378-069A-10	Sequence 10, Appl	497	10.8	54.0	38	1	US-08-373-124A-319	Sequence 319, App
C 425	10.8	54.0	20	2	US-08-790-374-3	Sequence 3, Appli	498	10.8	54.0	38	1	US-08-373-124A-575	Sequence 575, App
C 426	10.8	54.0	20	4	US-09-354-151-10	Sequence 10, Appl	499	10.8	54.0	38	1	US-08-373-124A-657	Sequence 657, App
C 427	10.8	54.0	20	4	US-09-679-299A-133	Sequence 133, App	500	10.8	54.0	38	1	US-08-373-124A-667	Sequence 667, App
C 428	10.8	54.0	21	1	US-08-399-986B-30	Sequence 30, Appl	501	10.8	54.0	38	1	US-08-373-124A-1342	Sequence 1342, Ap
C 429	10.8	54.0	21	1	US-08-493-754A-30	Sequence 30, Appl	502	10.8	54.0	38	1	US-08-373-124A-1716	Sequence 1716, Ap
C 430	10.8	54.0	21	2	US-08-687-080-170	Sequence 170, App	503	10.8	54.0	38	1	US-08-373-124A-1884	Sequence 1884, Ap
C 431	10.8	54.0	21	3	US-08-318-241-6	Sequence 45, Appl	504	10.8	54.0	38	1	US-08-435-634-743	Sequence 743, App
C 432	10.8	54.0	22	1	US-08-318-241-6	Sequence 6, Appli	505	10.8	54.0	38	1	US-08-435-628-319	Sequence 319, App
C 433	10.8	54.0	23	3	US-08-353-765-1	Sequence 2, Appli	506	10.8	54.0	38	1	US-08-435-628-575	Sequence 575, App
C 434	10.8	54.0	23	4	US-09-297-257-2	Sequence 2, Appli	507	10.8	54.0	38	1	US-08-435-628-657	Sequence 657, App
C 435	10.8	54.0	23	4	US-09-403-105-1	Sequence 1, Appli	508	10.8	54.0	38	1	US-08-435-628-667	Sequence 667, App
C 436	10.8	54.0	23	4	US-09-686-583B-61	Sequence 61, Appl	509	10.8	54.0	38	1	US-08-435-628-1342	Sequence 1342, Ap
C 437	10.8	54.0	24	1	US-08-166-160-13	Sequence 13, Appl	510	10.8	54.0	38	1	US-08-435-628-1716	Sequence 1716, Ap
C 438	10.8	54.0	24	3	US-09-050-159-92	Sequence 92, Appl	511	10.8	54.0	38	1	US-08-435-628-1884	Sequence 1884, Ap
C 439	10.8	54.0	26	1	US-08-429-121B-91	Sequence 91, Appl	512	10.8	54.0	38	1	US-08-292-620A-2068	Sequence 2068, Ap
C 440	10.8	54.0	26	2	US-09-003-067-91	Sequence 91, Appl	513	10.8	54.0	38	2	US-08-292-620A-2125	Sequence 2125, Ap
C 441	10.8	54.0	26	4	US-09-011-151-27	Sequence 27, Appl	514	10.8	54.0	38	3	US-09-071-845-2068	Sequence 2068, Ap
C 442	10.8	54.0	27	1	US-08-758-306-98	Sequence 98, Appl	515	10.8	54.0	38	3	US-09-071-845-2125	Sequence 2125, Ap
C 443	10.8	54.0	27	1	US-08-758-306-1034	Sequence 1034, Ap	516	10.8	54.0	38	4	US-09-371-772B-7386	Sequence 7386, Ap
C 444	10.8	54.0	27	3	US-08-985-162-921	Sequence 921, App	517	10.8	54.0	38	4	US-09-371-772B-7565	Sequence 7565, Ap
C 445	10.8	54.0	27	3	US-08-985-162-996	Sequence 996, App	518	10.8	54.0	38	4	US-09-371-772B-7666	Sequence 7666, Ap
C 446	10.8	54.0	27	3	US-08-985-162-1120	Sequence 1120, Ap	519	10.8	54.0	38	4	US-09-371-772B-7829	Sequence 7829, Ap
C 447	10.8	54.0	27	4	US-08-584-040-559	Sequence 559, App	520	10.8	54.0	38	4	US-09-371-772B-7891	Sequence 7891, Ap
C 448	10.8	54.0	27	4	US-08-584-040-3357	Sequence 3357, Ap	521	10.8	54.0	38	4	US-09-371-772B-8326	Sequence 8326, Ap
C 449	10.8	54.0	27	4	US-08-584-040-3732	Sequence 3732, Ap	522	10.8	54.0	38	4	US-09-371-772B-8779	Sequence 8779, Ap
C 450	10.8	54.0	27	4	US-08-584-040-4785	Sequence 4785, Ap	523	10.8	54.0	38	4	US-09-371-772B-9125	Sequence 9125, Ap
C 451	10.8	54.0	27	4	US-08-584-040-6713	Sequence 6713, Ap	524	10.8	54.0	38	4	US-09-371-772B-9793	Sequence 9793, Ap
C 452	10.8	54.0	27	4	US-08-679-645-968	Sequence 968, App	525	10.8	54.0	38	4	US-09-371-772B-9957	Sequence 9957, Ap
C 453	10.8	54.0	27	4	US-08-679-645-1050	Sequence 1050, Ap	526	10.8	54.0	38	4	US-09-371-772B-10348	Sequence 10348, A
C 454	10.8	54.0	27	4	US-08-679-645-1103	Sequence 1103, Ap	527	10.8	54.0	38	4	US-09-371-772B-10753	Sequence 10753, A
C 455	10.8	54.0	28	1	US-08-558-735-15	Sequence 15, Appl	528	10.8	54.0	38	4	US-09-371-772B-11585	Sequence 11585, A
C 456	10.8	54.0	28	3	US-08-906-480-15	Sequence 15, Appl	529	10.8	54.0	38	4	US-09-371-772B-11654	Sequence 11654, A
C 457	10.8	54.0	30	4	US-09-774-377-15	Sequence 15, Appl	530	10.8	54.0	38	4	US-09-371-772B-12215	Sequence 12215, A
C 458	10.8	54.0	30	4	US-09-425-585-11	Sequence 11, Appl	531	10.8	54.0	38	4	US-09-371-772B-12365	Sequence 12365, A
C 459	10.8	54.0	30	4	US-09-305-681-40	Sequence 40, Appl	532	10.8	54.0	38	4	US-09-371-772B-12520	Sequence 12520, A
C 460	10.8	54.0	30	4	US-09-305-681-42	Sequence 42, Appl	533	10.8	54.0	38	4	US-09-371-772B-12589	Sequence 12589, A
C 461	10.8	54.0	31	4	US-08-679-645-315	Sequence 315, App	534	10.8	54.0	38	4	US-09-371-772B-13375	Sequence 13375, A
C 462	10.8	54.0	31	4	US-09-686-583B-62	Sequence 62, Appl	535	10.8	54.0	38	4	US-09-371-772B-13579	Sequence 13579, A
C 463	10.8	54.0	32	4	US-09-468-738A-10	Sequence 10, Appl	536	10.8	54.0	38	4	US-09-371-772B-13736	Sequence 13736, A
C 464	10.8	54.0	32	4	US-09-468-738A-11	Sequence 11, Appl	537	10.8	54.0	38	4	US-09-371-772B-13815	Sequence 13815, A
C 465	10.8	54.0	32	4	US-09-940-019-10	Sequence 10, Appl	538	10.8	54.0	38	4		

539	10.8	54.0	38	4	US-09-371-772B-13842	Sequence 13842, A	612	10.6	53.0	32	1	US-08-391-339-24	Sequence 24, Appl
540	10.8	54.0	39	1	US-08-592-126-39	Sequence 39, Appl	613	10.6	53.0	32	1	US-08-391-339-25	Sequence 25, Appl
541	10.8	54.0	39	2	US-08-687-080-39	Sequence 39, Appl	614	10.6	53.0	32	1	US-08-484-274A-24	Sequence 24, Appl
542	10.8	54.0	39	2	US-08-687-080-39	Sequence 39, Appl	615	10.6	53.0	32	1	US-08-484-274A-25	Sequence 25, Appl
543	10.8	54.0	39	4	US-09-168-595-39	Sequence 39, Appl	616	10.6	53.0	32	5	PCT-US95-11985A-27	Sequence 27, Appl
544	10.8	54.0	40	1	US-08-344-820-4	Sequence 4, Appl	617	10.6	53.0	32	5	PCT-US95-11985A-28	Sequence 28, Appl
545	10.6	53.0	17	3	US-08-985-162-520	Sequence 520, App	618	10.6	53.0	32	5	PCT-US95-11985A-41	Sequence 41, Appl
546	10.6	53.0	17	4	US-09-371-772B-4651	Sequence 4551, Ap	619	10.6	53.0	33	1	US-07-771-022F-15	Sequence 15, Appl
547	10.6	53.0	18	1	US-07-929-119A-13	Sequence 13, Appl	620	10.6	53.0	33	1	US-08-242-098-6	Sequence 6, Appl
548	10.6	53.0	18	3	US-08-154-364-39	Sequence 19, Appl	621	10.6	53.0	33	4	US-09-713-678-20	Sequence 20, Appl
549	10.6	53.0	19	4	US-09-422-978-7411	Sequence 7411, Ap	622	10.6	53.0	34	3	US-09-358-972-232	Sequence 232, App
550	10.6	53.0	20	4	US-09-138-452A-6189	Sequence 6189, Ap	623	10.6	53.0	34	3	US-09-358-972-234	Sequence 234, App
551	10.6	53.0	21	1	US-08-379-078-507	Sequence 507, App	624	10.6	53.0	34	3	US-09-430-615-22	Sequence 22, Appl
552	10.6	53.0	21	2	US-08-702-105A-39	Sequence 39, Appl	625	10.6	53.0	34	3	US-09-430-615-24	Sequence 24, Appl
553	10.6	53.0	21	3	US-08-702-110A-39	Sequence 39, Appl	626	10.6	53.0	34	5	PCT-US95-11985A-42	Sequence 42, Appl
554	10.6	53.0	21	3	US-09-009-913-157	Sequence 157, App	627	10.6	53.0	35	4	US-09-813-781-125	Sequence 125, App
555	10.6	53.0	21	3	US-09-325-571-39	Sequence 39, Appl	628	10.6	53.0	36	1	US-08-403-762A-161	Sequence 161, App
556	10.6	53.0	21	4	US-07-974-409C-121	Sequence 121, App	629	10.6	53.0	36	1	US-08-403-762A-165	Sequence 165, App
557	10.6	53.0	21	5	PCT-US93-00977-121	Sequence 121, App	630	10.6	53.0	36	5	PCT-US95-11985A-43	Sequence 43, Appl
558	10.6	53.0	22	1	US-08-180-195-32	Sequence 32, Appl	631	10.6	53.0	38	1	US-08-485-971-11	Sequence 11, Appl
559	10.6	53.0	22	1	US-08-477-329-39	Sequence 32, Appl	632	10.6	53.0	38	1	US-08-275-876-11	Sequence 11, Appl
560	10.6	53.0	22	2	US-08-475-458-32	Sequence 32, Appl	633	10.6	53.0	38	1	US-08-383-754-11	Sequence 11, Appl
561	10.6	53.0	22	3	US-08-980-400-32	Sequence 32, Appl	634	10.6	53.0	38	1	US-08-485-978-11	Sequence 11, Appl
562	10.6	53.0	22	3	US-09-032-077-60	Sequence 60, Appl	635	10.6	53.0	38	2	US-08-486-814-11	Sequence 11, Appl
563	10.6	53.0	22	3	US-09-583-459A-32	Sequence 32, Appl	636	10.6	53.0	38	2	US-08-487-472-11	Sequence 11, Appl
564	10.6	53.0	22	4	US-09-583-210-32	Sequence 32, Appl	637	10.6	53.0	38	3	US-08-485-740-11	Sequence 11, Appl
565	10.6	53.0	22	4	US-09-583-449A-32	Sequence 32, Appl	638	10.6	53.0	38	3	US-09-162-184-11	Sequence 11, Appl
566	10.6	53.0	22	4	US-09-435-059-32	Sequence 32, Appl	639	10.6	53.0	38	3	US-09-161-902-11	Sequence 11, Appl
567	10.6	53.0	23	1	US-08-219-842-4	Sequence 4, Appl	640	10.6	53.0	38	3	US-09-489-777A-11	Sequence 11, Appl
568	10.6	53.0	23	1	US-08-451-096-4	Sequence 4, Appl	641	10.6	53.0	38	5	PCT-US95-08179-11	Sequence 11, Appl
569	10.6	53.0	23	2	US-08-810-599-27	Sequence 27, Appl	642	10.6	53.0	39	3	US-09-052-797-1	Sequence 1, Appl
570	10.6	53.0	23	3	US-08-413-740A-132	Sequence 132, App	643	10.4	52.0	17	1	US-08-332-453-3	Sequence 3, Appl
571	10.6	53.0	23	5	PCT-US95-04063-132	Sequence 132, App	644	10.4	52.0	17	1	US-08-373-124A-1615	Sequence 1615, Ap
572	10.6	53.0	24	1	US-08-685-764-11	Sequence 11, Appl	645	10.4	52.0	17	1	US-08-616-398-14	Sequence 14, Appl
573	10.6	53.0	24	3	US-08-486-857-1	Sequence 1, Appl	646	10.4	52.0	17	1	US-08-435-628-1615	Sequence 1615, Ap
574	10.6	53.0	24	3	US-08-513-974B-221	Sequence 11, Appl	647	10.4	52.0	17	4	US-08-584-040-8095	Sequence 8095, Ap
575	10.6	53.0	24	3	US-08-724-752-18	Sequence 18, Appl	648	10.4	52.0	17	4	US-09-371-772B-3878	Sequence 3878, Ap
576	10.6	53.0	24	5	PCT-US95-11985A-22	Sequence 22, Appl	649	10.4	52.0	18	2	US-08-359-705B-38	Sequence 38, Appl
577	10.6	53.0	24	5	PCT-US95-11985A-23	Sequence 23, Appl	650	10.4	52.0	18	2	US-08-286-846A-38	Sequence 38, Appl
578	10.6	53.0	24	5	PCT-US95-11985A-24	Sequence 24, Appl	651	10.4	52.0	18	2	US-08-457-880A-38	Sequence 38, Appl
579	10.6	53.0	24	5	PCT-US95-11985A-25	Sequence 25, Appl	652	10.4	52.0	18	2	US-08-927-722-9	Sequence 9, Appl
580	10.6	53.0	24	5	PCT-US95-11985A-34	Sequence 34, Appl	653	10.4	52.0	18	3	US-09-161-244-50	Sequence 50, Appl
581	10.6	53.0	24	5	PCT-US95-11985A-35	Sequence 35, Appl	654	10.4	52.0	18	3	US-08-444-622A-38	Sequence 38, Appl
582	10.6	53.0	25	1	US-07-771-022F-5	Sequence 5, Appl	655	10.4	52.0	18	3	US-09-156-923-38	Sequence 38, Appl
583	10.6	53.0	25	1	US-08-122-433-8	Sequence 8, Appl	656	10.4	52.0	18	3	US-08-964-877-4	Sequence 4, Appl
584	10.6	53.0	26	5	PCT-US95-11985A-36	Sequence 36, Appl	657	10.4	52.0	18	3	US-08-154-364-33	Sequence 33, Appl
585	10.6	53.0	27	1	US-08-137-117D-54	Sequence 54, Appl	658	10.4	52.0	18	3	US-08-154-364-34	Sequence 34, Appl
586	10.6	53.0	27	1	US-08-436-717-54	Sequence 54, Appl	659	10.4	52.0	18	4	US-09-721-822A-111	Sequence 111, App
587	10.6	53.0	28	5	PCT-US95-11985A-37	Sequence 37, Appl	660	10.4	52.0	18	4	US-09-378-069A-9	Sequence 9, Appl
588	10.6	53.0	29	1	US-07-805-567-24	Sequence 24, Appl	661	10.4	52.0	18	4	US-09-422-978-5504	Sequence 5504, Ap
589	10.6	53.0	29	1	US-08-105-483-106	Sequence 106, App	662	10.4	52.0	20	1	US-08-202-042-4	Sequence 4, Appl
590	10.6	53.0	29	1	US-08-220-151-63	Sequence 63, Appl	663	10.4	52.0	20	2	US-08-447-430A-19	Sequence 19, Appl
591	10.6	53.0	29	1	US-08-413-118-63	Sequence 63, Appl	664	10.4	52.0	20	2	US-08-447-430A-20	Sequence 20, Appl
592	10.6	53.0	29	1	US-08-224-657-40	Sequence 40, Appl	665	10.4	52.0	20	3	US-08-777-266A-42	Sequence 42, Appl
593	10.6	53.0	29	1	US-08-709-209-106	Sequence 106, App	666	10.4	52.0	20	3	US-09-290-640-9	Sequence 9, Appl
594	10.6	53.0	29	1	US-08-458-101-106	Sequence 106, App	667	10.4	52.0	20	4	US-09-326-186B-42	Sequence 42, Appl
595	10.6	53.0	29	2	US-08-184-009-39	Sequence 39, Appl	668	10.4	52.0	20	4	US-09-920-672-36	Sequence 36, Appl
596	10.6	53.0	29	2	US-08-486-963-28	Sequence 28, Appl	669	10.4	52.0	20	4	US-09-342-673-19	Sequence 19, Appl
597	10.6	53.0	29	2	US-08-417-210A-39	Sequence 39, Appl	670	10.4	52.0	20	4	US-09-342-673-20	Sequence 20, Appl
598	10.6	53.0	29	2	US-08-458-356-39	Sequence 39, Appl	671	10.4	52.0	20	4	US-09-422-978-10396	Sequence 10396, A
599	10.6	53.0	29	2	US-08-471-025-28	Sequence 28, Appl	672	10.4	52.0	20	4	US-09-508-264A-5	Sequence 5, Appl
600	10.6	53.0	29	2	US-08-658-665-28	Sequence 28, Appl	673	10.4	52.0	21	3	US-08-755-587-144	Sequence 144, App
601	10.6	53.0	29	3	US-08-473-446-63	Sequence 63, Appl	674	10.4	52.0	21	4	US-09-091-952A-18	Sequence 18, Appl
602	10.6	53.0	29	3	US-08-460-736-39	Sequence 39, Appl	675	10.4	52.0	21	4	US-09-422-978-10785	Sequence 10785, A
603	10.6	53.0	29	3	US-09-085-273-28	Sequence 28, Appl	676	10.4	52.0	22	1	US-08-156-792-3	Sequence 3, Appl
604	10.6	53.0	29	4	US-09-354-138-40	Sequence 40, Appl	677	10.4	52.0	22	1	US-08-156-792-7	Sequence 7, Appl
605	10.6	53.0	29	4	US-09-197-814-8	Sequence 8, Appl	678	10.4	52.0	22	1	US-08-729-447-13	Sequence 13, Appl
606	10.6	53.0	29	4	US-09-535-370-39	Sequence 39, Appl	679	10.4	52.0	23	2	US-08-674-149A-6	Sequence 6, Appl
607	10.6	53.0	29	4	US-09-920-581-8	Sequence 8, Appl	680	10.4	52.0	23	4	US-09-351-150A-53	Sequence 53, Appl
608	10.6	53.0	29	5	PCT-US96-00547-28	Sequence 28, Appl	681	10.4	52.0	24	1	US-08-052-404-4	Sequence 4, Appl
609	10.6	53.0	30	5	PCT-US95-11985A-38	Sequence 38, Appl	682	10.4	52.0	24	1	US-08-479-156-4	Sequence 4, Appl
610	10.6	53.0	30	5	PCT-US95-11985A-39	Sequence 39, Appl	683	10.4	52.0	24	2	US-08-481-793-22	Sequence 22, Appl
611	10.6	53.0	31	4	US-09-624-390-7	Sequence 7, Appl	684	10.4	52.0	24	2	US-08-354-326-22	Sequence 22, Appl

c 685	10.4	52.0	24	2	US-08-859-998-943	Sequence 943, App	758	10.4	52.0	37	3	US-08-973-124-178	Sequence 178, App
c 686	10.4	52.0	24	4	US-09-225-928-943	Sequence 943, App	759	10.4	52.0	37	3	US-08-973-124-179	Sequence 179, App
c 687	10.4	52.0	24	4	US-09-225-201B-943	Sequence 943, App	760	10.4	52.0	37	3	US-08-973-124-180	Sequence 180, App
c 688	10.4	52.0	24	4	US-09-922-146-5	Sequence 5, Appl	761	10.4	52.0	37	3	US-08-973-124-181	Sequence 181, App
c 689	10.4	52.0	24	5	PCT-US95-07068-22	Sequence 22, Appl	762	10.4	52.0	37	3	US-08-973-124-182	Sequence 182, App
c 690	10.4	52.0	24	5	US-08-702-344-37	Sequence 37, Appl	763	10.4	52.0	37	3	US-08-973-124-183	Sequence 183, App
c 691	10.4	52.0	26	1	US-08-859-998-1138	Sequence 1138, Ap	764	10.4	52.0	37	3	US-08-973-124-184	Sequence 184, App
c 692	10.4	52.0	26	2	US-08-859-998-1138	Sequence 1138, Ap	765	10.4	52.0	37	3	US-08-991-743C-89	Sequence 89, Appl
c 693	10.4	52.0	26	4	US-09-343-494-6	Sequence 1138, Ap	766	10.4	52.0	37	3	US-08-991-743C-90	Sequence 90, Appl
c 694	10.4	52.0	26	4	US-09-343-494-6	Sequence 1138, Ap	767	10.4	52.0	37	3	US-08-991-743C-91	Sequence 91, Appl
c 695	10.4	52.0	26	4	US-09-225-201B-1138	Sequence 1138, Ap	768	10.4	52.0	37	3	US-08-991-743C-92	Sequence 92, Appl
c 696	10.4	52.0	27	1	US-07-938-334C-15	Sequence 15, Appl	769	10.4	52.0	37	3	US-08-991-743C-93	Sequence 93, Appl
c 697	10.4	52.0	27	1	US-08-443-341-6	Sequence 6, Appl	770	10.4	52.0	37	3	US-08-991-743C-94	Sequence 94, Appl
c 698	10.4	52.0	27	1	US-08-443-341-6	Sequence 6, Appl	771	10.4	52.0	37	3	US-08-991-743C-95	Sequence 95, Appl
c 699	10.4	52.0	27	3	US-08-985-162-931	Sequence 931, App	772	10.4	52.0	37	3	US-08-851-486-89	Sequence 89, Appl
c 700	10.4	52.0	27	3	US-08-985-162-931	Sequence 931, App	773	10.4	52.0	37	3	US-08-851-486-90	Sequence 90, Appl
c 701	10.4	52.0	27	3	US-08-513-974B-284	Sequence 284, App	774	10.4	52.0	37	3	US-08-991-743C-92	Sequence 92, Appl
c 702	10.4	52.0	27	3	US-08-393-273E-6	Sequence 6, Appl	775	10.4	52.0	37	3	US-08-991-743C-93	Sequence 93, Appl
c 703	10.4	52.0	27	4	US-09-142-623-26	Sequence 26, Appl	776	10.4	52.0	37	3	US-08-991-743C-94	Sequence 94, Appl
c 704	10.4	52.0	27	4	US-08-584-040-4587	Sequence 4587, Ap	777	10.4	52.0	37	3	US-08-851-486-94	Sequence 94, Appl
c 705	10.4	52.0	27	4	US-08-584-040-4587	Sequence 4587, Ap	778	10.4	52.0	37	3	US-08-851-486-95	Sequence 95, Appl
c 706	10.4	52.0	27	4	US-08-443-580F-6	Sequence 4589, Ap	779	10.4	52.0	37	3	PCT-US96-08014-178	Sequence 178, App
c 707	10.4	52.0	27	4	US-09-545-686-7	Sequence 7, Appl	780	10.4	52.0	37	3	PCT-US96-08014-179	Sequence 179, App
c 708	10.4	52.0	27	4	US-08-571-263-6	Sequence 6, Appl	781	10.4	52.0	37	3	PCT-US96-08014-180	Sequence 180, App
c 709	10.4	52.0	27	5	PCT-US93-08157-6	Sequence 6, Appl	782	10.4	52.0	37	3	PCT-US96-08014-181	Sequence 181, App
c 710	10.4	52.0	28	4	US-09-142-623-15	Sequence 15, Appl	783	10.4	52.0	37	3	PCT-US96-08014-182	Sequence 182, App
c 711	10.4	52.0	29	1	US-08-452-633A-23	Sequence 23, Appl	784	10.4	52.0	37	3	PCT-US96-08014-183	Sequence 183, App
c 712	10.4	52.0	29	1	US-08-456-460C-23	Sequence 23, Appl	785	10.4	52.0	37	3	PCT-US96-08014-184	Sequence 184, App
c 713	10.4	52.0	29	3	US-08-574-396-33	Sequence 33, Appl	786	10.4	52.0	38	1	US-08-479-783A-83	Sequence 83, Appl
c 714	10.4	52.0	29	3	US-08-488-181-31	Sequence 31, Appl	787	10.4	52.0	38	1	US-08-479-783A-83	Sequence 83, Appl
c 715	10.4	52.0	29	3	US-08-973-568-33	Sequence 33, Appl	788	10.4	52.0	38	1	US-08-618-693A-2241	Sequence 2241, Ap
c 716	10.4	52.0	29	4	US-09-348-930A-10	Sequence 10, Appl	789	10.4	52.0	38	2	US-08-292-620A-8231	Sequence 8231, Ap
c 717	10.4	52.0	31	3	PCT-US94-05354-23	Sequence 23, Appl	790	10.4	52.0	38	2	US-09-157-206-1	Sequence 1, Appl
c 718	10.4	52.0	31	4	US-08-679-645-317	Sequence 317, App	791	10.4	52.0	38	3	US-09-447-863-1	Sequence 1, Appl
c 719	10.4	52.0	33	1	US-08-479-783A-84	Sequence 84, Appl	792	10.4	52.0	38	3	US-08-973-124-172	Sequence 172, App
c 720	10.4	52.0	33	1	US-08-479-783A-84	Sequence 84, Appl	793	10.4	52.0	38	3	US-08-991-743C-83	Sequence 83, Appl
c 721	10.4	52.0	33	1	US-08-438-639-21	Sequence 21, Appl	794	10.4	52.0	38	3	US-09-581-326-1	Sequence 1, Appl
c 722	10.4	52.0	33	1	US-07-813-338A-21	Sequence 21, Appl	795	10.4	52.0	38	3	US-09-907-074A-1	Sequence 1, Appl
c 723	10.4	52.0	33	3	US-08-441-971-96	Sequence 96, Appl	796	10.4	52.0	38	4	US-09-371-772B-9502	Sequence 9502, Ap
c 724	10.4	52.0	33	3	US-08-221-653-96	Sequence 96, Appl	797	10.4	52.0	38	4	US-09-371-772B-9534	Sequence 9534, Ap
c 725	10.4	52.0	33	3	US-08-442-144A-96	Sequence 96, Appl	798	10.4	52.0	38	4	US-09-371-772B-10272	Sequence 10272, A
c 726	10.4	52.0	33	3	US-09-155-107-47	Sequence 47, Appl	799	10.4	52.0	38	4	US-09-371-772B-10455	Sequence 10455, A
c 727	10.4	52.0	33	4	US-08-441-970-96	Sequence 96, Appl	800	10.4	52.0	38	4	US-09-371-772B-11686	Sequence 11686, A
c 728	10.4	52.0	33	4	US-09-246-461-1	Sequence 1, Appl	801	10.4	52.0	38	4	US-09-371-772B-11686	Sequence 11686, A
c 729	10.4	52.0	35	3	US-08-300-928C-49	Sequence 49, Appl	802	10.4	52.0	38	4	US-09-851-486-83	Sequence 83, Appl
c 730	10.4	52.0	35	3	US-08-430-944D-49	Sequence 49, Appl	803	10.4	52.0	38	5	PCT-US96-08014-172	Sequence 172, App
c 731	10.4	52.0	35	3	US-08-430-944D-49	Sequence 49, Appl	804	10.4	52.0	40	2	US-08-553-339-9	Sequence 9, Appl
c 732	10.4	52.0	35	3	US-08-431-184-49	Sequence 49, Appl	805	10.4	52.0	40	2	US-09-061-542-9	Sequence 9, Appl
c 733	10.4	52.0	35	3	US-08-431-184-49	Sequence 49, Appl	806	10.2	51.0	17	1	US-08-206-384-2	Sequence 2, Appl
c 734	10.4	52.0	36	1	US-08-291-932A-530	Sequence 530, App	807	10.2	51.0	17	3	US-08-752-722-2	Sequence 2, Appl
c 735	10.4	52.0	36	1	US-08-291-932A-733	Sequence 733, App	808	10.2	51.0	17	3	US-09-371-772B-5389	Sequence 5389, Ap
c 736	10.4	52.0	36	1	US-08-363-240A-456	Sequence 456, App	809	10.2	51.0	18	3	US-09-010-310-1	Sequence 1, Appl
c 737	10.4	52.0	36	1	US-08-363-240A-774	Sequence 774, App	810	10.2	51.0	18	3	US-09-461-697-278	Sequence 278, App
c 738	10.4	52.0	36	1	US-08-363-240A-775	Sequence 775, App	811	10.2	51.0	19	1	US-08-222-177A-78	Sequence 78, Appl
c 739	10.4	52.0	36	1	US-08-363-240A-900	Sequence 900, App	812	10.2	51.0	19	1	US-08-245-742A-5	Sequence 5, Appl
c 740	10.4	52.0	36	2	US-08-363-240A-979	Sequence 979, App	813	10.2	51.0	19	1	US-08-701-380-8	Sequence 8, Appl
c 741	10.4	52.0	36	2	US-08-292-620A-1464	Sequence 1464, Ap	814	10.2	51.0	19	1	US-08-465-483-5	Sequence 5, Appl
c 742	10.4	52.0	36	2	US-08-585-684B-425	Sequence 425, App	815	10.2	51.0	19	3	US-09-033-365A-42	Sequence 42, Appl
c 743	10.4	52.0	36	2	US-08-585-684B-2188	Sequence 2188, Ap	816	10.2	51.0	19	3	US-08-876-996-5	Sequence 5, Appl
c 744	10.4	52.0	36	3	US-09-071-845-1464	Sequence 1464, Ap	817	10.2	51.0	19	4	US-09-649-747A-72	Sequence 72, Appl
c 745	10.4	52.0	36	3	US-09-038-073-425	Sequence 425, App	818	10.2	51.0	19	4	US-09-422-978-4908	Sequence 4908, Ap
c 746	10.4	52.0	36	3	US-09-038-073-2188	Sequence 2188, Ap	819	10.2	51.0	19	4	US-09-422-978-8025	Sequence 8025, Ap
c 747	10.4	52.0	36	3	US-09-581-326-10	Sequence 10, Appl	820	10.2	51.0	19	4	US-09-536-393-9	Sequence 9, Appl
c 748	10.4	52.0	36	3	US-08-973-568-46	Sequence 46, Appl	821	10.2	51.0	19	5	PCT-US94-05700-5	Sequence 5, Appl
c 749	10.4	52.0	36	4	US-09-212-609B-27	Sequence 27, Appl	822	10.2	51.0	20	3	US-09-135-021-34	Sequence 34, Appl
c 750	10.4	52.0	36	4	US-09-307-074A-10	Sequence 10, Appl	823	10.2	51.0	20	3	US-09-358-683-39	Sequence 39, Appl
c 751	10.4	52.0	37	1	US-08-618-693-89	Sequence 89, Appl	824	10.2	51.0	20	3	US-09-135-020-36	Sequence 36, Appl
c 752	10.4	52.0	37	1	US-08-618-693-90	Sequence 90, Appl	825	10.2	51.0	20	3	US-09-135-010A-36	Sequence 36, Appl
c 753	10.4	52.0	37	1	US-08-618-693-91	Sequence 91, Appl	826	10.2	51.0	20	4	US-09-444-871-36	Sequence 36, Appl
c 754	10.4	52.0	37	1	US-08-618-693-92	Sequence 92, Appl	827	10.2	51.0	20	4	US-09-472-364-4	Sequence 4, Appl
c 755	10.4	52.0	37	1	US-08-618-693-93	Sequence 93, Appl	828	10.2	51.0	20	4	US-09-597-735-36	Sequence 36, Appl
c 756	10.4	52.0	37	1	US-08-618-693-94	Sequence 94, Appl	829	10.2	51.0	20	4	US-09-444-295-36	Sequence 36, Appl
c 757	10.4	52.0	37	1	US-08-618-693-95	Sequence 95, Appl	830	10.2	51.0	20	4	US-09-597-732-36	Sequence 36, Appl

831	10.2	51.0	20	4	US-09-422-978-7330	Sequence 7330, Ap	904	10.2	51.0	30	2	US-08-962-284-18	Sequence 18, Appl
832	10.2	51.0	20	4	US-09-198-452A-1816	Sequence 1816, Ap	905	10.2	51.0	30	3	US-08-978-741-13	Sequence 13, Appl
c 833	10.2	51.0	20	4	US-09-198-452A-5622	Sequence 5622, Ap	906	10.2	51.0	30	3	US-09-333-729A-11	Sequence 11, Appl
834	10.2	51.0	20	4	US-09-597-731-36	Sequence 36, Appl	c 907	10.2	51.0	30	4	US-09-341-007B-12	Sequence 12, Appl
835	10.2	51.0	20	5	PCT-US96-01008-7	Sequence 7, Appli	908	10.2	51.0	30	4	US-09-281-495-37	Sequence 37, Appl
c 836	10.2	51.0	21	1	US-08-378-078-513	Sequence 513, App	c 909	10.2	51.0	31	1	US-07-796-106-24	Sequence 24, Appl
c 837	10.2	51.0	21	1	US-08-378-078-514	Sequence 514, App	c 910	10.2	51.0	31	1	US-08-070-517-4	Sequence 4, Appli
c 838	10.2	51.0	21	1	US-08-378-078-515	Sequence 515, App	c 911	10.2	51.0	32	2	US-08-797-366-6	Sequence 6, Appli
839	10.2	51.0	21	1	US-08-443-642-4	Sequence 4, Appli	c 912	10.2	51.0	32	2	US-08-956-268-6	Sequence 6, Appli
840	10.2	51.0	21	3	US-08-997-211-4	Sequence 4, Appli	913	10.2	51.0	32	3	US-08-884-324-33	Sequence 33, Appl
c 841	10.2	51.0	21	3	US-09-273-565-86	Sequence 86, Appl	914	10.2	51.0	32	3	US-08-884-324-33	Sequence 33, Appl
c 842	10.2	51.0	21	4	US-07-974-409C-20	Sequence 20, Appl	c 915	10.2	51.0	32	3	US-08-845-546-8	Sequence 8, Appli
c 843	10.2	51.0	21	4	US-07-974-409C-127	Sequence 127, App	c 916	10.2	51.0	33	1	US-08-653-648A-56	Sequence 56, Appl
c 844	10.2	51.0	21	4	US-07-974-409C-128	Sequence 128, App	917	10.2	51.0	34	1	US-08-585-682-12	Sequence 12, Appl
c 845	10.2	51.0	21	4	US-07-974-409C-129	Sequence 129, App	918	10.2	51.0	34	1	US-08-585-682-13	Sequence 13, Appl
c 846	10.2	51.0	21	4	US-09-565-538-86	Sequence 86, Appl	919	10.2	51.0	34	1	US-08-585-682-15	Sequence 15, Appl
847	10.2	51.0	21	4	US-09-608-285A-10	Sequence 10, Appl	920	10.2	51.0	34	2	US-08-363-253-19	Sequence 19, Appl
c 848	10.2	51.0	21	4	US-09-661-468-86	Sequence 86, Appl	921	10.2	51.0	34	2	US-08-989-394-14	Sequence 14, Appl
849	10.2	51.0	21	4	US-09-350-836B-10	Sequence 10, Appl	922	10.2	51.0	34	3	US-08-081-180-14	Sequence 14, Appl
850	10.2	51.0	21	4	US-09-370-285-10	Sequence 10, Appl	923	10.2	51.0	34	3	US-09-040-786-14	Sequence 14, Appl
851	10.2	51.0	21	4	US-09-557-800C-10	Sequence 10, Appl	924	10.2	51.0	34	3	US-09-182-975-19	Sequence 19, Appl
852	10.2	51.0	21	4	US-09-132-368-13	Sequence 13, Appl	925	10.2	51.0	34	3	US-09-271-365-14	Sequence 14, Appl
c 853	10.2	51.0	21	4	US-09-976-165-86	Sequence 86, Appl	c 926	10.2	51.0	34	3	US-08-974-549A-473	Sequence 473, App
c 854	10.2	51.0	21	5	PCT-US93-00977-20	Sequence 20, Appl	927	10.2	51.0	34	4	US-05-628-959-14	Sequence 14, Appl
c 855	10.2	51.0	21	5	PCT-US93-00977-127	Sequence 127, App	928	10.2	51.0	34	4	US-03-604-013A-14	Sequence 14, Appl
c 856	10.2	51.0	21	5	PCT-US93-00977-128	Sequence 128, App	c 929	10.2	51.0	34	4	US-08-912-951-240	Sequence 240, App
857	10.2	51.0	21	5	PCT-US93-00977-129	Sequence 129, App	930	10.2	51.0	34	4	US-10-041-614-14	Sequence 14, Appl
858	10.2	51.0	21	6	5175147-2	Patent No. 5175147	931	10.2	51.0	36	1	US-08-311-760A-123	Sequence 123, App
859	10.2	51.0	21	6	5175147-16	Patent No. 5175147	932	10.2	51.0	36	1	US-08-311-760A-125	Sequence 125, App
860	10.2	51.0	21	6	5314872-5	Patent No. 5314872	933	10.2	51.0	36	1	US-08-311-760A-143	Sequence 143, App
861	10.2	51.0	21	6	5464943-32	Patent No. 5464943	934	10.2	51.0	36	1	US-08-311-760A-263	Sequence 263, App
c 862	10.2	51.0	22	2	US-08-534-479-5	Sequence 5, Appli	935	10.2	51.0	36	1	US-08-319-492B-228	Sequence 228, App
863	10.2	51.0	22	4	US-09-556-601-16	Sequence 16, Appl	936	10.2	51.0	36	1	US-08-319-492B-575	Sequence 575, App
c 864	10.2	51.0	23	2	US-08-809-297-23	Sequence 23, Appl	937	10.2	51.0	36	1	US-08-319-492B-575	Sequence 576, App
865	10.2	51.0	23	2	US-08-859-998-498	Sequence 498, App	938	10.2	51.0	36	1	US-08-373-124A-2625	Sequence 2625, Ap
866	10.2	51.0	23	3	US-08-513-974B-217	Sequence 217, App	939	10.2	51.0	36	1	US-08-291-932A-446	Sequence 446, App
867	10.2	51.0	23	4	US-09-225-928-498	Sequence 498, App	940	10.2	51.0	36	1	US-08-291-932A-478	Sequence 478, App
868	10.2	51.0	23	4	US-09-225-201B-498	Sequence 498, App	941	10.2	51.0	36	1	US-08-291-932A-486	Sequence 486, App
869	10.2	51.0	24	3	US-08-513-974B-229	Sequence 229, App	942	10.2	51.0	36	1	US-08-291-932A-667	Sequence 667, App
870	10.2	51.0	25	1	US-08-479-852-46	Sequence 46, Appl	943	10.2	51.0	36	1	US-08-291-932A-675	Sequence 675, App
871	10.2	51.0	25	1	US-08-479-852-126	Sequence 126, App	944	10.2	51.0	36	1	US-08-291-932A-676	Sequence 676, App
872	10.2	51.0	25	1	US-07-724-500B-18	Sequence 18, Appl	945	10.2	51.0	36	1	US-08-334-847-768	Sequence 768, App
873	10.2	51.0	25	2	US-08-462-646-46	Sequence 46, Appl	946	10.2	51.0	36	1	US-08-363-240A-373	Sequence 373, App
874	10.2	51.0	25	2	US-08-462-646-126	Sequence 126, App	947	10.2	51.0	36	1	US-08-363-240A-474	Sequence 474, App
875	10.2	51.0	25	2	US-08-629-001A-137	Sequence 137, App	948	10.2	51.0	36	1	US-08-363-240A-505	Sequence 505, App
876	10.2	51.0	25	2	US-08-461-418B-13	Sequence 13, Appl	949	10.2	51.0	36	1	US-08-363-240A-925	Sequence 925, App
c 877	10.2	51.0	25	2	US-08-859-998-1279	Sequence 1279, Ap	950	10.2	51.0	36	1	US-08-363-240A-995	Sequence 995, App
878	10.2	51.0	25	3	US-08-642-274D-216	Sequence 216, App	951	10.2	51.0	36	1	US-08-461-005-9	Sequence 9, Appli
879	10.2	51.0	25	3	US-09-013-406-46	Sequence 46, Appl	952	10.2	51.0	36	1	US-07-724-500B-6	Sequence 6, Appli
880	10.2	51.0	25	3	US-09-013-406-126	Sequence 126, App	953	10.2	51.0	36	1	US-08-311-486C-309	Sequence 309, App
c 881	10.2	51.0	25	3	US-09-245-041-29	Sequence 29, Appl	954	10.2	51.0	36	1	US-08-311-486C-336	Sequence 336, App
c 882	10.2	51.0	25	4	US-09-225-928-1279	Sequence 1279, Ap	955	10.2	51.0	36	1	US-08-311-486C-391	Sequence 391, App
883	10.2	51.0	25	4	US-09-255-899-13	Sequence 13, Appl	956	10.2	51.0	36	1	US-08-311-486C-913	Sequence 913, App
c 884	10.2	51.0	25	4	US-09-225-201B-1279	Sequence 1279, Ap	957	10.2	51.0	36	1	US-08-435-628-2625	Sequence 2625, Ap
c 885	10.2	51.0	25	4	US-09-181-585-14	Sequence 14, Appl	c 958	10.2	51.0	36	2	US-08-730-963-5	Sequence 5, Appli
c 886	10.2	51.0	26	1	US-08-623-891-84	Sequence 84, Appl	959	10.2	51.0	36	2	US-08-232-620A-782	Sequence 782, App
c 887	10.2	51.0	26	4	US-09-340-861-84	Sequence 84, Appl	960	10.2	51.0	36	2	US-08-232-620A-921	Sequence 921, App
c 888	10.2	51.0	26	4	US-07-796-106-10	Sequence 10, Appl	961	10.2	51.0	36	2	US-08-232-620A-1084	Sequence 1084, Ap
889	10.2	51.0	27	1	US-07-796-106-10	Sequence 10, Appl	962	10.2	51.0	36	2	US-08-232-620A-1274	Sequence 1274, Ap
c 890	10.2	51.0	27	1	US-08-479-852-45	Sequence 45, Appl	963	10.2	51.0	36	2	US-07-930-685-9	Sequence 9, Appli
c 891	10.2	51.0	27	1	US-08-479-852-125	Sequence 125, App	964	10.2	51.0	36	2	US-08-461-418B-14	Sequence 14, Appl
c 892	10.2	51.0	27	2	US-08-462-646-45	Sequence 45, Appl	965	10.2	51.0	36	2	US-08-585-684B-338	Sequence 338, App
c 893	10.2	51.0	27	2	US-08-462-646-125	Sequence 125, App	966	10.2	51.0	36	2	US-08-585-684B-350	Sequence 350, App
c 894	10.2	51.0	27	2	US-08-462-646-125	Sequence 125, App	967	10.2	51.0	36	2	US-08-585-684B-461	Sequence 461, App
c 895	10.2	51.0	27	3	US-08-513-974B-62	Sequence 62, Appl	968	10.2	51.0	36	2	US-08-585-684B-481	Sequence 481, App
896	10.2	51.0	27	3	US-08-513-974B-115	Sequence 115, Appl	969	10.2	51.0	36	2	US-08-585-684B-1025	Sequence 1025, Ap
c 897	10.2	51.0	27	3	US-09-013-406-45	Sequence 45, Appl	970	10.2	51.0	36	2	US-08-585-684B-1028	Sequence 1028, Ap
c 898	10.2	51.0	27	3	US-09-013-406-125	Sequence 125, App	971	10.2	51.0	36	2	US-08-585-684B-1534	Sequence 1534, Ap
899	10.2	51.0	27	5	PCT-US96-01008-10	Sequence 10, Appl	972	10.2	51.0	36	2	US-08-585-684B-1608	Sequence 1608, Ap
900	10.2	51.0	28	2	US-08-733-446-9	Sequence 9, Appli	973	10.2	51.0	36	2	US-08-585-684B-1948	Sequence 1948, Ap
901	10.2	51.0	28	4	US-08-679-493A-30	Sequence 30, Appl	974	10.2	51.0	36	2	US-08-585-684B-1949	Sequence 1949, Ap
902	10.2	51.0	29	4	US-08-679-493A-3	Sequence 3, Appli	975	10.2	51.0	36	2	US-08-585-684B-1974	Sequence 1974, Ap
903	10.2	51.0	30	1	US-08-136-993-17	Sequence 17, Appl	976	10.2	51.0	36	2	US-08-585-684B-1975	Sequence 1975, Ap

977 10.2 51.0 36 2 US-08-585-684B-1976 Sequence 1976, Ap
978 10.2 51.0 36 2 US-08-585-684B-2043 Sequence 2043, Ap
979 10.2 51.0 36 2 US-08-585-684B-2223 Sequence 2223, Ap
980 10.2 51.0 36 2 US-08-774-310-123 Sequence 123, App
981 10.2 51.0 36 2 US-08-774-310-125 Sequence 125, App
982 10.2 51.0 36 2 US-08-774-310-143 Sequence 143, App
983 10.2 51.0 36 2 US-08-774-310-263 Sequence 263, App
984 10.2 51.0 36 2 US-09-071-845-782 Sequence 782, App
985 10.2 51.0 36 3 US-09-071-845-921 Sequence 921, App
986 10.2 51.0 36 3 US-09-071-845-1084 Sequence 1084, App
987 10.2 51.0 36 3 US-09-071-845-1274 Sequence 1274, App
988 10.2 51.0 36 3 US-09-038-073-338 Sequence 338, App
989 10.2 51.0 36 3 US-09-038-073-350 Sequence 350, App
990 10.2 51.0 36 3 US-09-038-073-461 Sequence 461, App
991 10.2 51.0 36 3 US-09-038-073-481 Sequence 481, App
992 10.2 51.0 36 3 US-09-038-073-1025 Sequence 1025, App
993 10.2 51.0 36 3 US-09-038-073-1028 Sequence 1028, App
994 10.2 51.0 36 3 US-09-038-073-1534 Sequence 1534, App
995 10.2 51.0 36 3 US-09-038-073-1608 Sequence 1608, App
996 10.2 51.0 36 3 US-09-038-073-1948 Sequence 1948, App
997 10.2 51.0 36 3 US-09-038-073-1949 Sequence 1949, App
998 10.2 51.0 36 3 US-09-038-073-1974 Sequence 1974, App
999 10.2 51.0 36 3 US-09-038-073-1975 Sequence 1975, App
1000 10.2 51.0 36 3 US-09-038-073-1976 Sequence 1976, App

ALIGNMENTS

RESULT 1

US-08-468-447-8
; Sequence 8, Application US/08468447
; Patent No. 5576302
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook and Glenn Hoke
; TITLE OF INVENTION: Oligonucleotides For Modulating
; TITLE OF INVENTION: Hepatitis C Virus Having Phosphorothioate Linkages Of High Chirality
; TITLE OF INVENTION: Purity
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5576302ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,447
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 297,703
; FILING DATE: 29-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2008
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-468-447-8

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20
|||||

RESULT 2

US-08-469-851A-8
; Sequence 8, Application US/08469851A
; Patent No. 5587361
; GENERAL INFORMATION:
; APPLICANT: Cook and Hoke
; TITLE OF INVENTION: OLIGONUCLEOTIDES HAVING PHOSPHOROTHIOATE
; TITLE OF INVENTION: LINKAGES OF HIGH CHIRAL PURITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5587361ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,851A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 297,703
; FILING DATE: 29-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-851A-8

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20
|||||

RESULT 3
US-08-467-597A-8
; Sequence 8, Application US/08467597A
; Patent No. 5607923
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook and Glenn Hoke
; TITLE OF INVENTION: Oligonucleotides For Modulating
; TITLE OF INVENTION: Cytomegalovirus Having Phosphorothioate Linkages Of High Chirality
; TITLE OF INVENTION: Purity
; NUMBER OF SEQUENCES: 16


```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5607923ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,597A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 297,703
; FILING DATE: 29-AUG-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-467-597A-8
;
; Query Match 100.0%; Score 20; DB 1; Length 20;
; Best Local Similarity 100.0%; Pred. No. 0.3;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 GTTCTCGCTGGTGAGTTTCA 20
; Db 1 GTTCTCGCTGGTGAGTTTCA 20
;
; RESULT 4
; US-08-468-569A-8
; Sequence 8, Application US/08468569A
; Patent No. 5620963
; GENERAL INFORMATION:
; APPLICANT: Cook and Hoke
; TITLE OF INVENTION: OLIGONUCLEOTIDES FOR MODULATING PROTEIN
; TITLE OF INVENTION: KINASE C HAVING PHOSPHOROTHIOATE LINKAGES
; TITLE OF INVENTION: AND HIGH CHIRAL PURITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5620963ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,569A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 297,703
; FILING DATE: 29-AUG-1994
;
; Query Match 100.0%; Score 20; DB 1; Length 20;
; Best Local Similarity 100.0%; Pred. No. 0.3;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 GTTCTCGCTGGTGAGTTTCA 20
; Db 1 GTTCTCGCTGGTGAGTTTCA 20
;
; RESULT 5
; US-08-466-692A-8
; Sequence 8, Application US/08466692A
; Patent No. 5654284
; GENERAL INFORMATION:
; APPLICANT: Cook and Hoke
; TITLE OF INVENTION: OLIGONUCLEOTIDES FOR MODULATING RAF KINASE
; TITLE OF INVENTION: HAVING PHOSPHOROTHIOATE LINKAGES OF HIGH
; TITLE OF INVENTION: CHIRAL PURITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5654284ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,692A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 297,703
; FILING DATE: 29-AUG-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-466-692A-8
;
; Query Match 100.0%; Score 20; DB 1; Length 20;
; Best Local Similarity 100.0%; Pred. No. 0.3;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-468-569A-8
;
; Query Match 100.0%; Score 20; DB 1; Length 20;
; Best Local Similarity 100.0%; Pred. No. 0.3;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 GTTCTCGCTGGTGAGTTTCA 20
; Db 1 GTTCTCGCTGGTGAGTTTCA 20
;
; RESULT 5
; US-08-466-692A-8
; Sequence 8, Application US/08466692A
; Patent No. 5654284
; GENERAL INFORMATION:
; APPLICANT: Cook and Hoke
; TITLE OF INVENTION: OLIGONUCLEOTIDES FOR MODULATING RAF KINASE
; TITLE OF INVENTION: HAVING PHOSPHOROTHIOATE LINKAGES OF HIGH
; TITLE OF INVENTION: CHIRAL PURITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5654284ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,692A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 297,703
; FILING DATE: 29-AUG-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-466-692A-8
;
; Query Match 100.0%; Score 20; DB 1; Length 20;
; Best Local Similarity 100.0%; Pred. No. 0.3;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCTCGTGGTGAGTTTCA 20
Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 6
US-08-471-966A-8
; Sequence 8, Application US/08471966A
; Patent No. 5661134
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook and Glenn Hoke
; TITLE OF INVENTION: Oligonucleotides For Modulating Ha-ras or
; TITLE OF INVENTION: Ki-ras Having Phosphorothioate Linkages Of High Chiral Purity
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5661134ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,966A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 297,703
; FILING DATE: 29-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-471-966A-8

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 7
US-08-089-996-2
; Sequence 2, Application US/08089996
; Patent No. 5703054
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of protein
; TITLE OF INVENTION: Kinase C
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5703054ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
```

```
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/089,996
FILING DATE: 19930709
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: Yes
US-08-089-996-2

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGTGGTGAGTTTCA 20
Db 1 GTTCTCGTGGTGAGTTTCA 20

RESULT 8
US-08-612-775-1
; Sequence 1, Application US/08612775
; Patent No. 5744460
; GENERAL INFORMATION:
; APPLICANT: Miller, Marcel
; APPLICANT: Geiger, Thomas
; APPLICANT: Altmann, Karl-Heinz
; APPLICANT: Fabbro, Dorian
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Bennett, Clarence Frank
; TITLE OF INVENTION: Combinations for treatment of proliferative diseases
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation/Patent Department
; STREET: 520 White Plains Road/P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,775
FILING DATE: 07-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gruenfeld, No. 5744460bert
REGISTRATION NUMBER: 30,061
```


REFERENCE/DOCKET NUMBER: 4-20765/P1
TELEPHONE: 914-785-7120
TELEFAX: 914-785-7102
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "antisense oligonucleotide"
ANTI-SENSE: YES
US-08-612-775-1

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 9

US-08-478-178A-2
Sequence 2, Application US/08478178A
Patent No. 5882927
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
PROTEIN KINASE C
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5882927ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,178A
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumont
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1154
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-478-178A-2

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 10

US-08-488-177-2
Sequence 2, Application US/08488177
Patent No. 5885970
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
PROTEIN KINASE C
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5885970ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1995
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: YES
US-08-488-177-2

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 11

US-08-481-072A-2
Sequence 2, Application US/08481072A
Patent No. 5916807
GENERAL INFORMATION:
APPLICANT: Nicholas Dean, C. Frank Bennett
TITLE OF INVENTION: Oligonucleotide Modulation of
PROTEIN KINASE C
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz
ADDRESSEE: Mackiewicz & No. 5916807ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia

```
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,072A
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Rebecca Ralph Gaumond
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-481-072A-2

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 12
US-08-664-336-2
; Sequence 2, Application US/08664336
; Patent No. 5922686
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of Protein
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5922686ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 720 kb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/664,336
; FILING DATE: herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 852,852
; FILING DATE: March 16, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 089,996
; FILING DATE: July 9, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
```

```
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2345
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
; US-08-664-336-2

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 13
US-08-601-269-1
; Sequence 1, Application US/08601269
; Patent No. 5948998
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, Pierre Martin, and Karl-Heinz Altmann
; TITLE OF INVENTION: Methoxyethoxy Oligonucleotides for Modulation of
; TITLE OF INVENTION: Protein Kinase C Expression
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 5948998ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 720 kb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/601,269
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/478,178
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-601-269-1

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
```

Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 14

US-08-481-066A-2
; Sequence 2, Application US/08481066A
; Patent No. 5950996
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett
; TITLE OF INVENTION: Oligonucleotide Modulation of
; TITLE OF INVENTION: Protein Kinase C
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; ADDRESSEE: Mackiewicz & No. 595096ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481.066A
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: March 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Rebecca Ralph Gaumond
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-1154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-481-066A-2

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20

Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 15

US-08-578-615A-2
; Sequence 2, Application US/08578615A
; Patent No. 6015892
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
; TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase C
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578.615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: ISIS-1568
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-578-615A-2

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20

Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 16

US-08-578-615A-121
; Sequence 121, Application US/08578615A
; Patent No. 6015892
; GENERAL INFORMATION:
; APPLICANT: Nicholas Dean, C. Frank Bennett and Russell, T. Boggs
; TITLE OF INVENTION: Oligonucleotide Modulation of Protein Kinase C
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6015892ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578.615A
FILING DATE: 11-JAN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 852,852
FILING DATE: 16-MAR-1992
APPLICATION NUMBER: 08/089,996
FILING DATE: 09-JUL-1993
APPLICATION NUMBER: 08/199,779
FILING DATE: 22-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard

```
;
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-1568
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ANTI-SENSE: yes
;
US-08-578-615A-121

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
DB 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 17
US-08-950-779-4
; Sequence 4, Application US/08950779
; Patent No. 6114519
; GENERAL INFORMATION:
; APPLICANT: Cole, Douglas L.
; APPLICANT: Ravikumar, Vasalinga T.
; APPLICANT: Cheruvallath, Zacharia S.
; TITLE OF INVENTION: Synthesis of Sulfurized Oligonucleotides
; FILE REFERENCE: ISIS2585
; CURRENT APPLICATION NUMBER: US/08/950,779
; CURRENT FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: No. 6114519el Sequence
US-08-950-779-4

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
DB 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 18
US-09-094-714A-29
; Sequence 29, Application US/09094714A
; Patent No. 6117847
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett, Nicholas M. Dean
; TITLE OF INVENTION: OLIGONUCLEOTIDES FOR ENHANCED MODULATION OF
; TITLE OF INVENTION: PROTEIN KINASE C EXPRESSION
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6117847ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
```

```
;
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/094,714A
; FILING DATE: June 15, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,269
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/478,178
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/089,996
; FILING DATE: 09-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/852,852
; FILING DATE: 16-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-094-714A-29
```

```
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCTCGCTGGTGAGTTTCA 20
DB 1 GTTCTCGCTGGTGAGTTTCA 20
```

```
RESULT 19
US-09-249-730-217
; Sequence 217, Application US/09249730
; Patent No. 6121000
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
; FILE REFERENCE: 032396-040
; CURRENT APPLICATION NUMBER: US/09/249,730
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-249-730-217
```

```
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GTTCTCGCTGGTGAGTTTCA 20
DB 1 GTTCTCGCTGGTGAGTTTCA 20
```

```
RESULT 20
US-09-117-901-1
```

```
; Sequence 1, Application US/091117901
; Patent No. 6153599
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Methoxyethoxy Oligonucleotides for Modulation of
; TITLE OF INVENTION: Protein Kinase C Expression
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6153599-ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/117,901
; FILING DATE: 07-JAN-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/601,269
; FILING DATE: 14-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 36,534
; REFERENCE/DOCKET NUMBER: ISNO-0058
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-117-901-1
;
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 21
US-09-414-145-4
; Sequence 4, Application US/0941415
; Patent No. 6160152
; GENERAL INFORMATION:
; APPLICANT: Capaldi, Daniel C
; APPLICANT: Ravikumar, Vasulunga T
; TITLE OF INVENTION: Improved Process For The Synthesis Of Oligomeric
; FILE REFERENCE: ISIS4173
; CURRENT APPLICATION NUMBER: US/09/414,145
; PRIOR FILING DATE: 1999-10-07
; PRIOR FILING DATE: 1993-02-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6160152el
; OTHER INFORMATION: Sequence
```

```
US-09-414-145-4
;
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 22
US-08-398-901-1
; Sequence 1, Application US/08398901
; Patent No. 6166197
; GENERAL INFORMATION:
; APPLICANT: Cook, Philip Dan
; APPLICANT: Sanghvi, Yogesh S.
; APPLICANT: Sprankle, Kelly G.
; APPLICANT: Ross, Bruce S.
; APPLICANT: Griffey, Rich H.
; TITLE OF INVENTION: Oligomeric Compounds Having
; TITLE OF INVENTION: Pyrimidine Nucleotide(s) With 2' and 5
; TITLE OF INVENTION: Substitutions
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,901
; FILING DATE: March 6, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Caldwell
; REGISTRATION NUMBER: 28,937
; REFERENCE/DOCKET NUMBER: ISIS-0719
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Nucleic Acid Analog
;
US-08-398-901-1
;
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 23
US-08-398-901-2
; Sequence 2, Application US/08398901
```

```

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,901
FILING DATE: March 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: John W. Caldwell
REGISTRATION NUMBER: 28,937
REFERENCE/DOCKET NUMBER: ISIS-0719
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Nucleic Acid Analog
US-08-398-901-3

Query Match          100.0%;   Score 20;
Best Local Similarity 70.0%;   Pred No. 0;
Matches    14;   Conservative    6; Mismatched    0

Qy      1  GTTCTCGCTGGTGAGTTCA 20
       |:|::|||::|||
Db      1  GUUCUCCGTGCGAGUUUCA 20

RESULT 25
US-09-144-883C-4
Sequence 4, Application US/09144883C
Patent No. 6175004
GENERAL INFORMATION:
APPLICANT: Ross, Bruce S
TITLE OF INVENTION: Improved Process for t
TITLE OF INVENTION: Incorporating 2-Aminoac
FILE REFERENCE: ISIS33158
CURRENT APPLICATION NUMBER: US/09/144,883C
CURRENT FILING DATE: 1998-09-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)
OTHER INFORMATION: 5-methyl
NAME/KEY: misc_feature
LOCATION: (6)
OTHER INFORMATION: 5-methyl
NAME/KEY: misc_feature
LOCATION: (8)
OTHER INFORMATION: 5-methyl
NAME/KEY: modified_base
LOCATION: (14)
OTHER INFORMATION: 2-aminoadenosine
```

```
; NAME/KEY: misc_feature
; LOCATION: (19)
; OTHER INFORMATION: 5-methyl
; NAME/KEY: modified_base
; LOCATION: (20)
; OTHER INFORMATION: 2-aminoadenosine
; OTHER INFORMATION: Description of Artificial Sequence: No. 6175004el Sequence
US-09-144-883C-4

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 26
US-08-894-899-27
; Sequence 27, Application US/08894899
; Patent No. 6222025
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Sanghvi, Yogesh S.
; APPLICANT: Ross, Bruce S.
; APPLICANT: Griffey, Rich H.
; APPLICANT: Sprinker, Robert H.
; APPLICANT: Sprankle, Kelly G.
; TITLE OF INVENTION: Improved Process For The Synthesis Of 2'-O-Substituted Pyrimidin
; FILE REFERENCE: ISIS-2167
; CURRENT APPLICATION NUMBER: US/08/894,899
; CURRENT FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: PCT/US96/03174
; PRIOR FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: 08/475,467
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/398,901
; PRIOR FILING DATE: 1995-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: No. 6222025el Sequence
US-08-894-899-27

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 27
US-08-894-899-28
; Sequence 28, Application US/08894899
; Patent No. 6222025
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Sanghvi, Yogesh S.
; APPLICANT: Ross, Bruce S.
; APPLICANT: Griffey, Rich H.
; APPLICANT: Sprinker, Robert H.
; APPLICANT: Sprankle, Kelly G.
; TITLE OF INVENTION: Improved Process For The Synthesis Of 2'-O-Substituted Pyrimidin
; FILE REFERENCE: ISIS-2167
; CURRENT APPLICATION NUMBER: US/08/894,899
; CURRENT FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: PCT/US96/03174
; PRIOR FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: 08/475,467
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/398,901
; PRIOR FILING DATE: 1995-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: No. 6222025el Sequence
US-08-894-899-27

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20
```

```
; CURRENT APPLICATION NUMBER: US/08/894,899
; CURRENT FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: PCT/US96/03174
; PRIOR FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: 08/475,467
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/398,901
; PRIOR FILING DATE: 1995-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: No. 6222025el Sequence
US-08-894-899-28

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 70.0%; Pred. No. 0.3;
Matches 14; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GUUCUCGCTGGTGAGUUUCA 20

RESULT 28
US-08-894-899-29
; Sequence 29, Application US/08894899
; Patent No. 6222025
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Sanghvi, Yogesh S.
; APPLICANT: Ross, Bruce S.
; APPLICANT: Griffey, Rich H.
; APPLICANT: Sprinker, Robert H.
; APPLICANT: Sprankle, Kelly G.
; TITLE OF INVENTION: Improved Process For The Synthesis Of 2'-O-Substituted Pyrimidin
; FILE REFERENCE: ISIS-2167
; CURRENT APPLICATION NUMBER: US/08/894,899
; CURRENT FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: PCT/US96/03174
; PRIOR FILING DATE: 1996-03-06
; PRIOR APPLICATION NUMBER: 08/475,467
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/398,901
; PRIOR FILING DATE: 1995-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: No. 6222025el Sequence
US-08-894-899-29

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 70.0%; Pred. No. 0.3;
Matches 14; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GUUCUCGCTGGTGAGUUUCA 20

RESULT 29
US-09-177-953-4
; Sequence 4, Application US/09177953
; Patent No. 6274725
; GENERAL INFORMATION:
```

```
; APPLICANT: Sanghvi, Yogesh
; APPLICANT: Ravikumar, Vasulinga T.
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: ISIS3148
; CURRENT APPLICATION NUMBER: US/09/177,953
; CURRENT FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-09-177-953-4
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 30
US-09-177-953-13
; Sequence 13, Application US/09177953
; Patent No. 6274725
; GENERAL INFORMATION:
; APPLICANT: Sanghvi, Yogesh
; APPLICANT: Ravikumar, Vasulinga T.
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: ISIS3148
; CURRENT APPLICATION NUMBER: US/09/177,953
; CURRENT FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-09-177-953-13
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 31
US-09-177-953-27
; Sequence 27, Application US/09177953
; Patent No. 6274725
; GENERAL INFORMATION:
; APPLICANT: Sanghvi, Yogesh
; APPLICANT: Ravikumar, Vasulinga T.
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: ISIS3148
; CURRENT APPLICATION NUMBER: US/09/177,953
; CURRENT FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-09-177-953-27
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 32
US-09-177-953-35
; Sequence 35, Application US/09177953
; Patent No. 6274725
; GENERAL INFORMATION:
; APPLICANT: Sanghvi, Yogesh
; APPLICANT: Ravikumar, Vasulinga T.
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: ISIS3148
; CURRENT APPLICATION NUMBER: US/09/177,953
; CURRENT FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-09-177-953-35
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 33
US-09-177-953-42
; Sequence 42, Application US/09177953
; Patent No. 6274725
; GENERAL INFORMATION:
; APPLICANT: Sanghvi, Yogesh
; APPLICANT: Ravikumar, Vasulinga T.
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: ISIS3148
; CURRENT APPLICATION NUMBER: US/09/177,953
; CURRENT FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-09-177-953-42
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 33
US-09-177-953-42
; Sequence 42, Application US/09177953
; Patent No. 6274725
; GENERAL INFORMATION:
; APPLICANT: Sanghvi, Yogesh
; APPLICANT: Ravikumar, Vasulinga T.
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: ISIS3148
; CURRENT APPLICATION NUMBER: US/09/177,953
; CURRENT FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-09-177-953-42
Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20
```


; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6274725e1 Sequence
US-09-177-953-42

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 34
US-09-078-954-13
; Sequence 13, Application US/09078954
; Patent No. 6287591

; GENERAL INFORMATION:

; APPLICANT: SEMPLE, Sean C.

; APPLICANT: Klimuk, Sandra K.

; APPLICANT: Harasym, Troy

; APPLICANT: Hope, Michael J.

; APPLICANT: Ansell, Steven M.

; APPLICANT: Cullis, Pieter

; APPLICANT: Scherrer, Peter

; APPLICANT: Geiser, Timothy

; APPLICANT: Zon, Gerald

; APPLICANT: Debever, Dan

; TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic Agents in

; TITLE OF INVENTION: Lipid Vesicles

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Oppedahl & Larson

; STREET: PO Box 5270

; CITY: Frisco

; STATE: CO

; COUNTRY: USA

; ZIP: 80443-5270

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS 5.0

; SOFTWARE: Word Perfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/078,954

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/856,374

; FILING DATE: 14-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Marina T. Larson

; REGISTRATION NUMBER: 32,038

; REFERENCE/DOCKET NUMBER: INEX.P-003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (970) 668-2050

; TELEFAX: (970) 668-2082

; TELEX:

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; HYPOTHETICAL: no

; ANTI-SENSE: yes

; US-09-078-954-13

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 35

US-09-225-749-2

; Sequence 2, Application US/09225749

; Patent No. 6300320

; GENERAL INFORMATION:

; APPLICANT: Dean, Nicholas M.

; APPLICANT: McKay, Robert, A.

; TITLE OF INVENTION: Modulation of c-jun using inhibitors of protein kinase C

; FILE REFERENCE: ISIS3313

; CURRENT APPLICATION NUMBER: US/09/225,749

; CURRENT FILING DATE: 1999-01-05

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: antisense sequence

; US-09-225-749-2

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 36

US-09-379-718-4

; Sequence 4, Application US/09379718

; Patent No. 6310047

; GENERAL INFORMATION:

; APPLICANT: Farrell, Nicholas

; APPLICANT: Kloster, Miriam

; TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in

; FILE REFERENCE: Farrell/Kloster

; CURRENT APPLICATION NUMBER: US/09/379,718

; CURRENT FILING DATE: 1999-08-24

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: oligonucleotides for gene therapy

; US-09-379-718-4

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 37

US-09-111-678-4

; Sequence 4, Application US/09111678

; Patent No. 6326478

; GENERAL INFORMATION:

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APPLICANT: Cheruvallath, Zacharia S
APPLICANT: Ravikumar, Vasulunga T
APPLICANT: Cole, Douglas L
TITLE OF INVENTION: Process For The Synthesis Of Oligomeric Compounds
FILE REFERENCE: ISIS2853
CURRENT APPLICATION NUMBER: US/09/111,678
CURRENT FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6326478e1
OTHER INFORMATION: Sequence
US-09-111-678-4

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
DB 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 38
US-08-829-637A-2
Sequence 2, Application US/08829637A
Patent No. 6339066
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Phillip Dan Cook
APPLICANT: Nicholas Dean
APPLICANT: Glenn Hoke
TITLE OF INVENTION: OLIGONUCLEOTIDES WHICH HAVE
TITLE OF INVENTION: PHOSPHOROTHIATE LINKAGES OF HIGH CHIRAL PURITY AND
TITLE OF INVENTION: WHICH MODULATE ai, aii, k, n, AND ISOFORMS OF
TITLE OF INVENTION: PROTEIN KINASE C
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Caldwell (28,937) Woodcock
ADDRESSEE: Washburn Kurtz Mackiewicz & No. 6339066ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,637A
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,066
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,129
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,851
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,569
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/089,996
FILING DATE: 09-JUL-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/058,023
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,007
FILING DATE: 16-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,760
FILING DATE: 15-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,852
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00243
FILING DATE: 11-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/566,977
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,358
FILING DATE: 11-JAN-1990
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: ISIS-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ANTI-SENSE: yes
US-08-829-637A-2

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
DB 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 39
US-09-287-175-4
Sequence 4, Application US/09287175
Patent No. 6379698
GENERAL INFORMATION:
APPLICANT: LEAMON, Christopher P
TITLE OF INVENTION: FUSOGENIC LIPIDS AND VESICLES
FILE REFERENCE: 049202/2002
CURRENT APPLICATION NUMBER: US/09/287,175
CURRENT FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide
US-09-287-175-4

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||

Db 1 GTTCTCGCTGGTGAGTTTCA 20

```

RESULT 40
US-09-349-659-4
; Sequence 4, Application US/09349659
; Patent No. 6399756
; GENERAL INFORMATION:
; APPLICANT: Cheruvallath, Zacharia S
; APPLICANT: Ravikumar, Vasulinga T
; APPLICANT: Cole, Douglas L
; TITLE OF INVENTION: Improved Process For The Synthesis Of Oligomeric
; TITLE OF INVENTION: Compounds
; FILE REFERENCE: ISIS3837
; CURRENT APPLICATION NUMBER: US/09/349,659
; CURRENT FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 09/111,678
; PRIOR FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6399756el
; OTHER INFORMATION: Sequence
US-09-349-659-4

```

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

Search completed: January 24, 2004, 15:37:19
 Job time : 67 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 24, 2004, 15:05:33 ; Search time 224 Seconds

(without alignments)

319.328 Million cell updates/sec

Title: US-10-002-884A-5

Sequence: 1 gtctcgctggtgatttca 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2356869 seqs, 1788235258 residues

Total number of hits satisfying chosen parameters: 1221896

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	10	US-09-835-371-38	Sequence 38, Appl
2	20	100.0	20	11	US-09-835-370-38	Sequence 38, Appl
3	20	100.0	20	11	US-09-931-732-18	Sequence 18, Appl
4	20	100.0	20	11	US-09-747-009-27	Sequence 27, Appl
5	20	100.0	20	11	US-09-747-009-28	Sequence 28, Appl
6	20	100.0	20	11	US-09-747-009-29	Sequence 29, Appl
7	20	100.0	20	11	US-09-876-242-5	Sequence 5, Appl
8	20	100.0	20	11	US-09-935-316-4	Sequence 4, Appl
9	20	100.0	20	11	US-09-902-953-4	Sequence 4, Appl
10	20	100.0	20	12	US-10-444-445-4	Sequence 4, Appl
11	20	100.0	20	12	US-10-437-263-23	Sequence 23, Appl
12	20	100.0	20	12	US-10-437-275-23	Sequence 23, Appl
13	20	100.0	20	12	US-10-447-136-217	Sequence 217, Appl
14	20	100.0	20	12	US-09-895-480A-13	Sequence 13, Appl
15	20	100.0	20	13	US-09-895-480A-13	Sequence 13, Appl

Sequence 3, Appl	20	100.0	20	13	US-10-262-318-3	Sequence 3, Appl
Sequence 4, Appl	20	100.0	20	13	US-10-290-587-4	Sequence 4, Appl
Sequence 5, Appl	20	100.0	20	13	US-10-348-485-2	Sequence 2, Appl
Sequence 6, Appl	20	100.0	20	13	US-10-337-004-5	Sequence 5, Appl
Sequence 14, Appl	20	100.0	20	13	US-10-337-004-6	Sequence 6, Appl
Sequence 22, Appl	20	100.0	20	13	US-10-365-623-14	Sequence 14, Appl
Sequence 4, Appl	20	100.0	20	13	US-10-080-979-22	Sequence 22, Appl
Sequence 13, Appl	20	100.0	20	13	US-10-318-628-4	Sequence 4, Appl
Sequence 27, Appl	20	100.0	20	13	US-10-318-628-13	Sequence 13, Appl
Sequence 35, Appl	20	100.0	20	13	US-10-318-628-27	Sequence 27, Appl
Sequence 42, Appl	20	100.0	20	13	US-10-318-628-35	Sequence 35, Appl
Sequence 3, Appl	20	100.0	20	13	US-10-318-628-42	Sequence 42, Appl
Sequence 1, Appl	20	100.0	20	14	US-10-103-906-3	Sequence 3, Appl
Sequence 4, Appl	20	100.0	20	14	US-10-002-802A-1	Sequence 1, Appl
Sequence 49, Appl	20	100.0	20	15	US-10-071-822A-4	Sequence 4, Appl
Sequence 57, Appl	20	100.0	20	15	US-10-029-598-49	Sequence 49, Appl
Sequence 58, Appl	20	100.0	20	15	US-10-029-598-57	Sequence 57, Appl
Sequence 1, Appl	20	100.0	20	15	US-10-123-435-1	Sequence 1, Appl
Sequence 5, Appl	20	100.0	20	15	US-10-002-884A-5	Sequence 5, Appl
Sequence 42, Appl	20	100.0	20	15	US-10-142-566-42	Sequence 42, Appl
Sequence 23, Appl	20	100.0	20	15	US-10-290-545-23	Sequence 23, Appl
Sequence 19, Appl	19	95.0	19	11	US-09-370-541-19	Sequence 19, Appl
Sequence 19, Appl	19	95.0	19	11	US-09-370-541-19	Sequence 19, Appl
Sequence 21, Appl	19	95.0	19	13	US-10-318-628-19	Sequence 19, Appl
Sequence 5, Appl	18	90.0	18	11	US-09-996-263-5	Sequence 5, Appl
Sequence 52, Appl	18	90.0	18	13	US-10-348-485-52	Sequence 52, Appl
Sequence 6, Appl	17	85.0	17	11	US-09-996-263-6	Sequence 6, Appl
Sequence 53, Appl	17	85.0	17	13	US-10-348-485-53	Sequence 53, Appl
Sequence 38, Appl	17	85.0	17	13	US-10-352-586-6	Sequence 38, Appl
Sequence 11814, A	16	80.0	17	15	US-10-142-566-38	Sequence 38, Appl
Sequence 2199, Ap	15	68.0	25	15	US-10-098-263B-111814	Sequence 2199, Ap
Sequence 17, Appl	14	67.0	24	11	US-09-940-185-2199	Sequence 17, Appl
Sequence 28, Appl	21	66.0	21	10	US-09-966-147-28	Sequence 28, Appl
Sequence 24, Appl	21	66.0	21	12	US-10-172-526-24	Sequence 24, Appl
Sequence 28, Appl	21	66.0	21	13	US-10-374-463-28	Sequence 28, Appl
Sequence 51446, A	25	65.0	25	15	US-10-098-263B-51446	Sequence 51446, A
Sequence 1799, Ap	31	65.0	31	9	US-09-801-274-1799	Sequence 1799, Ap
Sequence 12541, A	25	64.0	25	15	US-10-215-113-12541	Sequence 12541, A
Sequence 11, Appl	30	64.0	30	12	US-10-182-329-11	Sequence 11, Appl
Sequence 68194, A	25	63.0	25	15	US-10-098-263B-68194	Sequence 68194, A
Sequence 2, Appl	27	63.0	27	13	US-10-394-194-2	Sequence 2, Appl
Sequence 4, Appl	27	62.0	27	13	US-10-366-504-4	Sequence 4, Appl
Sequence 1224, Ap	38	62.0	38	13	US-09-792-818-1224	Sequence 1224, Ap
Sequence 44, Appl	20	61.0	20	10	US-09-974-052-44	Sequence 44, Appl
Sequence 44, Appl	20	61.0	20	10	US-09-974-051-44	Sequence 44, Appl
Sequence 5517, Ap	20	61.0	20	11	US-09-974-516-44	Sequence 5517, Ap
Sequence 5125, Ap	22	61.0	22	13	US-10-032-585-5125	Sequence 5125, Ap
Sequence 265, App	23	61.0	23	12	US-10-411-954-265	Sequence 265, App
Sequence 336, Appl	23	61.0	23	12	US-10-411-954-336	Sequence 336, Appl
Sequence 5, Appl	23	61.0	23	13	US-10-160-078-5	Sequence 5, Appl
Sequence 28, Appl	25	61.0	25	9	US-09-822-263-28	Sequence 28, Appl
Sequence 28, Appl	25	61.0	25	13	US-09-882-263-28	Sequence 28, Appl
Sequence 47667, A	25	61.0	25	15	US-10-098-263B-47667	Sequence 47667, A
Sequence 51564, A	25	61.0	25	15	US-10-098-263B-51564	Sequence 51564, A
Sequence 83394, A	25	61.0	25	15	US-10-098-263B-83394	Sequence 83394, A
Sequence 125841, A	25	61.0	25	15	US-10-098-263B-125841	Sequence 125841, A
Sequence 36, Appl	25	61.0	25	16	US-10-273-334-36	Sequence 36, Appl
Sequence 1, Appl	19	60.0	19	12	US-10-426-159-8	Sequence 1, Appl
Sequence 8, Appl	21	60.0	21	13	US-10-209-676-30	Sequence 8, Appl
Sequence 50, Appl	22	60.0	22	9	US-09-847-842-8	Sequence 50, Appl
Sequence 61, Appl	22	60.0	22	11	US-09-940-244-50	Sequence 61, Appl
Sequence 50, Appl	22	60.0	22	11	US-09-982-667-61	Sequence 50, Appl
Sequence 9, Appl	22	60.0	22	13	US-10-290-386-50	Sequence 9, Appl
Sequence 50, Appl	22	60.0	22	14	US-10-033-297-50	Sequence 50, Appl
Sequence 61, Appl	22	60.0	22	14	US-10-081-806-61	Sequence 61, Appl
Sequence 2, Appl	22	60.0	22	15	US-10-210-682-2	Sequence 2, Appl
Sequence 445, App	25	60.0	25	11	US-09-754-853A-445	Sequence 445, App

89	12	60.0	25	15	US-10-098-263B-76855	Sequence 76855, A	c 162	11.8	59.0	24	13	US-10-017-084A-233	Sequence 233, App
90	12	60.0	25	15	US-10-098-263B-78094	Sequence 78094, A	c 163	11.8	59.0	24	13	US-10-017-084A-233	Sequence 233, App
91	12	60.0	25	15	US-10-098-263B-111813	Sequence 111813, A	c 164	11.8	59.0	24	13	US-10-013-916A-233	Sequence 233, App
92	12	60.0	29	13	US-10-336-638-446	Sequence 446, App	c 165	11.8	59.0	24	13	US-10-143-026B-233	Sequence 233, App
93	12	60.0	30	13	US-09-416-579A-6	Sequence 6, Appl	c 166	11.8	59.0	24	13	US-10-013-918A-233	Sequence 233, App
94	12	60.0	30	13	US-10-084-706-41	Sequence 41, Appl	c 167	11.8	59.0	24	13	US-10-013-923A-233	Sequence 233, App
95	12	60.0	30	13	US-10-084-706-42	Sequence 42, Appl	c 168	11.8	59.0	24	13	US-10-013-925A-233	Sequence 233, App
96	12	60.0	31	12	US-09-912-263-27	Sequence 27, Appl	c 169	11.8	59.0	24	13	US-10-013-927A-233	Sequence 233, App
97	12	60.0	38	11	US-10-388-918A-15	Sequence 15, Appl	c 170	11.8	59.0	24	13	US-10-013-928A-233	Sequence 233, App
98	12	60.0	39	10	US-09-797-941A-28	Sequence 28, Appl	c 171	11.8	59.0	24	13	US-10-017-081A-233	Sequence 233, App
99	12	60.0	39	10	US-09-797-941A-29	Sequence 29, Appl	c 172	11.8	59.0	24	15	US-10-167-749-233	Sequence 233, App
100	12	60.0	39	12	US-10-411-066-46	Sequence 46, Appl	c 173	11.8	59.0	24	15	US-10-013-921A-233	Sequence 233, App
101	11.8	59.0	18	10	US-09-969-373-1783	Sequence 1783, Ap	c 174	11.8	59.0	24	15	US-10-013-929A-233	Sequence 233, App
102	11.8	59.0	18	10	US-09-733-444-21	Sequence 21, Appl	c 175	11.8	59.0	24	15	US-10-016-177A-233	Sequence 233, App
103	11.8	59.0	18	13	US-10-279-454-21	Sequence 21, Appl	c 176	11.8	59.0	24	15	US-10-166-709A-233	Sequence 233, App
104	11.8	59.0	20	12	US-10-289-762-1681	Sequence 1681, Ap	c 177	11.8	59.0	24	15	US-10-098-263B-78509	Sequence 78509, A
105	11.8	59.0	23	12	US-10-175-492-5	Sequence 5, Appl	c 178	11.8	59.0	25	15	US-10-098-263B-78509	Sequence 78509, A
106	11.8	59.0	24	10	US-09-978-295A-233	Sequence 233, App	c 179	11.8	59.0	25	15	US-10-098-263B-78509	Sequence 78509, A
107	11.8	59.0	24	10	US-09-978-295A-233	Sequence 233, App	c 180	11.8	59.0	25	15	US-10-098-263B-78509	Sequence 78509, A
108	11.8	59.0	24	10	US-09-978-192A-233	Sequence 233, App	c 181	11.8	59.0	28	13	US-09-995-225-25	Sequence 25, Appl
109	11.8	59.0	24	10	US-09-999-832A-233	Sequence 233, App	c 182	11.8	59.0	28	13	US-10-247-813-12	Sequence 12, Appl
110	11.8	59.0	24	11	US-09-978-189-233	Sequence 233, App	c 183	11.8	59.0	29	13	US-10-247-813-12	Sequence 12, Appl
111	11.8	59.0	24	11	US-09-978-608A-233	Sequence 233, App	c 184	11.8	59.0	29	13	US-10-243-581B-11	Sequence 11, Appl
112	11.8	59.0	24	11	US-09-978-585A-233	Sequence 233, App	c 185	11.8	59.0	33	10	US-09-974-052-47	Sequence 47, Appl
113	11.8	59.0	24	11	US-09-978-403A-233	Sequence 233, App	c 186	11.8	59.0	33	10	US-09-974-052-47	Sequence 47, Appl
114	11.8	59.0	24	11	US-09-978-403A-233	Sequence 233, App	c 187	11.8	59.0	33	11	US-09-974-051-47	Sequence 47, Appl
115	11.8	59.0	24	11	US-09-978-564A-233	Sequence 233, App	c 188	11.8	59.0	33	11	US-09-974-051-47	Sequence 47, Appl
116	11.8	59.0	24	11	US-09-999-833A-233	Sequence 233, App	c 189	11.8	59.0	36	9	US-09-504-231A-1810	Sequence 1810, Ap
117	11.8	59.0	24	11	US-09-981-915A-233	Sequence 233, App	c 190	11.8	59.0	36	9	US-09-504-231A-1810	Sequence 1810, Ap
118	11.8	59.0	24	11	US-09-978-824A-233	Sequence 233, App	c 191	11.8	59.0	36	13	US-10-440-850-1251	Sequence 1251, Ap
119	11.8	59.0	24	11	US-09-978-824A-233	Sequence 233, App	c 192	11.8	59.0	36	13	US-10-440-850-1251	Sequence 1251, Ap
120	11.8	59.0	24	11	US-09-978-193A-233	Sequence 233, App	c 193	11.8	59.0	36	13	US-10-440-850-1251	Sequence 1251, Ap
121	11.8	59.0	24	11	US-09-978-193A-233	Sequence 233, App	c 194	11.8	59.0	36	13	US-10-440-850-1251	Sequence 1251, Ap
122	11.8	59.0	24	11	US-09-999-830A-233	Sequence 233, App	c 195	11.8	59.0	36	13	US-10-440-850-1251	Sequence 1251, Ap
123	11.8	59.0	24	11	US-09-978-197B-233	Sequence 233, App	c 196	11.8	59.0	36	15	US-10-056-414-421	Sequence 421, App
124	11.8	59.0	24	11	US-09-978-643A-233	Sequence 233, App	c 197	11.8	59.0	36	15	US-10-056-414-421	Sequence 421, App
125	11.8	59.0	24	12	US-10-013-919A-233	Sequence 233, App	c 198	11.8	59.0	37	9	US-09-504-231A-1810	Sequence 1810, Ap
126	11.8	59.0	24	12	US-10-145-093A-233	Sequence 233, App	c 199	11.8	59.0	37	9	US-09-504-231A-1810	Sequence 1810, Ap
127	11.8	59.0	24	12	US-09-978-375A-233	Sequence 233, App	c 200	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
128	11.8	59.0	24	13	US-09-978-188A-233	Sequence 233, App	c 201	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
129	11.8	59.0	24	13	US-09-978-188A-233	Sequence 233, App	c 202	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
130	11.8	59.0	24	13	US-10-143-031A-233	Sequence 233, App	c 203	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
131	11.8	59.0	24	13	US-10-002-967A-233	Sequence 233, App	c 204	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
132	11.8	59.0	24	13	US-10-017-083A-233	Sequence 233, App	c 205	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
133	11.8	59.0	24	13	US-10-143-030A-233	Sequence 233, App	c 206	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
134	11.8	59.0	24	13	US-10-145-128A-233	Sequence 233, App	c 207	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
135	11.8	59.0	24	13	US-10-145-128A-233	Sequence 233, App	c 208	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
136	11.8	59.0	24	13	US-10-017-191A-233	Sequence 233, App	c 209	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
137	11.8	59.0	24	13	US-10-143-028A-233	Sequence 233, App	c 210	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
138	11.8	59.0	24	13	US-10-143-028A-233	Sequence 233, App	c 211	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
139	11.8	59.0	24	13	US-10-145-029A-233	Sequence 233, App	c 212	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
140	11.8	59.0	24	13	US-10-145-029A-233	Sequence 233, App	c 213	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
141	11.8	59.0	24	13	US-10-013-926A-233	Sequence 233, App	c 214	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
142	11.8	59.0	24	13	US-10-145-017A-233	Sequence 233, App	c 215	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
143	11.8	59.0	24	13	US-10-164-728A-233	Sequence 233, App	c 216	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
144	11.8	59.0	24	13	US-10-165-067A-233	Sequence 233, App	c 217	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
145	11.8	59.0	24	13	US-10-145-124A-233	Sequence 233, App	c 218	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
146	11.8	59.0	24	13	US-10-165-502A-233	Sequence 233, App	c 219	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
147	11.8	59.0	24	13	US-10-165-247A-233	Sequence 233, App	c 220	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
148	11.8	59.0	24	13	US-09-978-194A-233	Sequence 233, App	c 221	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
149	11.8	59.0	24	13	US-09-978-68A-233	Sequence 233, App	c 222	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
150	11.8	59.0	24	13	US-09-999-829A-233	Sequence 233, App	c 223	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
151	11.8	59.0	24	13	US-10-013-922A-233	Sequence 233, App	c 224	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
152	11.8	59.0	24	13	US-10-017-086A-233	Sequence 233, App	c 225	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
153	11.8	59.0	24	13	US-10-145-087A-233	Sequence 233, App	c 226	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
154	11.8	59.0	24	13	US-10-164-822A-233	Sequence 233, App	c 227	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
155	11.8	59.0	24	13	US-10-164-822A-233	Sequence 233, App	c 228	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
156	11.8	59.0	24	13	US-09-978-299A-233	Sequence 233, App	c 229	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
157	11.8	59.0	24	13	US-09-978-544A-233	Sequence 233, App	c 230	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
158	11.8	59.0	24	13	US-09-978-665A-233	Sequence 233, App	c 231	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
159	11.8	59.0	24	13	US-09-978-802A-233	Sequence 233, App	c 232	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
160	11.8	59.0	24	13	US-10-013-924A-233	Sequence 233, App	c 233	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap
161	11.8	59.0	24	13	US-10-020-445A-233	Sequence 233, App	c 234	11.8	59.0	38	11	US-09-848-754A-3875	Sequence 3875, Ap

C 235	11.6	58.0	25	9	US-09-844-915-2	Sequence 2, Appli	308	11.2	56.0	17	11	US-09-776-474-1103	Sequence 1103, Ap
236	11.6	58.0	25	15	US-10-098-2638-130	Sequence 130, App	309	11.2	56.0	19	12	US-10-349-143-6251	Sequence 6251, Ap
237	11.6	58.0	25	15	US-10-098-2638-2612	Sequence 2612, Ap	310	11.2	56.0	20	10	US-09-957-688A-7	Sequence 4, Appli
238	11.6	58.0	25	15	US-10-098-2638-36085	Sequence 36085, A	C 311	11.2	56.0	20	11	US-09-940-244-77	Sequence 77, Appl
239	11.6	58.0	25	15	US-10-098-2638-51445	Sequence 51445, A	C 312	11.2	56.0	20	11	US-09-770-107-12	Sequence 12, Appl
240	11.6	58.0	25	15	US-10-098-2638-87996	Sequence 87996, A	C 313	11.2	56.0	20	12	US-10-190-366-41	Sequence 41, Appl
241	11.6	58.0	25	15	US-10-098-2638-112432	Sequence 112432, A	C 314	11.2	56.0	20	12	US-10-190-366-238	Sequence 238, App
242	11.6	58.0	25	15	US-10-098-2638-126756	Sequence 126756, A	C 315	11.2	56.0	20	12	US-10-289-762-3774	Sequence 3774, Ap
243	11.6	58.0	27	8	US-08-860-844-7	Sequence 7, Appli	C 316	11.2	56.0	20	13	US-10-290-386-77	Sequence 77, Appl
244	11.6	58.0	27	8	US-08-860-844-8	Sequence 8, Appli	C 317	11.2	56.0	20	14	US-10-033-297-77	Sequence 77, Appl
245	11.6	58.0	27	9	US-09-766-095-44	Sequence 44, Appl	C 318	11.2	56.0	21	9	US-09-765-081-404	Sequence 404, App
246	11.6	58.0	27	9	US-09-766-095-124	Sequence 124, App	C 319	11.2	56.0	21	13	US-10-084-839-3093	Sequence 3093, Ap
247	11.6	58.0	27	13	US-10-244-490-17	Sequence 17, Appl	C 320	11.2	56.0	21	14	US-10-020-038-5	Sequence 5, Appli
248	11.6	58.0	27	13	US-10-407-543-7	Sequence 7, Appli	C 321	11.2	56.0	21	15	US-10-153-275-9	Sequence 9, Appli
249	11.6	58.0	27	13	US-10-407-543-8	Sequence 8, Appli	C 322	11.2	56.0	21	15	US-10-274-095-43	Sequence 43, Appl
C 250	11.6	58.0	28	11	US-09-308-207-40	Sequence 40, Appl	C 323	11.2	56.0	22	14	US-10-066-498-8	Sequence 8, Appli
251	11.6	58.0	29	10	US-09-887-879-12	Sequence 12, Appl	C 324	11.2	56.0	22	14	US-10-066-498-24	Sequence 24, Appl
252	11.6	58.0	29	10	US-09-993-234-10	Sequence 10, Appl	C 325	11.2	56.0	24	11	US-09-940-185-535	Sequence 535, App
253	11.6	58.0	29	10	US-09-992-964-12	Sequence 12, Appl	C 326	11.2	56.0	25	10	US-09-789-453A-10	Sequence 10, Appl
254	11.6	58.0	29	12	US-10-423-448-4	Sequence 4, Appli	C 327	11.2	56.0	25	11	US-09-730-2898-1367	Sequence 1367, Ap
255	11.6	58.0	29	13	US-10-442-383-12	Sequence 12, Appl	C 328	11.2	56.0	25	11	US-09-730-2898-1368	Sequence 1368, Ap
256	11.6	58.0	29	13	US-10-288-917-4	Sequence 4, Appli	C 329	11.2	56.0	25	11	US-09-730-2898-1369	Sequence 1369, Ap
257	11.6	58.0	29	14	US-10-080-455-6	Sequence 6, Appli	C 330	11.2	56.0	25	11	US-09-730-2898-1370	Sequence 1370, Ap
258	11.6	58.0	29	14	US-10-052-798-4	Sequence 4, Appli	C 331	11.2	56.0	25	11	US-09-730-2898-1371	Sequence 1371, Ap
259	11.6	58.0	29	14	US-10-081-280-10	Sequence 10, Appl	C 332	11.2	56.0	25	11	US-09-730-2898-1372	Sequence 1372, Ap
260	11.6	58.0	29	14	US-10-112-793-10	Sequence 10, Appl	C 333	11.2	56.0	25	11	US-09-730-2898-1373	Sequence 1373, Ap
261	11.6	58.0	29	15	US-10-112-193-14	Sequence 14, Appl	C 334	11.2	56.0	25	11	US-09-730-2898-1374	Sequence 1374, Ap
262	11.6	58.0	32	10	US-09-031-629A-5	Sequence 5, Appli	C 335	11.2	56.0	25	11	US-09-730-2898-1375	Sequence 1375, Ap
C 263	11.6	58.0	33	10	US-09-797-941A-39	Sequence 39, Appl	C 336	11.2	56.0	25	11	US-09-730-2898-1376	Sequence 1376, Ap
264	11.6	58.0	35	15	US-10-235-682-8	Sequence 8, Appli	C 337	11.2	56.0	25	11	US-09-730-2898-1377	Sequence 1377, Ap
C 265	11.6	58.0	35	15	US-10-235-682-9	Sequence 9, Appli	C 338	11.2	56.0	25	11	US-09-730-2898-1378	Sequence 1378, Ap
266	11.6	58.0	37	8	US-08-860-844-38	Sequence 38, Appl	C 339	11.2	56.0	25	11	US-09-730-2898-1379	Sequence 1379, Ap
267	11.6	58.0	37	13	US-10-407-543-38	Sequence 38, Appl	C 340	11.2	56.0	25	11	US-09-730-2898-1380	Sequence 1380, Ap
268	11.6	58.0	38	11	US-09-888-326-417	Sequence 417, App	C 341	11.2	56.0	25	11	US-09-730-2898-1381	Sequence 1381, Ap
269	11.6	58.0	38	11	US-09-776-479-148	Sequence 148, App	C 342	11.2	56.0	25	11	US-09-730-2898-1382	Sequence 1382, Ap
270	11.6	58.0	38	15	US-10-112-653-141	Sequence 141, App	C 343	11.2	56.0	25	11	US-09-730-2898-1383	Sequence 1383, Ap
271	11.6	58.0	38	15	US-10-017-995-148	Sequence 148, App	C 344	11.2	56.0	25	11	US-09-730-2898-1384	Sequence 1384, Ap
272	11.6	58.0	40	16	US-10-260-212-14	Sequence 14, Appl	C 345	11.2	56.0	25	11	US-09-730-2898-1385	Sequence 1385, Ap
C 273	11.4	57.0	13	13	US-10-156-433-35	Sequence 35, Appl	C 346	11.2	56.0	25	11	US-09-730-2898-1386	Sequence 1386, Ap
C 274	11.4	57.0	13	13	US-10-112-814-35	Sequence 35, Appl	C 347	11.2	56.0	25	15	US-10-215-112-12667	Sequence 12667, A
275	11.4	57.0	14	15	US-10-146-058-64	Sequence 64, Appl	C 348	11.2	56.0	25	15	US-10-215-112-14154	Sequence 14154, A
276	11.4	57.0	18	10	US-09-263-959-1160	Sequence 1160, Ap	C 349	11.2	56.0	25	15	US-10-098-2638-17761	Sequence 17761, A
277	11.4	57.0	20	9	US-09-815-656-35	Sequence 35, Appl	C 350	11.2	56.0	25	15	US-10-098-2638-35833	Sequence 35833, A
278	11.4	57.0	20	12	US-10-189-267-74	Sequence 74, Appl	C 351	11.2	56.0	25	15	US-10-098-2638-35834	Sequence 35834, A
C 279	11.4	57.0	20	12	US-10-189-267-214	Sequence 214, App	C 352	11.2	56.0	25	15	US-10-098-2638-41992	Sequence 41992, A
C 280	11.4	57.0	21	15	US-10-120-187A-8	Sequence 8, Appli	C 353	11.2	56.0	25	15	US-10-098-2638-48010	Sequence 48010, A
281	11.4	57.0	22	13	US-10-168-445-178	Sequence 178, App	C 354	11.2	56.0	25	15	US-10-098-2638-50025	Sequence 50025, A
C 282	11.4	57.0	22	13	US-10-168-445-189	Sequence 189, App	C 355	11.2	56.0	25	15	US-10-098-2638-51529	Sequence 51529, A
C 283	11.4	57.0	23	13	US-10-320-095-14	Sequence 14, Appl	C 356	11.2	56.0	25	15	US-10-098-2638-59812	Sequence 59812, A
284	11.4	57.0	24	11	US-09-040-736-16	Sequence 16, Appl	C 357	11.2	56.0	25	15	US-10-098-2638-74219	Sequence 74219, A
285	11.4	57.0	25	11	US-09-940-185-679	Sequence 679, App	C 358	11.2	56.0	25	15	US-10-098-2638-106476	Sequence 106476, A
286	11.4	57.0	25	11	US-09-940-185-4645	Sequence 4645, App	C 359	11.2	56.0	26	9	US-09-989-002-21	Sequence 21, Appl
287	11.4	57.0	25	11	US-09-776-191-57	Sequence 57, Appl	C 360	11.2	56.0	26	13	US-10-441-126-21	Sequence 21, Appl
288	11.4	57.0	25	15	US-10-092-004A-7	Sequence 7, Appli	C 361	11.2	56.0	28	13	US-10-084-839-3091	Sequence 3091, Ap
C 289	11.4	57.0	25	15	US-10-215-112-11390	Sequence 11390, Ap	C 362	11.2	56.0	30	9	US-09-828-313-46	Sequence 46, Appl
290	11.4	57.0	25	15	US-10-215-112-9670	Sequence 9670, Ap	C 363	11.2	56.0	31	9	US-09-801-274-1453	Sequence 1453, Ap
291	11.4	57.0	25	15	US-10-215-112-12050	Sequence 12050, A	C 364	11.2	56.0	31	11	US-09-912-263-533	Sequence 533, App
292	11.4	57.0	25	15	US-10-098-2638-42244	Sequence 42244, A	C 365	11.2	56.0	32	10	US-09-843-777-23	Sequence 23, Appl
293	11.4	57.0	25	15	US-10-098-2638-53607	Sequence 53607, A	C 366	11.2	56.0	37	13	US-10-217-933-56	Sequence 56, Appl
C 294	11.4	57.0	25	15	US-10-098-2638-94582	Sequence 94582, A	C 367	11.2	56.0	38	13	US-09-405-032-165	Sequence 165, App
C 295	11.4	57.0	26	12	US-09-750-980D-43	Sequence 43, Appl	C 368	11.2	56.0	40	13	US-10-109-349A-192	Sequence 192, App
296	11.4	57.0	31	11	US-09-361-077-383	Sequence 383, App	C 369	11	55.0	18	9	US-09-104-654-4	Sequence 4, Appli
C 297	11.4	57.0	32	12	US-10-317-444-105	Sequence 105, App	C 370	11	55.0	19	13	US-10-251-117-784	Sequence 784, App
298	11.4	57.0	32	12	US-10-317-444-106	Sequence 106, App	C 371	11	55.0	19	13	US-10-251-117-1091	Sequence 1091, Ap
C 299	11.4	57.0	33	13	US-09-852-370-38	Sequence 38, Appl	C 372	11	55.0	20	12	US-10-173-817-6	Sequence 6, Appli
C 300	11.4	57.0	33	13	US-10-002-244-8	Sequence 8, Appli	C 373	11	55.0	20	13	US-09-813-432-75	Sequence 75, Appl
C 301	11.4	57.0	33	13	US-10-002-244-44	Sequence 44, Appl	C 374	11	55.0	20	13	US-10-348-485-116	Sequence 116, App
C 302	11.4	57.0	33	13	US-10-341-567-6	Sequence 6, Appli	C 375	11	55.0	20	13	US-10-203-939-35	Sequence 35, Appl
C 303	11.4	57.0	33	16	US-10-087-286-30	Sequence 30, Appl	C 376	11	55.0	20	13	US-10-174-364-75	Sequence 75, Appl
304	11.4	57.0	38	11	US-09-948-754A-3885	Sequence 3885, Ap	C 377	11	55.0	21	10	US-09-908-500A-28	Sequence 28, Appl
305	11.4	57.0	38	15	US-10-156-306-4587	Sequence 4587, Ap	C 378	11	55.0	21	12	US-10-170-096A-9	Sequence 9, Appli
306	11.2	56.0	17	11	US-09-776-474-454	Sequence 454, App	C 379	11	55.0	21	13	US-10-148-351-13	Sequence 13, Appl
307	11.2	56.0	17	11	US-09-776-474-1102	Sequence 1102, App	C 380	11	55.0	22	11	US-09-973-473-3	Sequence 3, Appli

c 381	11	55.0	23	9	US-09-187-289-7	Sequence 7, Appli	454	11	55.0	36	14	US-10-027-632-176541	Sequence 176541, A
c 382	11	55.0	23	9	US-09-187-289-8	Sequence 8, Appli	455	11	55.0	37	13	US-10-027-632-52497	Sequence 52497, A
c 383	11	55.0	23	13	US-10-032-585-4663	Sequence 4663, Ap	456	11	55.0	37	13	US-10-027-632-52514	Sequence 52514, A
c 384	11	55.0	24	13	US-10-132-069-21	Sequence 21, Appl	457	11	55.0	37	14	US-10-027-632-52497	Sequence 52497, A
c 385	11	55.0	25	9	US-09-402-100-25	Sequence 25, Appl	458	11	55.0	37	14	US-10-027-632-52514	Sequence 52514, A
c 386	11	55.0	25	9	US-09-866-108-12647	Sequence 12647, A	c 459	11	55.0	37	15	US-10-022-832-41	Sequence 41, Appl
c 387	11	55.0	25	9	US-09-866-108-12648	Sequence 12648, A	c 460	11	55.0	38	9	US-09-894-884A-15	Sequence 15, Appl
c 388	11	55.0	25	9	US-09-866-108-12649	Sequence 12649, A	c 461	11	55.0	38	10	US-09-996-650A-16	Sequence 16, Appl
c 389	11	55.0	25	9	US-09-866-108-12650	Sequence 12650, A	c 462	11	55.0	38	10	US-09-909-650A-3	Sequence 3, Appli
c 390	11	55.0	25	9	US-09-866-108-12651	Sequence 12651, A	c 463	11	55.0	38	10	US-09-884-948-16	Sequence 16, Appl
c 391	11	55.0	25	9	US-09-866-108-12652	Sequence 12652, A	c 464	11	55.0	38	13	US-10-317-832-224	Sequence 224, App
c 392	11	55.0	25	9	US-09-866-108-12653	Sequence 12653, A	c 465	11	55.0	40	9	US-09-245-802-38	Sequence 38, Appl
c 393	11	55.0	25	11	US-09-864-636A-2222	Sequence 2222, Ap	c 466	11	55.0	40	13	US-09-963-827B-132	Sequence 132, App
c 394	11	55.0	25	13	US-10-084-839-2222	Sequence 2222, Ap	c 467	10.8	54.0	17	9	US-09-866-108-2319	Sequence 2319, Ap
c 395	11	55.0	25	15	US-10-215-112-2435	Sequence 2435, Ap	c 468	10.8	54.0	17	9	US-09-866-108-2320	Sequence 2320, Ap
c 396	11	55.0	25	15	US-10-215-112-2561	Sequence 2561, Ap	c 469	10.8	54.0	17	9	US-09-866-108-2321	Sequence 2321, Ap
c 397	11	55.0	25	15	US-10-215-112-3310	Sequence 3310, Ap	c 470	10.8	54.0	17	9	US-09-866-108-2322	Sequence 2322, Ap
c 398	11	55.0	25	15	US-10-215-112-3436	Sequence 3436, Ap	c 471	10.8	54.0	17	11	US-09-730-289B-1	Sequence 1, Appli
c 399	11	55.0	25	15	US-10-215-112-11890	Sequence 11890, A	c 472	10.8	54.0	17	13	US-10-338-777-324	Sequence 324, App
c 400	11	55.0	25	15	US-10-215-112-13995	Sequence 13995, A	c 473	10.8	54.0	17	15	US-10-156-306-4373	Sequence 4373, Ap
c 401	11	55.0	25	15	US-10-215-112-14734	Sequence 14734, A	c 474	10.8	54.0	17	15	US-10-156-306-4779	Sequence 4779, Ap
c 402	11	55.0	25	15	US-10-098-263B-27	Sequence 27, Appl	c 475	10.8	54.0	17	15	US-10-156-306-4780	Sequence 4780, Ap
c 403	11	55.0	25	15	US-10-098-263B-1188	Sequence 1188, Ap	c 476	10.8	54.0	18	10	US-09-969-373-3194	Sequence 3194, Ap
c 404	11	55.0	25	15	US-10-098-263B-9367	Sequence 9367, Ap	c 477	10.8	54.0	19	13	US-10-225-023-689	Sequence 689, App
c 405	11	55.0	25	15	US-10-098-263B-9819	Sequence 9819, Ap	c 478	10.8	54.0	19	13	US-10-225-023-1427	Sequence 1427, Ap
c 406	11	55.0	25	15	US-10-098-263B-16639	Sequence 16639, A	c 479	10.8	54.0	20	9	US-09-802-669-117	Sequence 117, App
c 407	11	55.0	25	15	US-10-098-263B-16640	Sequence 16640, A	c 480	10.8	54.0	20	11	US-09-915-814-37	Sequence 37, Appl
c 408	11	55.0	25	15	US-10-098-263B-21149	Sequence 21149, A	c 481	10.8	54.0	20	11	US-09-972-607-14	Sequence 14, Appl
c 409	11	55.0	25	15	US-10-098-263B-21150	Sequence 21150, A	c 482	10.8	54.0	20	13	US-10-169-983-55	Sequence 55, Appl
c 410	11	55.0	25	15	US-10-098-263B-23341	Sequence 23341, A	c 483	10.8	54.0	20	13	US-10-169-983-55	Sequence 55, Appl
c 411	11	55.0	25	15	US-10-098-263B-24040	Sequence 24040, A	c 484	10.8	54.0	20	13	US-10-206-561-17	Sequence 17, Appl
c 412	11	55.0	25	15	US-10-098-263B-26362	Sequence 26362, A	c 485	10.8	54.0	20	13	US-09-767-421-49	Sequence 49, Appl
c 413	11	55.0	25	15	US-10-098-263B-35920	Sequence 35920, A	c 486	10.8	54.0	20	15	US-10-211-522-13	Sequence 13, Appl
c 414	11	55.0	25	15	US-10-098-263B-41077	Sequence 41077, A	c 487	10.8	54.0	20	15	US-10-144-000-5	Sequence 5, Appli
c 415	11	55.0	25	15	US-10-098-263B-54458	Sequence 54458, A	c 488	10.8	54.0	22	13	US-10-073-054-11	Sequence 11, Appl
c 416	11	55.0	25	15	US-10-098-263B-67873	Sequence 67873, A	c 489	10.8	54.0	22	13	US-10-073-054-14	Sequence 14, Appl
c 417	11	55.0	25	15	US-10-098-263B-68193	Sequence 68193, A	c 490	10.8	54.0	22	15	US-10-061-375A-3	Sequence 3, Appli
c 418	11	55.0	25	15	US-10-098-263B-69194	Sequence 69194, A	c 491	10.8	54.0	23	9	US-09-833-918-1	Sequence 1, Appli
c 419	11	55.0	25	15	US-10-098-263B-103004	Sequence 103004, A	c 492	10.8	54.0	23	11	US-09-991-936-1948	Sequence 1948, Ap
c 420	11	55.0	25	15	US-10-098-263B-113171	Sequence 113171, A	c 493	10.8	54.0	23	12	US-10-080-334-357	Sequence 357, App
c 421	11	55.0	25	15	US-10-098-263B-113172	Sequence 113172, A	c 494	10.8	54.0	23	12	US-10-080-334-360	Sequence 360, App
c 422	11	55.0	25	15	US-10-098-263B-114282	Sequence 114282, A	c 495	10.8	54.0	23	13	US-10-401-324-61	Sequence 61, Appl
c 423	11	55.0	25	15	US-10-098-263B-115224	Sequence 115224, A	c 496	10.8	54.0	23	14	US-10-105-662-2	Sequence 2, Appli
c 424	11	55.0	25	15	US-10-098-263B-120498	Sequence 120498, A	c 497	10.8	54.0	24	9	US-09-822-263-22	Sequence 22, Appl
c 425	11	55.0	25	15	US-10-098-263B-124000	Sequence 124000, A	c 498	10.8	54.0	24	11	US-09-940-185-3638	Sequence 3638, Ap
c 426	11	55.0	25	15	US-10-098-263B-127535	Sequence 127535, A	c 499	10.8	54.0	24	13	US-09-862-263-22	Sequence 22, Appl
c 427	11	55.0	25	15	US-10-098-263B-130789	Sequence 130789, A	c 500	10.8	54.0	24	13	US-10-032-585-4558	Sequence 4558, Ap
c 428	11	55.0	27	9	US-09-949-145-61	Sequence 61, Appl	c 501	10.8	54.0	25	9	US-09-866-108-5248	Sequence 5248, Ap
c 429	11	55.0	27	11	US-09-954-987B-209	Sequence 209, App	c 502	10.8	54.0	25	9	US-09-866-108-5249	Sequence 5249, Ap
c 430	11	55.0	27	13	US-10-272-502A-20	Sequence 20, Appl	c 503	10.8	54.0	25	9	US-09-866-108-5250	Sequence 5250, Ap
c 431	11	55.0	27	15	US-10-066-007-20	Sequence 20, Appl	c 504	10.8	54.0	25	9	US-09-866-108-5251	Sequence 5251, Ap
c 432	11	55.0	28	9	US-09-799-760-16	Sequence 16, Appl	c 505	10.8	54.0	25	9	US-09-866-108-5252	Sequence 5252, Ap
c 433	11	55.0	30	9	US-09-875-519A-8	Sequence 8, Appli	c 506	10.8	54.0	25	9	US-09-866-108-5253	Sequence 5253, Ap
c 434	11	55.0	30	13	US-10-084-706-33	Sequence 33, Appl	c 507	10.8	54.0	25	9	US-09-866-108-5254	Sequence 5254, Ap
c 435	11	55.0	30	13	US-10-084-706-35	Sequence 35, Appl	c 508	10.8	54.0	25	9	US-09-866-108-5255	Sequence 5255, Ap
c 436	11	55.0	30	13	US-10-084-706-43	Sequence 43, Appl	c 509	10.8	54.0	25	9	US-09-866-108-5256	Sequence 5256, Ap
c 437	11	55.0	30	13	US-10-084-706-44	Sequence 44, Appl	c 510	10.8	54.0	25	9	US-09-866-108-5257	Sequence 5257, Ap
c 438	11	55.0	30	13	US-10-325-720-33	Sequence 33, Appl	c 511	10.8	54.0	25	9	US-09-866-108-5258	Sequence 5258, Ap
c 439	11	55.0	30	13	US-10-325-720-35	Sequence 35, Appl	c 512	10.8	54.0	25	9	US-09-866-108-5259	Sequence 5259, Ap
c 440	11	55.0	30	13	US-10-351-189-33	Sequence 33, Appl	c 513	10.8	54.0	25	11	US-09-754-853A-621	Sequence 621, App
c 441	11	55.0	30	13	US-10-351-189-35	Sequence 35, Appl	c 514	10.8	54.0	25	11	US-09-730-289B-1366	Sequence 1366, Ap
c 442	11	55.0	30	14	US-10-004-201-26	Sequence 26, Appl	c 515	10.8	54.0	25	11	US-09-730-289B-3280	Sequence 3280, Ap
c 443	11	55.0	31	14	US-10-004-201-28	Sequence 28, Appl	c 516	10.8	54.0	25	15	US-10-215-112-980	Sequence 980, App
c 444	11	55.0	31	14	US-09-740-332-6769	Sequence 6769, Ap	c 517	10.8	54.0	25	15	US-10-215-112-2703	Sequence 2703, Ap
c 445	11	55.0	31	13	US-09-817-879-6769	Sequence 6769, Ap	c 518	10.8	54.0	25	15	US-10-098-263B-19765	Sequence 19765, A
c 446	11	55.0	33	9	US-09-817-414-5	Sequence 5, Appli	c 519	10.8	54.0	25	15	US-10-098-263B-19765	Sequence 19765, A
c 447	11	55.0	34	11	US-09-864-636A-961	Sequence 961, App	c 520	10.8	54.0	25	15	US-10-098-263B-21339	Sequence 21339, A
c 448	11	55.0	34	11	US-09-864-636A-961	Sequence 961, App	c 521	10.8	54.0	25	15	US-10-098-263B-21340	Sequence 21340, A
c 449	11	55.0	34	13	US-10-084-839-961	Sequence 961, App	c 522	10.8	54.0	25	15	US-10-098-263B-25523	Sequence 25523, A
c 450	11	55.0	34	13	US-10-084-839-961	Sequence 961, App	c 523	10.8	54.0	25	15	US-10-098-263B-32707	Sequence 32707, A
c 451	11	55.0	36	10	US-09-797-941A-33	Sequence 33, Appl	c 524	10.8	54.0	25	15	US-10-098-263B-37268	Sequence 37268, A
c 452	11	55.0	36	13	US-10-214-419-7	Sequence 7, Appli	c 525	10.8	54.0	25	15	US-10-098-263B-41070	Sequence 41070, A
c 453	11	55.0	36	13	US-10-027-632-176541	Sequence 176541, A	c 526	10.8	54.0	25	15	US-10-098-263B-54903	Sequence 54903, A

527	10.8	54.0	25	15	US-10-098-263B-54904	Sequence 54904, A	600	10.8	54.0	38	11	US-09-776-474-1710	Sequence 1665, Ap
528	10.8	54.0	25	15	US-10-098-263B-63102	Sequence 63102, A	601	10.8	54.0	38	11	US-09-776-474-1710	Sequence 1710, Ap
529	10.8	54.0	25	15	US-10-098-263B-67549	Sequence 67549, A	602	10.8	54.0	38	11	US-09-776-474-1710	Sequence 1844, Ap
530	10.8	54.0	25	15	US-10-098-263B-73077	Sequence 73077, A	603	10.8	54.0	38	11	US-09-930-423-2184	Sequence 2184, Ap
531	10.8	54.0	25	15	US-10-098-263B-84630	Sequence 84630, A	604	10.8	54.0	38	11	US-09-930-423-2259	Sequence 2259, Ap
532	10.8	54.0	25	15	US-10-098-263B-94251	Sequence 94251, A	605	10.8	54.0	38	11	US-09-930-423-2259	Sequence 2259, Ap
533	10.8	54.0	25	15	US-10-098-263B-102791	Sequence 102791, A	606	10.8	54.0	38	11	US-09-930-423-2259	Sequence 2259, Ap
534	10.8	54.0	25	15	US-10-098-263B-104260	Sequence 104260, A	607	10.8	54.0	38	11	US-09-780-164-1209	Sequence 1209, Ap
535	10.8	54.0	25	15	US-10-098-263B-107077	Sequence 107077, A	608	10.8	54.0	38	11	US-09-780-164-1209	Sequence 1209, Ap
536	10.8	54.0	25	15	US-10-098-263B-113879	Sequence 113879, A	609	10.8	54.0	38	11	US-09-745-237A-2184	Sequence 2184, Ap
537	10.8	54.0	25	15	US-10-098-263B-114853	Sequence 114853, A	610	10.8	54.0	38	13	US-09-745-237A-2184	Sequence 2184, Ap
538	10.8	54.0	25	15	US-10-098-263B-114854	Sequence 114854, A	611	10.8	54.0	38	13	US-09-745-237A-2447	Sequence 2447, Ap
539	10.8	54.0	25	15	US-10-098-263B-123747	Sequence 123747, A	612	10.8	54.0	38	13	US-09-792-818-1148	Sequence 1148, Ap
540	10.8	54.0	25	15	US-10-098-263B-125085	Sequence 125085, A	613	10.8	54.0	38	13	US-09-792-818-1148	Sequence 1148, Ap
541	10.8	54.0	25	15	US-09-791-489-23	Sequence 489, A	614	10.8	54.0	38	13	US-09-792-818-1377	Sequence 1377, Ap
542	10.8	54.0	27	11	US-09-961-077-968	Sequence 968, Ap	615	10.8	54.0	38	13	US-09-792-818-1377	Sequence 1377, Ap
543	10.8	54.0	27	11	US-09-961-077-1050	Sequence 1050, Ap	616	10.8	54.0	38	13	US-10-230-006-343	Sequence 343, Ap
544	10.8	54.0	27	11	US-09-961-077-1103	Sequence 1103, Ap	617	10.8	54.0	38	13	US-10-230-006-343	Sequence 343, Ap
545	10.8	54.0	29	12	US-10-383-773-1	Sequence 1, Appl	618	10.8	54.0	38	15	US-10-156-306-735	Sequence 735, Ap
546	10.8	54.0	29	13	US-10-071-962-4	Sequence 4, Appl	619	10.8	54.0	38	15	US-10-156-306-735	Sequence 735, Ap
547	10.8	54.0	29	13	US-10-400-487-12	Sequence 12, Appl	620	10.8	54.0	38	15	US-10-156-306-772	Sequence 772, Ap
548	10.8	54.0	30	10	US-09-953-321-11	Sequence 11, Appl	621	10.8	54.0	38	15	US-10-156-306-1779	Sequence 1779, Ap
549	10.8	54.0	30	10	US-10-084-706-41	Sequence 41, Appl	622	10.8	54.0	38	15	US-10-156-306-2101	Sequence 2101, Ap
550	10.8	54.0	30	13	US-10-084-706-42	Sequence 42, Appl	623	10.8	54.0	38	15	US-10-156-306-2258	Sequence 2258, Ap
551	10.8	54.0	31	9	US-09-801-274-941	Sequence 941, Appl	624	10.8	54.0	38	15	US-10-156-306-4621	Sequence 4621, Ap
552	10.8	54.0	31	11	US-09-961-077-315	Sequence 315, Appl	625	10.8	54.0	38	15	US-10-156-306-5261	Sequence 5261, Ap
553	10.8	54.0	31	11	US-09-912-263-471	Sequence 471, Appl	626	10.8	54.0	38	15	US-10-156-306-5375	Sequence 5375, Ap
554	10.8	54.0	31	13	US-10-401-324-62	Sequence 62, Appl	627	10.6	53.0	17	9	US-10-156-306-5565	Sequence 5565, Ap
555	10.8	54.0	32	10	US-09-940-037A-10	Sequence 10, Appl	628	10.6	53.0	17	11	US-10-393-602-39	Sequence 39, Appl
556	10.8	54.0	32	10	US-09-940-037A-11	Sequence 11, Appl	629	10.6	53.0	17	11	US-09-866-108-9513	Sequence 9513, Ap
557	10.8	54.0	34	10	US-09-797-941A-34	Sequence 34, Appl	630	10.6	53.0	17	13	US-09-848-754A-520	Sequence 520, Ap
558	10.8	54.0	34	13	US-10-401-344-21	Sequence 21, Appl	631	10.6	53.0	17	13	US-09-740-332-3163	Sequence 3163, Ap
559	10.8	54.0	35	10	US-09-771-009-62	Sequence 62, Appl	632	10.6	53.0	19	12	US-09-817-879-3163	Sequence 3163, Ap
560	10.8	54.0	36	9	US-09-504-231A-1882	Sequence 1882, Ap	633	10.6	53.0	19	12	US-10-339-793-421	Sequence 421, Ap
561	10.8	54.0	36	9	US-09-504-231A-2188	Sequence 2188, Ap	634	10.6	53.0	19	12	US-10-349-143-7411	Sequence 7411, Ap
562	10.8	54.0	36	9	US-09-504-231A-2713	Sequence 2713, Ap	635	10.6	53.0	20	12	US-10-225-023-606	Sequence 606, Ap
563	10.8	54.0	36	9	US-09-504-231A-2726	Sequence 2726, Ap	636	10.6	53.0	20	12	US-10-225-023-1344	Sequence 1344, Ap
564	10.8	54.0	36	9	US-09-504-231A-2726	Sequence 2726, Ap	637	10.6	53.0	20	12	US-10-187-659A-59	Sequence 59, Appl
565	10.8	54.0	36	9	US-09-504-231A-2726	Sequence 2726, Ap	638	10.6	53.0	20	12	US-10-289-762-6189	Sequence 6189, Ap
566	10.8	54.0	36	9	US-09-504-231A-2726	Sequence 2726, Ap	639	10.6	53.0	20	12	US-10-376-566-34	Sequence 34, Appl
567	10.8	54.0	36	9	US-09-504-231A-2726	Sequence 2726, Ap	640	10.6	53.0	20	12	US-10-094-743-3316	Sequence 3316, Ap
568	10.8	54.0	36	9	US-09-504-231A-2726	Sequence 2726, Ap	641	10.6	53.0	21	10	US-09-848-585-39	Sequence 39, Appl
569	10.8	54.0	36	11	US-09-903-412-26	Sequence 2, Appl	642	10.6	53.0	21	11	US-09-972-115A-46	Sequence 46, Appl
570	10.8	54.0	36	11	US-09-903-412-26	Sequence 2, Appl	643	10.6	53.0	22	12	US-09-955-363-32	Sequence 32, Appl
571	10.8	54.0	36	13	US-10-165-155-26	Sequence 26, Appl	644	10.6	53.0	22	12	US-09-985-198-285	Sequence 285, Appl
572	10.8	54.0	36	13	US-10-165-155-26	Sequence 26, Appl	645	10.6	53.0	22	13	US-09-912-976-76	Sequence 15, Appl
573	10.8	54.0	36	13	US-10-440-850-1556	Sequence 1556, Ap	646	10.6	53.0	22	13	US-09-912-976-76	Sequence 76, Appl
574	10.8	54.0	36	13	US-10-440-850-1556	Sequence 1556, Ap	647	10.6	53.0	22	13	US-10-402-017-18	Sequence 18, Appl
575	10.8	54.0	36	13	US-10-440-850-1556	Sequence 1556, Ap	648	10.6	53.0	22	15	US-10-216-122-148	Sequence 148, Ap
576	10.8	54.0	36	13	US-10-440-850-1556	Sequence 1556, Ap	649	10.6	53.0	22	15	US-10-216-122-148	Sequence 148, Ap
577	10.8	54.0	36	13	US-10-440-850-1556	Sequence 1556, Ap	650	10.6	53.0	23	11	US-09-978-600-132	Sequence 132, Ap
578	10.8	54.0	36	14	US-10-008-620-2	Sequence 2, Appl	651	10.6	53.0	23	8	US-08-591-4868-30	Sequence 30, Appl
579	10.8	54.0	37	9	US-09-504-231A-3145	Sequence 3145, Ap	652	10.6	53.0	24	10	US-09-169-048-9	Sequence 9, Appl
580	10.8	54.0	37	9	US-09-504-231A-3145	Sequence 3145, Ap	653	10.6	53.0	24	11	US-09-815-981-2	Sequence 2, Appl
581	10.8	54.0	37	11	US-09-848-754A-9473	Sequence 9473, Ap	654	10.6	53.0	24	11	US-09-815-981-2	Sequence 2, Appl
582	10.8	54.0	38	11	US-09-780-533A-2806	Sequence 2806, Ap	655	10.6	53.0	24	11	US-09-815-981-2	Sequence 2, Appl
583	10.8	54.0	38	11	US-09-780-533A-2813	Sequence 2813, Ap	656	10.6	53.0	24	11	US-09-815-981-2	Sequence 2, Appl
584	10.8	54.0	38	11	US-09-780-533A-3033	Sequence 3033, Ap	657	10.6	53.0	24	11	US-09-815-981-2	Sequence 2, Appl
585	10.8	54.0	38	11	US-09-780-533A-3033	Sequence 3033, Ap	658	10.6	53.0	24	11	US-09-815-981-2	Sequence 2, Appl
586	10.8	54.0	38	11	US-09-780-533A-3136	Sequence 3136, Ap	659	10.6	53.0	24	11	US-09-815-981-2	Sequence 2, Appl
587	10.8	54.0	38	11	US-09-780-533A-3773	Sequence 3773, Ap	660	10.6	53.0	24	13	US-09-997-209-9	Sequence 9, Appl
588	10.8	54.0	38	11	US-09-780-533A-4154	Sequence 4154, Ap	661	10.6	53.0	24	13	US-09-839-469-9	Sequence 9, Appl
589	10.8	54.0	38	11	US-09-877-478-3756	Sequence 3756, Ap	662	10.6	53.0	24	13	US-10-086-745-2	Sequence 2, Appl
590	10.8	54.0	38	11	US-09-877-478-3756	Sequence 3756, Ap	663	10.6	53.0	24	13	US-10-086-745-2	Sequence 2, Appl
591	10.8	54.0	38	11	US-09-877-478-3756	Sequence 3756, Ap	664	10.6	53.0	24	13	US-09-898-200-12	Sequence 12, Appl
592	10.8	54.0	38	11	US-09-877-478-3756	Sequence 3756, Ap	665	10.6	53.0	24	13	US-10-235-119-2	Sequence 2, Appl
593	10.8	54.0	38	11	US-09-848-754A-3948	Sequence 3948, Ap	666	10.6	53.0	25	9	US-09-866-108-14405	Sequence 14405, A
594	10.8	54.0	38	11	US-09-848-754A-4049	Sequence 4049, Ap	667	10.6	53.0	25	9	US-09-866-108-14406	Sequence 14406, A
595	10.8	54.0	38	11	US-09-848-754A-4058	Sequence 4058, Ap	668	10.6	53.0	25	9	US-09-866-108-14407	Sequence 14407, A
596	10.8	54.0	38	11	US-09-848-754A-4329	Sequence 4329, Ap	669	10.6	53.0	25	9	US-09-866-108-14408	Sequence 14408, A
597	10.8	54.0	38	11	US-09-848-754A-4671	Sequence 4671, Ap	670	10.6	53.0	25	9	US-09-866-108-14409	Sequence 14409, A
598	10.8	54.0	38	11	US-09-848-754A-4732	Sequence 4732, Ap	671	10.6	53.0	25	9	US-09-866-108-14410	Sequence 14410, A
599	10.8	54.0	38	11	US-09-848-754A-5279	Sequence 5279, Ap	672	10.6	53.0	25	9	US-09-866-108-14411	Sequence 14411, A
					Sequence 5456, Ap							US-09-866-108-14412	Sequence 14412, A
					Sequence 1437, Ap							US-09-866-108-14413	Sequence 14413, A
												US-10-215-112-1605	Sequence 1605, Ap
												US-10-215-112-10218	Sequence 10218, A
												US-10-215-112-11977	Sequence 11977, A
												US-10-215-112-12103	Sequence 12103, A
												US-10-215-112-12874	Sequence 12874, A
												US-10-215-112-13810	Sequence 13810, A
												US-10-098-263B-5721	Sequence 5721, Ap
												US-10-098-263B-5722	Sequence 5722, Ap

c 673	10.6	53.0	25	15	US-10-098-263B-6208	Sequence 6208, Ap	c 746	10.6	53.0	40	13	US-09-963-827B-124	Sequence 124, App
c 674	10.6	53.0	25	15	US-10-098-263B-7860	Sequence 7860, Ap	747	10.6	53.0	40	15	US-10-133-205-2	Sequence 2, Appl
c 675	10.6	53.0	25	15	US-10-098-263B-21265	Sequence 21265, A	748	10.4	52.0	17	10	US-09-263-959-42	Sequence 42, Appl
c 676	10.6	53.0	25	15	US-10-098-263B-21745	Sequence 21745, A	c 749	10.4	52.0	18	10	US-09-969-373-3746	Sequence 3746, Ap
c 677	10.6	53.0	25	15	US-10-098-263B-23057	Sequence 23057, A	750	10.4	52.0	18	10	US-09-966-147-38	Sequence 38, Appl
c 678	10.6	53.0	25	15	US-10-098-263B-34095	Sequence 34095, A	751	10.4	52.0	18	10	US-09-887-880-41	Sequence 41, Appl
c 679	10.6	53.0	25	15	US-10-098-263B-35449	Sequence 35449, A	c 752	10.4	52.0	18	12	US-10-371-099-46	Sequence 46, Appl
c 680	10.6	53.0	25	15	US-10-098-263B-47668	Sequence 47668, A	c 753	10.4	52.0	18	12	US-10-371-099-47	Sequence 47, Appl
c 681	10.6	53.0	25	15	US-10-098-263B-50616	Sequence 50616, A	c 754	10.4	52.0	18	12	US-10-349-143-5504	Sequence 5504, Ap
c 682	10.6	53.0	25	15	US-10-098-263B-51563	Sequence 51563, A	c 755	10.4	52.0	18	12	US-10-371-122-46	Sequence 46, Appl
c 683	10.6	53.0	25	15	US-10-098-263B-53977	Sequence 53977, A	c 756	10.4	52.0	18	12	US-10-371-122-47	Sequence 47, Appl
c 684	10.6	53.0	25	15	US-10-098-263B-54605	Sequence 54605, A	757	10.4	52.0	18	13	US-10-327-776-9	Sequence 9, Appl
c 685	10.6	53.0	25	15	US-10-098-263B-63430	Sequence 63430, A	758	10.4	52.0	18	13	US-10-374-469-38	Sequence 38, Appl
c 686	10.6	53.0	25	15	US-10-098-263B-81635	Sequence 81635, A	c 759	10.4	52.0	18	13	US-10-423-007-28	Sequence 28, Appl
c 687	10.6	53.0	25	15	US-10-098-263B-81636	Sequence 81636, A	c 760	10.4	52.0	20	9	US-03-802-669-9	Sequence 9, Appl
c 688	10.6	53.0	25	15	US-10-098-263B-83393	Sequence 83393, A	c 761	10.4	52.0	20	11	US-09-766-450-43	Sequence 43, Appl
c 689	10.6	53.0	25	15	US-10-098-263B-95291	Sequence 95291, A	c 762	10.4	52.0	20	11	US-09-972-469-58	Sequence 58, Appl
c 690	10.6	53.0	25	15	US-10-098-263B-108495	Sequence 108495, A	c 763	10.4	52.0	20	11	US-09-915-485-36	Sequence 36, Appl
c 691	10.6	53.0	25	15	US-10-098-263B-110621	Sequence 110621, A	c 764	10.4	52.0	20	11	US-09-918-187-72	Sequence 72, Appl
c 692	10.6	53.0	25	15	US-10-098-263B-114359	Sequence 114359, A	c 765	10.4	52.0	20	12	US-10-408-571A-6	Sequence 6, Appl
c 693	10.6	53.0	25	15	US-10-098-263B-119336	Sequence 119336, A	c 766	10.4	52.0	20	12	US-10-349-143-10396	Sequence 10396, A
c 694	10.6	53.0	25	15	US-10-098-263B-121324	Sequence 121324, A	767	10.4	52.0	20	13	US-10-380-913-7	Sequence 7, Appl
c 695	10.6	53.0	25	15	US-10-098-263B-123793	Sequence 123793, A	c 768	10.4	52.0	20	13	US-09-843-377-40	Sequence 40, Appl
c 696	10.6	53.0	25	15	US-10-098-263B-125842	Sequence 125842, A	c 769	10.4	52.0	20	13	US-09-851-871-42	Sequence 42, Appl
c 697	10.6	53.0	25	15	US-09-808-602-38	Sequence 38, Appl	c 770	10.4	52.0	21	9	US-09-736-863-13	Sequence 13, Appl
c 698	10.6	53.0	26	11	US-09-800-199-36	Sequence 36, Appl	c 771	10.4	52.0	21	11	US-09-796-679-22	Sequence 22, Appl
c 699	10.6	53.0	26	12	US-10-417-923-31	Sequence 31, Appl	c 772	10.4	52.0	21	13	US-10-349-143-10785	Sequence 10785, A
c 700	10.6	53.0	26	16	US-10-338-694-4	Sequence 4, Appl	c 773	10.4	52.0	21	13	US-10-251-598-18	Sequence 18, Appl
c 701	10.6	53.0	27	13	US-10-079-167-9	Sequence 9, Appl	c 774	10.4	52.0	22	12	US-10-024-212-161	Sequence 161, App
c 702	10.6	53.0	29	9	US-09-745-763-161	Sequence 161, App	c 775	10.4	52.0	23	10	US-09-969-373-4441	Sequence 4441, App
c 703	10.6	53.0	29	10	US-09-920-581-8	Sequence 8, Appl	c 776	10.4	52.0	24	11	US-09-922-146-5	Sequence 5, Appl
c 704	10.6	53.0	29	11	US-09-951-061A-40	Sequence 40, Appl	c 777	10.4	52.0	24	11	US-09-940-185-1699	Sequence 1699, Ap
c 705	10.6	53.0	29	13	US-10-371-421-8	Sequence 8, Appl	c 778	10.4	52.0	24	11	US-09-940-185-2170	Sequence 2170, Ap
c 706	10.6	53.0	29	15	US-10-267-384-39	Sequence 39, Appl	c 779	10.4	52.0	24	13	US-09-940-185-2177	Sequence 2177, Ap
c 707	10.6	53.0	29	15	US-10-060-585-16	Sequence 16, Appl	c 780	10.4	52.0	25	13	US-10-061-201-2824	Sequence 2824, Ap
c 708	10.6	53.0	30	13	US-10-295-362-14	Sequence 14, Appl	c 781	10.4	52.0	25	13	US-10-061-201-2825	Sequence 2825, Ap
c 709	10.6	53.0	31	9	US-09-801-274-660	Sequence 660, App	c 782	10.4	52.0	25	13	US-10-061-201-2826	Sequence 2826, Ap
c 710	10.6	53.0	31	9	US-09-801-274-928	Sequence 928, App	c 783	10.4	52.0	25	13	US-10-061-201-2827	Sequence 2827, Ap
c 711	10.6	53.0	31	11	US-09-870-759-145	Sequence 145, App	c 784	10.4	52.0	25	13	US-10-061-201-2828	Sequence 2828, Ap
c 712	10.6	53.0	31	11	US-09-912-263-436	Sequence 436, App	c 785	10.4	52.0	25	13	US-10-061-201-2829	Sequence 2829, Ap
c 713	10.6	53.0	31	13	US-10-379-981-7	Sequence 7, Appl	c 786	10.4	52.0	25	13	US-10-296-540-46	Sequence 46, Appl
c 714	10.6	53.0	31	13	US-09-751-708A-145	Sequence 145, App	c 787	10.4	52.0	25	15	US-10-215-112-2723	Sequence 2723, Ap
c 715	10.6	53.0	32	9	US-09-740-668A-49	Sequence 49, Appl	c 788	10.4	52.0	25	15	US-10-215-112-2849	Sequence 2849, Ap
c 716	10.6	53.0	32	11	US-09-977-418-89	Sequence 89, Appl	c 789	10.4	52.0	25	15	US-10-215-112-4041	Sequence 4041, Ap
c 717	10.6	53.0	32	11	US-09-977-033A-89	Sequence 89, Appl	c 790	10.4	52.0	25	15	US-10-215-112-4164	Sequence 4164, Ap
c 718	10.6	53.0	32	12	US-09-977-819B-89	Sequence 89, Appl	c 791	10.4	52.0	25	15	US-10-215-112-5891	Sequence 5891, Ap
c 719	10.6	53.0	32	13	US-09-389-782-10	Sequence 10, Appl	c 792	10.4	52.0	25	15	US-10-215-112-13687	Sequence 13687, A
c 720	10.6	53.0	32	13	US-09-977-751C-89	Sequence 89, Appl	c 793	10.4	52.0	25	15	US-10-098-263B-895	Sequence 895, App
c 721	10.6	53.0	32	13	US-10-119-431-32	Sequence 32, Appl	c 794	10.4	52.0	25	15	US-10-098-263B-7181	Sequence 7181, Ap
c 722	10.6	53.0	32	13	US-09-736-116-32	Sequence 32, Appl	c 795	10.4	52.0	25	15	US-10-098-263B-7182	Sequence 7182, Ap
c 723	10.6	53.0	32	13	US-09-977-639A-89	Sequence 89, Appl	c 796	10.4	52.0	25	15	US-10-098-263B-10168	Sequence 10168, A
c 724	10.6	53.0	33	10	US-09-729-520-8	Sequence 8, Appl	c 797	10.4	52.0	25	15	US-10-098-263B-11623	Sequence 11623, A
c 725	10.6	53.0	33	13	US-10-164-085-20	Sequence 20, Appl	c 798	10.4	52.0	25	15	US-10-098-263B-11623	Sequence 11623, A
c 726	10.6	53.0	33	13	US-10-002-750-20	Sequence 20, Appl	c 799	10.4	52.0	25	15	US-10-098-263B-15777	Sequence 15777, A
c 727	10.6	53.0	33	14	US-10-008-620-8	Sequence 8, Appl	c 800	10.4	52.0	25	15	US-10-098-263B-15778	Sequence 15778, A
c 728	10.6	53.0	33	15	US-10-002-720-20	Sequence 20, Appl	c 801	10.4	52.0	25	15	US-10-098-263B-22201	Sequence 22201, A
c 729	10.6	53.0	33	15	US-10-272-041-20	Sequence 20, Appl	c 802	10.4	52.0	25	15	US-10-098-263B-22202	Sequence 22202, A
c 730	10.6	53.0	34	9	US-09-790-417-232	Sequence 232, App	c 803	10.4	52.0	25	15	US-10-098-263B-22855	Sequence 22855, A
c 731	10.6	53.0	34	9	US-09-790-417-234	Sequence 234, App	c 804	10.4	52.0	25	15	US-10-098-263B-26587	Sequence 26587, A
c 732	10.6	53.0	36	11	US-09-853-079-156	Sequence 156, App	c 805	10.4	52.0	25	15	US-10-098-263B-27840	Sequence 27840, A
c 733	10.6	53.0	36	11	US-09-853-079-162	Sequence 162, App	c 806	10.4	52.0	25	15	US-10-098-263B-28208	Sequence 28208, A
c 734	10.6	53.0	38	10	US-09-874-389-11	Sequence 11, Appl	c 807	10.4	52.0	25	15	US-10-098-263B-32089	Sequence 32089, A
c 735	10.6	53.0	38	12	US-09-921-650-11	Sequence 11, Appl	c 808	10.4	52.0	25	15	US-10-098-263B-32090	Sequence 32090, A
c 736	10.6	53.0	38	12	US-09-241-347-11	Sequence 11, Appl	c 809	10.4	52.0	25	15	US-10-098-263B-32090	Sequence 32090, A
c 737	10.6	53.0	38	12	US-10-453-483-62	Sequence 62, Appl	c 810	10.4	52.0	25	15	US-10-098-263B-34619	Sequence 34619, A
c 738	10.6	53.0	38	13	US-10-301-516-8	Sequence 8, Appl	c 811	10.4	52.0	25	15	US-10-098-263B-42243	Sequence 42243, A
c 739	10.6	53.0	38	13	US-10-326-671-51	Sequence 51, Appl	c 812	10.4	52.0	25	15	US-10-098-263B-44050	Sequence 44050, A
c 740	10.6	53.0	38	15	US-10-032-393-62	Sequence 62, Appl	c 813	10.4	52.0	25	15	US-10-098-263B-45022	Sequence 45022, A
c 741	10.6	53.0	39	13	US-10-021-632-58408	Sequence 58408, A	c 814	10.4	52.0	25	15	US-10-098-263B-52711	Sequence 52711, A
c 742	10.6	53.0	39	14	US-10-027-632-58408	Sequence 58408, A	c 815	10.4	52.0	25	15	US-10-098-263B-52711	Sequence 52711, A
c 743	10.6	53.0	39	15	US-10-237-563-61	Sequence 61, Appl	c 816	10.4	52.0	25	15	US-10-098-263B-5317	Sequence 5317, A
c 744	10.6	53.0	40	13	US-09-963-827B-110	Sequence 110, App	c 817	10.4	52.0	25	15	US-10-098-263B-53608	Sequence 53608, A
c 745	10.6	53.0	40	13	US-09-963-827B-116	Sequence 116, App	c 818	10.4	52.0	25	15	US-10-098-263B-55491	Sequence 55491, A
												US-10-098-263B-55699	Sequence 55699, A

Sequence 166, App
 Sequence 29, Appl
 Sequence 1377, Ap
 Sequence 3291, Ap
 Sequence 14, Appl
 Sequence 4271, Ap
 Sequence 165, App
 Sequence 3130, Ap
 Sequence 4074, Ap
 Sequence 5573, Ap
 Sequence 7723, Ap
 Sequence 11834, A
 Sequence 12590, A
 Sequence 10581, A
 Sequence 19909, A
 Sequence 20781, A
 Sequence 21045, A
 Sequence 21242, A
 Sequence 23486, A
 Sequence 24090, A
 Sequence 25083, A
 Sequence 28294, A
 Sequence 33816, A
 Sequence 40492, A
 Sequence 42768, A
 Sequence 43882, A
 Sequence 45914, A
 Sequence 4816, A
 Sequence 49776, A
 Sequence 51034, A
 Sequence 54304, A
 Sequence 54761, A
 Sequence 59395, A
 Sequence 60023, A
 Sequence 60381, A
 Sequence 60723, A

ALIGNMENTS

RESULT 1
 US-09-835-371-38
 ; Sequence 38, Application US/09835371
 ; Publication No. US20020187473A1
 ; GENERAL INFORMATION:
 ; APPLICANT: UHLMANN, Eugen
 ; APPLICANT: BREIPOHL, Gerhard
 ; APPLICANT: WILL, David W
 ; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES, AND AGENTS AND
 ; TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
 ; FILE REFERENCE: 02481.1743 SEQUENCE LISTING
 ; CURRENT APPLICATION NUMBER: US/09/835,371
 ; CURRENT FILING DATE: 2001-04-17
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 38
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: base sequence
 ; OTHER INFORMATION: of PNA targeting CMV
 US-09-835-371-38

Query Match 100.0%; Score 20; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 2
 US-09-835-370-38
 ; Sequence 38, Application US/09835370
 ; Publication No. US20030022172A1
 ; GENERAL INFORMATION:
 ; APPLICANT: UHLMANN, EUGEN
 ; APPLICANT: BREIPOHL, GERHARD
 ; APPLICANT: WILL, DAVID W
 ; TITLE OF INVENTION: POLYAMIDE NUCLEIC ACID DERIVATIVES AND AGENTS AND
 ; TITLE OF INVENTION: PROCESSES FOR PREPARING THEM
 ; FILE REFERENCE: 02481.1742 SEQUENCE LISTING
 ; CURRENT APPLICATION NUMBER: US/09/835,370
 ; CURRENT FILING DATE: 2001-04-17
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 38
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
 ; OTHER INFORMATION: base sequence of PNA derivatives that bind to
 ; OTHER INFORMATION: viral and cellular targets
 US-09-835-370-38

Query Match 100.0%; Score 20; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 3
 US-09-931-732-18
 ; Sequence 18, Application US/09931732
 ; Publication No. US20030045488A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Bob D.
 ; APPLICANT: Riley, Timothy A.
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES COMPRISING
 ; TITLE OF INVENTION: UNIVERSAL AND/OR DEGENERATE BASES
 ; FILE REFERENCE: OASBIO.001C1
 ; CURRENT APPLICATION NUMBER: US/09/931,732
 ; CURRENT FILING DATE: 2001-08-16
 ; PRIOR APPLICATION NUMBER: PCT/US00/09293
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: US 60/128,377
 ; PRIOR FILING DATE: 1999-04-08
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic oligonucleotide primers
 US-09-931-732-18

Query Match 100.0%; Score 20; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 4
 US-09-747-009-27
 ; Sequence 27, Application US/09747009

```
; Publication No. US20030050454A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Sanghvi, Yogesh S.
; APPLICANT: Ross, Bruce S.
; APPLICANT: Griffey, Rich H.
; APPLICANT: Springer, Robert H.
; APPLICANT: Sprankle, Kelly G.
; TITLE OF INVENTION: Improved Process For The Synthesis Of 2'-O-Substituted Pyrimidine
; TITLE OF INVENTION: Oligomeric Compounds Therefrom
; FILE REFERENCE: ISIS-4684
; CURRENT APPLICATION NUMBER: US/09/747,009
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 08/894,899
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: PCT/US96/03174
; PRIOR FILING DATE: 1996-01-07
; PRIOR APPLICATION NUMBER: 08/475,467
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/398,901
; PRIOR FILING DATE: 1995-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20030050454A1el Sequence
US-09-747-009-27

Query Match      100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCTCGCTGCTGAGTTTCA 20
Db      1 GTTCTCGCTGCTGAGTTTCA 20

RESULT 5
US-09-747-009-28
; Sequence 28, Application US/09747009
; Publication No. US20030050454A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Sanghvi, Yogesh S.
; APPLICANT: Ross, Bruce S.
; APPLICANT: Griffey, Rich H.
; APPLICANT: Springer, Robert H.
; APPLICANT: Sprankle, Kelly G.
; TITLE OF INVENTION: Improved Process For The Synthesis Of 2'-O-Substituted Pyrimidine
; TITLE OF INVENTION: Oligomeric Compounds Therefrom
; FILE REFERENCE: ISIS-4684
; CURRENT APPLICATION NUMBER: US/09/747,009
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 08/894,899
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: PCT/US96/03174
; PRIOR FILING DATE: 1996-01-07
; PRIOR APPLICATION NUMBER: 08/475,467
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/398,901
; PRIOR FILING DATE: 1995-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20030050454A1el Sequence
US-09-747-009-29

Query Match      100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCTCGCTGCTGAGTTTCA 20
Db      1 GTTCTCGCTGCTGAGTTTCA 20

RESULT 6
US-09-747-009-29
; Sequence 29, Application US/09747009
; Publication No. US20030050454A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Sanghvi, Yogesh S.
; APPLICANT: Ross, Bruce S.
; APPLICANT: Griffey, Rich H.
; APPLICANT: Springer, Robert H.
; APPLICANT: Sprankle, Kelly G.
; TITLE OF INVENTION: Improved Process For The Synthesis Of 2'-O-Substituted Pyrimidine
; TITLE OF INVENTION: Oligomeric Compounds Therefrom
; FILE REFERENCE: ISIS-4684
; CURRENT APPLICATION NUMBER: US/09/747,009
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 08/894,899
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: PCT/US96/03174
; PRIOR FILING DATE: 1996-01-07
; PRIOR APPLICATION NUMBER: 08/475,467
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/398,901
; PRIOR FILING DATE: 1995-03-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. US20030050454A1el Sequence
US-09-747-009-29

Query Match      100.0%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 14; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCTCGCTGCTGAGTTTCA 20
Db      1 GUUCUCGCTGCTGAGUUUCA 20

RESULT 7
US-09-876-242-5
; Sequence 5, Application US/09876242
; Publication No. US20030055241A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Max N.
; APPLICANT: Arthur, John Charles
; APPLICANT: VanSooy, Kent
; APPLICANT: Scozzari, Anthony N.
; TITLE OF INVENTION: Processes Of Purifying Oligonucleotides
; FILE REFERENCE: ISIS4728
; CURRENT APPLICATION NUMBER: US/09/876,242
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
```

; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide
 US-09-876-242-5

Query Match 100.0%; Score 20; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 8
 US-09-935-316-4
 ; Sequence 4, Application US/09935316
 ; Publication No. US20030083286A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weinbach, Susan
 ; APPLICANT: Tillman, Lloyd G.
 ; APPLICANT: Geary, Richard H.
 ; APPLICANT: Hardee, Gregory E.
 ; TITLE OF INVENTION: Pulsatile Release Compositions And Methods For Enhanced Intestina
 ; TITLE OF INVENTION: Absorption
 ; FILE REFERENCE: ISIS4823
 ; CURRENT APPLICATION NUMBER: US/09/935,316
 ; CURRENT FILING DATE: 2001-08-22
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-935-316-4

Query Match 100.0%; Score 20; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 9
 US-09-902-953-4
 ; Sequence 4, Application US/09902953
 ; Publication No. US20030096770A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Krotz, Achim
 ; APPLICANT: Mehta, Rahul
 ; TITLE OF INVENTION: Enhancement Of The Stability Of Oligonucleotides Comprising
 ; TITLE OF INVENTION: Phosphorothioate Linkages By Addition Of Water Soluble Antioxi
 ; FILE REFERENCE: ISIS-4797
 ; CURRENT APPLICATION NUMBER: US/09/902,953
 ; CURRENT FILING DATE: 2001-07-11
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-902-953-4

Query Match 100.0%; Score 20; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 10
 US-09-944-493-4
 ; Sequence 4, Application US/09944493
 ; Publication No. US20030124196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weinbach, Susan
 ; APPLICANT: Tillman, Lloyd G.
 ; APPLICANT: Geary, Richard H.
 ; APPLICANT: Hardee, Gregory E.
 ; TITLE OF INVENTION: Pulsatile Release Compositions And Methods For Enhanced Intestir
 ; TITLE OF INVENTION: Absorption
 ; FILE REFERENCE: ISIS4823
 ; CURRENT APPLICATION NUMBER: US/09/944,493
 ; CURRENT FILING DATE: 2001-08-21
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-944-493-4

Query Match 100.0%; Score 20; DB 11; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 11
 US-10-444-445-4
 ; Sequence 4, Application US/10444445
 ; Publication No. US20030229220A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Capaldi, Daniel C
 ; APPLICANT: Ravikumar, Vasulunga T
 ; APPLICANT: Cole, Douglas L
 ; TITLE OF INVENTION: Processes For The Synthesis Of Oligomers Using Phosphoramidite
 ; TITLE OF INVENTION: Compositions
 ; FILE REFERENCE: ISIS5196
 ; CURRENT APPLICATION NUMBER: US/10/444,445
 ; CURRENT FILING DATE: 2003-05-23
 ; PRIOR APPLICATION NUMBER: 09/306,278
 ; PRIOR FILING DATE: 1999-05-06
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 4
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic construct
 US-10-444-445-4

Query Match 100.0%; Score 20; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
 |||||
 Db 1 GTTCTCGCTGGTGAGTTTCA 20

```
RESULT 12
US-10-437-263-23
; Sequence 23, Application US/10437263
; Publication No. US20040009943A1
; GENERAL INFORMATION:
; APPLICANT: Sample, Sean
; APPLICANT: Tam, Ying K.
; APPLICANT: Chikh, Ghania
; APPLICANT: Hope, Michael J.
; TITLE OF INVENTION: PATHOGEN VACCINES AND METHODS FOR USING THE SAME
; FILE REFERENCE: A-72216/TAL
; CURRENT APPLICATION NUMBER: US/10/437,263
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/454,298
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-437-263-23

Query Match      100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCTCGCTGGTGAGTTTCA 20
      |||||||
Db      1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 13
US-10-437-275-23
; Sequence 23, Application US/10437275
; Publication No. US20040009944A1
; GENERAL INFORMATION:
; APPLICANT: Sample, Sean
; APPLICANT: Klimuk, Sandra
; APPLICANT: Chikh, Ghania
; TITLE OF INVENTION: METHYLATED IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND METHODS OF
; FILE REFERENCE: A-72158/TAL
; CURRENT APPLICATION NUMBER: US/10/437,275
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/290,545
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-437-275-23

Query Match      100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCTCGCTGGTGAGTTTCA 20
      |||||||
Db      1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 14
US-10-447-136-217
; Sequence 217, Application US/10447136
; Publication No. US20040009948A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
; FILE REFERENCE: 032396-023
; CURRENT APPLICATION NUMBER: US/10/447,136
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/249,247
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/023,040
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/039,959
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 08/904,901
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-10-447-136-217

Query Match      100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTTCTCGCTGGTGAGTTTCA 20
      |||||||
Db      1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 15
US-09-895-480A-13
; Sequence 13, Application US/09895480A
; Publication No. US20030129221A1
; GENERAL INFORMATION:
; APPLICANT: Inex Pharmaceuticals Inc.
; TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic
; Agents in Lipid Vesicles
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson LLP
; STREET: PO Box 5068
; CITY: Dillon
; STATE: CO
; COUNTRY: US
; ZIP: 80435
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/895,480A
; FILING DATE: 29-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: <Unknown>
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: <Unknown>
```

```
;
; TELEFAX: <Unknown>
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: other nucleic acid
;   HYPOTHETICAL: no
;   ANTI-SENSE: yes
;   SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-895-480A-13

Query Match      100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 16
US-10-262-318-3
; Sequence 3, Application US/10262318
; Publication No. US20030144198A1
; GENERAL INFORMATION:
; APPLICANT: Copharos
; APPLICANT: Collins, Douglas A.
; TITLE OF INVENTION: ADMINISTRATION OF TRANSPORT PROTEINS WITH CONJUGATED COBALAMIN
; TITLE OF INVENTION: DELIVER AGENTS
; FILE REFERENCE: COP1012
; CURRENT APPLICATION NUMBER: US/10/262,318
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide-- 3521/CGP, 64128A (Isis, No. US20030144198A1)
US-10-262-318-3

Query Match      100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 17
US-10-290-587-4
; Sequence 4, Application US/10290587
; Publication No. US20030149260A1
; GENERAL INFORMATION:
; APPLICANT: Chervallath, Zacharia S.
; APPLICANT: Ravikumar, Vasulinga T.
; APPLICANT: Cole, Douglas L.
; TITLE OF INVENTION: Process For The Synthesis Of Oligomeric Compounds
; FILE REFERENCE: ISIS-5108
; CURRENT APPLICATION NUMBER: US/10/290,587
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 10/016,465
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 09/349,659
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4

Query Match      100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 18
US-10-348-485-2
; Sequence 2, Application US/10348485
; Publication No. US20030148989A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Holmlund, Jon T.
; APPLICANT: Doerr, F. Andrew
; TITLE OF INVENTION: Oligonucleotide Modulation Of Protein Kinase C
; FILE REFERENCE: ISIS4954
; CURRENT APPLICATION NUMBER: US/10/348,485
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/10/025,139
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 08/829,637
; PRIOR FILING DATE: 1997-03-31
; PRIOR APPLICATION NUMBER: US 08/478,178
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/089,996
; PRIOR FILING DATE: 1993-07-09
; PRIOR APPLICATION NUMBER: US 07/852,852
; PRIOR FILING DATE: 1992-03-16
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-485-2

Query Match      100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 19
US-10-337-004-5
; Sequence 5, Application US/10337004
; Publication No. US20030153742A1
; GENERAL INFORMATION:
; APPLICANT: Krotz, Achim H.
; APPLICANT: Ravikumar, Vasulinga T.
; TITLE OF INVENTION: Purification Of Oligonucleotides
; FILE REFERENCE: ISIS111
; CURRENT APPLICATION NUMBER: US/10/337,004
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 09/495,398
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
```

```
;
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-290-587-4

Query Match      100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 18
US-10-348-485-2
; Sequence 2, Application US/10348485
; Publication No. US20030148989A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Holmlund, Jon T.
; APPLICANT: Doerr, F. Andrew
; TITLE OF INVENTION: Oligonucleotide Modulation Of Protein Kinase C
; FILE REFERENCE: ISIS4954
; CURRENT APPLICATION NUMBER: US/10/348,485
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/10/025,139
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 08/829,637
; PRIOR FILING DATE: 1997-03-31
; PRIOR APPLICATION NUMBER: US 08/478,178
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/089,996
; PRIOR FILING DATE: 1993-07-09
; PRIOR APPLICATION NUMBER: US 07/852,852
; PRIOR FILING DATE: 1992-03-16
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-485-2

Query Match      100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 19
US-10-337-004-5
; Sequence 5, Application US/10337004
; Publication No. US20030153742A1
; GENERAL INFORMATION:
; APPLICANT: Krotz, Achim H.
; APPLICANT: Ravikumar, Vasulinga T.
; TITLE OF INVENTION: Purification Of Oligonucleotides
; FILE REFERENCE: ISIS111
; CURRENT APPLICATION NUMBER: US/10/337,004
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 09/495,398
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
```

; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-337-004-5

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 20

US-10-337-004-6
; Sequence 6, Application US/10337004
; Publication No. US20030153742A1
; GENERAL INFORMATION:
; APPLICANT: Krotz, Achim H.
; APPLICANT: Ravikumar, Vasulunga T.
; TITLE OF INVENTION: Purification Of Oligonucleotides
; FILE REFERENCE: ISIS5111
; CURRENT APPLICATION NUMBER: US/10/337,004
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 09/495,398
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-337-004-6

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 21

US-10-365-623-14
; Sequence 14, Application US/10365623
; Publication No. US20030166512A1
; GENERAL INFORMATION:
; APPLICANT: Xie, Dong
; TITLE OF INVENTION: Protein Carrier System for Therapeutic Oligonucleotides
; FILE REFERENCE: 63024.000001
; CURRENT APPLICATION NUMBER: US/10/365,623
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide directed against human PKC-alpha
US-10-365-623-14

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 22

US-10-080-979-22
; Sequence 22, Application US/10080979
; Publication No. US20030191075A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Philip Dan
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Bennett, Frank C.
; TITLE OF INVENTION: Oligonucleotide Conjugates For Hepatic Delivery
; FILE REFERENCE: ISIS-5028
; CURRENT APPLICATION NUMBER: US/10/080,979
; CURRENT FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-080-979-22

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.5;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|:|
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 23

US-10-318-628-4
; Sequence 4, Application US/10318628
; Publication No. US20030191304A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Ravikumar, Vasulunga T.
; APPLICANT: Sanghvi, Yogesh
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: ISIS4855
; CURRENT APPLICATION NUMBER: US/10/318,628
; CURRENT FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: 09/177,953
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-318-628-4

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 24

US-10-318-628-13

; Sequence 13, Application US/10318628
; Publication No. US20030191304A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Ravikumar, Vasulinga T.
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: IS184855
; CURRENT APPLICATION NUMBER: US/10/318,628
; PRIOR FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: 09/177,953
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; SOFTWARE: PatentIn version 3.2
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-318-628-13

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 25
US-10-318-628-27
; Sequence 27, Application US/10318628
; Publication No. US20030191304A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Ravikumar, Vasulinga T.
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: IS184855
; CURRENT APPLICATION NUMBER: US/10/318,628
; PRIOR FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: 09/177,953
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; SOFTWARE: PatentIn version 3.2
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-318-628-27

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 26
US-10-318-628-35
; Sequence 35, Application US/10318628
; Publication No. US20030191304A1
; GENERAL INFORMATION:

; APPLICANT: Manoharan, Muthiah
; APPLICANT: Ravikumar, Vasulinga T.
; APPLICANT: Sanghvi, Yogesh
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: IS184855
; CURRENT APPLICATION NUMBER: US/10/318,628
; PRIOR FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: 09/177,953
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-318-628-35

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 27
US-10-318-628-42
; Sequence 42, Application US/10318628
; Publication No. US20030191304A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Ravikumar, Vasulinga T.
; APPLICANT: Sanghvi, Yogesh
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: IS184855
; CURRENT APPLICATION NUMBER: US/10/318,628
; PRIOR FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: 09/177,953
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-318-628-42

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 28
US-10-103-906-3
; Sequence 3, Application US/10103906
; Publication No. US20020156286A1
; GENERAL INFORMATION:
; APPLICANT: Kretz, Achim H.
; APPLICANT: McElroy, Bethany M.
; TITLE OF INVENTION: Methods for Removing Dimethoxytrityl Groups From

; TITLE OF INVENTION: Oligonucleotides
; FILE REFERENCE: ISIS-3349
; CURRENT APPLICATION NUMBER: US/10/103,906
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US/05/271,220
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-103-906-3

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 29

US-10-002-802A-1
; Sequence 1, Application US/10002802A
; Publication No. US20020197720A1
; GENERAL INFORMATION:
; APPLICANT: Uhler, Michael D.
; TITLE OF INVENTION: Surface Transfection and Expression Procedure
; FILE REFERENCE: UM-06669
; CURRENT APPLICATION NUMBER: US/10/002,802A
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/245,892
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/305,552
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/960,454
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-002-802A-1

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 30

US-10-071-822A-4
; Sequence 4, Application US/10071822A
; Publication No. US2003027780A1
; GENERAL INFORMATION:
; APPLICANT: Hardee, Gregory E.
; APPLICANT: Tillman, Lloyd G.
; APPLICANT: Gonzales-Ferreiro, Maria
; APPLICANT: Mehta, Rahul C.
; APPLICANT: Teng, Ching-Leou
; TITLE OF INVENTION: Multiparticulate Formulation
; FILE REFERENCE: ISIS4947
; CURRENT APPLICATION NUMBER: US/10/071,822A
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/256,515

; PRIOR FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Sequence
US-10-071-822A-4

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 31

US-10-029-598-49
; Sequence 49, Application US/10029598
; Publication No. US20030040497A1
; GENERAL INFORMATION:
; APPLICANT: Teng, Ching-Leou
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Tillman, Lloyd
; APPLICANT: Hardee, Gregory E.
; APPLICANT: Ecker, David J.
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Compositions And Methods For No. US20030040497A1-Parental Delive
; FILE REFERENCE: ISIS4945
; CURRENT APPLICATION NUMBER: US/10/029,598
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 08/082,624
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: 09/315,298
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Sequence
; NAME/KEY: misc feature
; LOCATION: (1)-(20)
; OTHER INFORMATION: Phosphorothioate linkage
US-10-029-598-49

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 32

US-10-029-598-57
; Sequence 57, Application US/10029598
; Publication No. US20030040497A1
; GENERAL INFORMATION:
; APPLICANT: Teng, Ching-Leou
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Tillman, Lloyd
; APPLICANT: Hardee, Gregory E.
; APPLICANT: Ecker, David J.
; APPLICANT: Manoharan, Muthiah
; TITLE OF INVENTION: Compositions And Methods For No. US20030040497A1-Parental Delive

```

; OTHER INFORMATION: 2'-O-methoxythyl
; NAME/KEY: misc_feature
; LOCATION: (15)..(19)
; OTHER INFORMATION: 2'-O-methoxythyl
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: 5'-methyl
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: 5'-methyl
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 5'-methyl
; NAME/KEY: misc_feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: Phosphorothioate linkage
; US-10-029-598-58

Query Match      100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 34
US-10-123-435-1
; Sequence 1, Application US/10123435
; Publication No. US20030077827A1
; GENERAL INFORMATION:
; APPLICANT: Uhler, Michael D.
; TITLE OF INVENTION: Surface Transfection and Expression Procedure
; FILE REFERENCE: UM-06983
; CURRENT APPLICATION NUMBER: US/10/123,435
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/245,892
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/305,552
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/960,454
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 10/002,802
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-123-435-1

Query Match      100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
   |||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 35
US-10-002-884A-5
; Sequence 5, Application US/10002884A
; Publication No. US20030087810A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Cy A
; APPLICANT: Benimetskaya, Lyuba
; APPLICANT: Guzzo-Pernell, Nancy
; TITLE OF INVENTION: PEPTIDES THAT COMPLEX WITH ANTISENSE OLIGONUCLEOTIDES WHICH DON
; TITLE OF INVENTION: PKC-PROTEIN EXPRESSION IN CELLS
; FILE REFERENCE: 0575/63293

```

; CURRENT APPLICATION NUMBER: US/10/002, 884A
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: ANTISENSE OLIGONUCLEOTIDE
US-10-002-884A-5

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 36
US-10-142-566-42
; Sequence 42, Application US/10142566
; Publication No. US20030119016A1
; GENERAL INFORMATION:
; APPLICANT: Riley, Timothy A.
; APPLICANT: Brown, Bob D.
; APPLICANT: Arnold, Lyle J.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES WITH INCREASED RNASE SENSITIVITY
; FILE REFERENCE: OASBIO.003DV1
; CURRENT APPLICATION NUMBER: US/10/142,566
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US 09/136,080
; PRIOR FILING DATE: 1998-08-18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-142-566-42

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 37
US-10-290-545-23
; Sequence 23, Application US/10290545
; Publication No. US20030125292A1
; GENERAL INFORMATION:
; APPLICANT: Semple, Sean
; APPLICANT: Klimuk, Sandy
; APPLICANT: Yuan, Zuan-Ning
; TITLE OF INVENTION: Improved Mucosal Vaccines and Methods for Using the Same
; FILE REFERENCE: A-71854/PAL/AXG
; CURRENT APPLICATION NUMBER: US/10/290,545
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-290-545-23

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 GTTCTCGCTGGTGAGTTTCA 20

RESULT 38
US-09-370-541-19
; Sequence 19, Application US/09370541
; Publication No. US20030088079A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Nucleosidic Compounds And Oligomeric
; FILE REFERENCE: ISIS3993
; CURRENT APPLICATION NUMBER: US/09/370,541
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: 09/130,973
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 09/016,520
; EARLIER FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; EARLIER APPLICATION NUMBER: 09/344,260
; EARLIER FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
US-09-370-541-19

Query Match 95.0%; Score 19; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTTTCA 20
|||||
Db 1 TTCTCGCTGGTGAGTTTCA 19

RESULT 39
US-10-318-628-19
; Sequence 19, Application US/10318628
; Publication No. US20030191304A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Ravikumar, Vasulunga T.
; APPLICANT: Sanghvi, Yogesh
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: ISIS4855
; CURRENT APPLICATION NUMBER: US/10/318,628
; CURRENT FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: 09/177,953
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 19
; TYPE: DNA

```
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(6)
/ OTHER INFORMATION: 2' O MOE, phosphorothioate internucleotide
/ OTHER INFORMATION: linkages
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (6)..(15)
/ OTHER INFORMATION: phosphorothioate internucleotide linkages
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (15)..(19)
/ OTHER INFORMATION: 2' O MOE, phosphorothioated internucleotide
/ OTHER INFORMATION: linkages
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (19)..(19)
/ OTHER INFORMATION: 2' O MOE linkages
US-10-318-628-19

Query Match          95.0%; Score 19; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TTCTCGCTGGTGAGTTTCA 20
        |||||
Db       1 TTCTCGCTGGTGAGTTTCA 19

Search completed: January 24, 2004, 16:32:36
Job time : 244 secs

/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(6)
/ OTHER INFORMATION: 2' O MOE, phosphorothioate internucleotide
/ OTHER INFORMATION: linkages
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (6)..(15)
/ OTHER INFORMATION: phosphorothioate internucleotide linkages
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (15)..(19)
/ OTHER INFORMATION: 2' O MOE, phosphorothioated internucleotide
/ OTHER INFORMATION: linkages
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (19)..(19)
/ OTHER INFORMATION: 2' O MOE linkages
US-10-318-628-19

Query Match          95.0%; Score 19; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TTCTCGCTGGTGAGTTTCA 20
        |||||
Db       1 TTCTCGCTGGTGAGTTTCA 19

RESULT 40
US-10-318-628-21
; Sequence 21, Application US/10318628
; Publication No. US20030191304A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Ravikumar, Vasulunga T.
; APPLICANT: Sanghvi, Yogesh
; TITLE OF INVENTION: Activators For Oligonucleotide Synthesis
; FILE REFERENCE: ISIS4855
; CURRENT APPLICATION NUMBER: US/10/318,628
; CURRENT FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: 09/177,953
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/087,757
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(5)
; OTHER INFORMATION: 2' O MOE, phosphodiester internucleotide
; OTHER INFORMATION: linkages
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)..(6)
; OTHER INFORMATION: 2' O MOE, phosphorothioate internucleotide
; OTHER INFORMATION: linkages
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6)..(15)
; OTHER INFORMATION: phosphorothioate internucleotide
; OTHER INFORMATION: linkages
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)..(19)
; OTHER INFORMATION: 2' O MOE, phosphorothioated internucleotide
; OTHER INFORMATION: linkages
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2' O MOE linkages
US-10-318-628-19

Query Match          95.0%; Score 19; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TTCTCGCTGGTGAGTTTCA 20
        |||||
Db       1 TTCTCGCTGGTGAGTTTCA 19

Search completed: January 24, 2004, 16:32:36
Job time : 244 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 24, 2004, 14:14:56 ; Search time 1830 Seconds

(without alignments)
265.623 Million cell updates/sec

Title: US-10-002-884A-5

Perfect score: 20

Sequence: 1 gttctcgctggtgatttca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 71908

Minimum DB seq length: 0

Maximum DB seq length: 40

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

EST:*

1: em_estba:*

2: em_esthm:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12.6	63.0	40	9	AI020727 ua9h09.r
2	12.2	61.0	33	28	BH907017 SALK_0373
3	12.2	61.0	34	28	BH904365 SALK_1043
4	12.2	61.0	39	29	CC459602 SALK_1307

5	11.6	58.0	30	28	AZ307649	1M0009E19
6	11.6	58.0	32	29	BZ352394	BZ352394 SALK_0789
7	11.6	58.0	34	28	AZ495085	AZ495085 IM0330114
8	11.6	58.0	37	9	AA866679	AA866679 ud07b12.r
9	11.6	58.0	37	28	BH840631	BH840631 KG05933-5
10	11.6	58.0	37	29	BZ352489	BZ352489 SALK_0807
11	11.2	56.0	33	28	BH812422	BH812422 SALK_0617
12	11.2	56.0	36	29	BZ354295	BZ354295 SALK_1234
13	11	55.0	18	28	AQ026356	AQ026356 1(3)IG554
14	11	55.0	24	28	AZ776659	AZ776659 2M0010C02
15	11	55.0	27	28	AQ026157	AQ026157 1(3)00506
16	11	55.0	27	28	AQ073772	AQ073772 EP(3)3136
17	11	55.0	27	28	AQ073845	AQ073845 EP(3)3236
18	11	55.0	30	28	AZ788334	AZ788334 2M0035B19
19	11	55.0	30	28	AZ837449	AZ837449 2M0132C15
20	11	55.0	31	9	AA929219	AA929219 vt29e03.r
21	11	55.0	31	28	BH904243	BH904243 SALK_1041
22	11	55.0	32	28	BH904234	BH904234 SALK_1041
23	11	55.0	34	9	AI416615	AI416615 ea17a05.y
24	11	55.0	34	10	BG339578	BG339578 602437433
25	11	55.0	34	10	BG340055	BG340055 602438218
26	11	55.0	37	9	AI766095	AI766095 wh70a04.x
27	11	55.0	37	29	TA11C07P	TA11C07P T. brucei
28	11	55.0	39	29	BZ768960	BZ768960 SALK_1413
29	10.8	54.0	23	28	AZ514463	AZ514463 IM0361A19
30	10.8	54.0	24	28	AZ764581	AZ764581 IM0561I03
31	10.8	54.0	33	28	AZ352257	AZ352257 IM0090G11
32	10.8	54.0	40	29	BZ661620	BZ661620 SALK_0250
33	10.6	53.0	28	9	A1338568	A1338568 qq98g03.x
34	10.6	53.0	31	28	AZ344319	AZ344319 IM0078G16
35	10.6	53.0	31	28	AZ950542	AZ950542 2M0214I08
36	10.6	53.0	31	29	TA238C03Q	TA238C03Q T. brucei
37	10.6	53.0	33	28	AZ780156	AZ780156 2M0017B15
38	10.6	53.0	33	28	AZ946219	AZ946219 2M0207K24
39	10.6	53.0	35	9	AL675283	AL675283 AL675283
40	10.6	53.0	35	9	AL678369	AL678369 AL678369
41	10.6	53.0	35	9	AL781896	AL781896 AL781896
42	10.6	53.0	35	9	AL788690	AL788690 AL788690
43	10.6	53.0	35	9	AL789547	AL789547 AL789547
44	10.6	53.0	35	9	AL789903	AL789903 AL789903
45	10.6	53.0	35	9	AL792560	AL792560 AL792560
46	10.6	53.0	35	9	AL793701	AL793701 AL793701
47	10.6	53.0	35	9	AL850640	AL850640 AL850640
48	10.6	53.0	35	9	AL894852	AL894852 AL894852
49	10.6	53.0	36	9	AL776321	AL776321 AL776321
50	10.6	53.0	36	9	AL777656	AL777656 AL777656
51	10.6	53.0	36	9	AL868644	AL868644 AL868644
52	10.6	53.0	37	9	AL885188	AL885188 AL885188
53	10.6	53.0	39	9	AL776617	AL776617 AL776617
54	10.6	53.0	39	29	AG216711	AG216711 Drosophila
55	10.6	53.0	40	9	AA878858	AA878858 of84e04.s
56	10.6	53.0	40	29	BZ593226	BZ593226 SALK_0682
57	10.4	52.0	25	29	TA353F07Q	TA353F07Q T. brucei
58	10.4	52.0	30	28	AZ307481	AZ307481 IM0009011
59	10.4	52.0	31	28	BH902749	BH902749 SALK_0988
60	10.4	52.0	32	28	BH861153	BH861153 SALK_0345
61	10.4	52.0	33	29	TA210G07Q	TA210G07Q T. brucei
62	10.4	52.0	35	28	AZ796974	AZ796974 2M0052M23
63	10.4	52.0	36	28	AZ311632	AZ311632 2M0059N10
64	10.4	52.0	39	28	AZ424411	AZ424411 IM0204F04
65	10.4	52.0	40	9	AA811948	AA811948 ob74e04.s
66	10.2	51.0	22	9	AI153897	AI153897 ud50d11.r
67	10.2	51.0	25	28	AZ981731	AZ981731 2M0262G13
68	10.2	51.0	26	9	AU254495	AU254495 AU254495
69	10.2	51.0	27	28	AZ506095	AZ506095 IM0347A01
70	10.2	51.0	27	29	TA187C01P	TA187C01P T. brucei
71	10.2	51.0	29	28	AZ801486	AZ801486 2M0059P23
72	10.2	51.0	32	29	TA222D01P	TA222D01P T. brucei
73	10.2	51.0	33	9	AV853989	AV853989 AV853989
74	10.2	51.0	33	28	AZ352257	AZ352257 IM0090G11
75	10.2	51.0	33	28	BH863017	BH863017 SALK_0929
76	10.2	51.0	34	28	AZ803964	AZ803964 2M0064D09
77	10.2	51.0	34	29	BZ355267	BZ355267 SALK_1265

78	10.2	51.0	35	29	DM545539	AJ545539 Drosophil	151	9.6	48.0	30	28	A2812009	AZ812009 2M0078J20
79	10.2	51.0	40	9	AI078713	AI078713 oxy12C09.s	C 152	9.6	48.0	30	29	B2352917	BZ352917 SALK_1194
C 80	10.2	51.0	40	9	AI157055	AI157055 udi1d02.r	C 153	9.6	48.0	31	9	AA862388	AA862388 OG95A03.s
C 81	10.2	51.0	40	29	BX185505	BX185505 Danio rer	154	9.6	48.0	32	28	AZ513928	AZ513928 1M0360G15
C 82	10.2	51.0	19	28	AZ774477	AZ774477 2M0004A03	155	9.6	48.0	32	28	AZ990657	AZ990657 2M0274C03
C 83	10.2	51.0	21	28	AZ490638	AZ490638 1M0323B13	C 156	9.6	48.0	33	28	AZ635442	AZ635442 1M0491K13
C 84	10.2	51.0	21	28	AZ661642	AZ661642 1M0540M18	157	9.6	48.0	33	28	BH747174	BH747174 SALK_0119
C 85	10.2	51.0	23	28	AZ635716	AZ635716 1M0493H18	C 158	9.6	48.0	34	29	BZ596672	BZ596672 SALK_0994
C 86	10.2	51.0	27	28	AZ627967	AZ627967 1M0476I06	C 159	9.6	48.0	35	9	AL682947	AL682947 AL682947
C 87	10.2	51.0	27	28	BH863828	BH863828 SALK_0946	C 160	9.6	48.0	35	9	AL851597	AL851597 AL851597
C 88	10.2	51.0	29	28	AZ306174	AZ306174 1M0007G07	161	9.6	48.0	35	28	AZ310047	AZ310047 1M0018M10
C 89	10.2	51.0	31	9	AI554671	AI554671 t227A02.x	162	9.6	48.0	35	28	AZ823097	AZ823097 2M0096K19
C 90	10.2	51.0	31	9	AI798567	AI798567 t237C12.x	C 163	9.6	48.0	36	12	BH395940	BH395940 5009-0-14
C 91	10.2	51.0	31	9	AV963392	AV963392 AV963392	C 164	9.6	48.0	37	28	AZ666528	AZ666528 1M0548A18
C 92	10.2	51.0	31	10	BF011373	BF011373 601559150	C 165	9.6	48.0	37	29	AG218076	AG218076 Drosophil
C 93	10.2	51.0	31	28	BH811132	BH811132 SALK_0575	C 166	9.6	48.0	37	29	DR68G5T	DR68G5T Danio rer
C 94	10.2	51.0	31	28	BH812156	BH812156 SALK_0612	C 167	9.6	48.0	37	29	AZ383812Q	AZ383812Q T. brucei
C 95	10.2	51.0	32	28	AZ307875	AZ307875 1M010TH18	C 168	9.6	48.0	38	28	AZ770404	AZ770404 1M0571P20
C 96	10.2	51.0	33	28	AZ489566	AZ489566 1M0322P02	C 169	9.6	48.0	38	28	AZ857140	AZ857140 2M0161O21
C 97	10.2	51.0	33	29	TA124F05P	TA124F05P T. brucei	170	9.6	48.0	38	28	BH612014	BH612014 SALK_0320
C 98	10.2	51.0	34	9	AI083546	AI083546 ox79B08.x	C 171	9.6	48.0	39	9	AL896025	AL896025 AL896025
C 99	10.2	51.0	34	29	BZ355267	BZ355267 SALK_1265	C 172	9.6	48.0	40	9	AA861998	AA861998 O145R06.s
C 100	10.2	51.0	34	29	AL754880	AL754880 Arabidops	C 173	9.6	48.0	40	9	AA906556	AA906556 OK93E04.s
C 101	10.2	51.0	36	28	AZ397955	AZ397955 1M0163I10	174	9.6	48.0	40	9	AI000125	AI000125 os43A04.s
C 102	10.2	51.0	36	28	AZ444039	AZ444039 1M0239H07	C 175	9.6	48.0	40	28	AZ322671	AZ322671 1M0043N11
C 103	10.2	51.0	36	28	AZ507727	AZ507727 1M0349D04	176	9.6	48.0	40	28	AZ537263	AZ537263 AST-2P031
C 104	10.2	51.0	36	28	AZ809373	AZ809373 2M0073A20	177	9.6	48.0	40	28	BH619099	BH619099 SALK_0402
C 105	10.2	51.0	36	28	AZ812410	AZ812410 2M0079M01	178	9.6	48.0	40	28	BH533139	BH533139 SALK_0767
C 106	10.2	51.0	37	9	AI912881	AI912881 t220D08.x	179	9.6	48.0	40	29	BZ583820	BZ583820 3590_1_46
C 107	10.2	51.0	37	28	AZ595462	AZ595462 1M0408P03	180	9.6	48.0	40	29	CC037274	CC037274 3591_1_86
C 108	10.2	51.0	37	29	TA304B02Q	TA304B02Q T. brucei	C 181	9.6	48.0	40	29	BX121044	BX121044 Danio rer
C 109	10.2	51.0	38	28	AZ336879	AZ336879 1M0670I18	182	9.4	47.0	23	28	AZ794418	AZ794418 2M0048M10
C 110	10.2	51.0	38	28	AZ947417	AZ947417 2M0210D11	C 183	9.4	47.0	23	28	AZ808894	AZ808894 2M0072G09
C 111	10.2	51.0	39	12	B065029	B065029 B065029	C 184	9.4	47.0	24	28	AZ478403	AZ478403 1M0298N21
C 112	10.2	51.0	40	9	AA910968	AA910968 ck67B03.s	C 185	9.4	47.0	24	29	TA57D02P	TA57D02P T. brucei
C 113	10.2	51.0	40	28	AQ072891	AQ072891 EP(2)2087	C 186	9.4	47.0	25	9	AI744368	AI744368 tr10B10.x
C 114	9.8	49.0	20	28	AZ627859	AZ627859 1M0476E04	187	9.4	47.0	25	28	BH759431	BH759431 KG04006-5
C 115	9.8	49.0	22	9	AI047954	AI047954 vnl8f09.x	C 188	9.4	47.0	25	29	TA383A06P	TA383A06P T. brucei
C 116	9.8	49.0	22	28	AZ35450	AZ35450 2M0129L12	C 189	9.4	47.0	26	28	AZ436027	AZ436027 1M0233C06
C 117	9.8	49.0	23	9	AZ254193	AZ254193 AU254193	C 190	9.4	47.0	26	28	AZ780294	AZ780294 2M0017G01
C 118	9.8	49.0	23	14	D18239	D18239 MUSGS00519	C 191	9.4	47.0	28	9	AI497442	AI497442 fb53F02.x
C 119	9.8	49.0	25	28	AI000890	AI000890 os56H04.s	C 192	9.4	47.0	28	9	AI687005	AI687005 TP81F02.x
C 120	9.8	49.0	25	28	AZ364139	AZ364139 1M0110A14	C 193	9.4	47.0	28	28	AZ324675	AZ324675 1M0046A14
C 121	9.8	49.0	25	28	BH759548	BH759548 KG04960-5	C 194	9.4	47.0	28	28	AZ432111	AZ432111 1M0217E05
C 122	9.8	49.0	28	9	AU260122	AU260122 AU260122	C 195	9.4	47.0	28	28	AZ806132	AZ806132 2M0680O02
C 123	9.8	49.0	31	28	AQ026325	AQ026325 I(3)J5E2	196	9.4	47.0	28	28	AZ946024	AZ946024 2M0207E07
C 124	9.8	49.0	31	29	BZ354380	BZ354380 SALK_1248	197	9.4	47.0	29	28	AZ307834	AZ307834 1M0010M12
C 125	9.8	49.0	33	28	AZ305164	AZ305164 1M0005M08	198	9.4	47.0	29	28	BZ384399	BZ384399 SALK_1354
C 126	9.8	49.0	34	9	AI098964	AI098964 ue34d12.y	199	9.4	47.0	30	28	AZ345704	AZ345704 1M0080G05
C 127	9.8	49.0	34	29	BZ377406	BZ377406 SALK_0808	C 200	9.4	47.0	30	28	TA277C08Q	TA277C08Q T. brucei
C 128	9.8	49.0	34	29	BZ381221	BZ381221 SALK_1164	C 201	9.4	47.0	31	28	AZ580546	AZ580546 1M0368A24
C 129	9.8	49.0	35	9	AZ237255	AZ237255 AU237255	C 202	9.4	47.0	31	29	TA247B09Q	TA247B09Q T. brucei
C 130	9.8	49.0	37	9	AZ239975	AZ239975 AU239975	C 203	9.4	47.0	32	9	AU259613	AU259613 AU259613
C 131	9.8	49.0	37	14	H43693	H43693 Y080B05.s1	C 204	9.4	47.0	32	29	AB082183	AB082183 Drosophil
C 132	9.8	49.0	37	28	AZ481957	AZ481957 1M0306F12	C 205	9.4	47.0	32	29	AB760995	AB760995 Arabidops
C 133	9.8	49.0	37	29	BZ377442	BZ377442 SALK_0809	C 206	9.4	47.0	33	14	CA900115	CA900115 PCSC08163
C 134	9.8	49.0	37	29	BZ380722	BZ380722 SALK_1155	C 207	9.4	47.0	33	28	AZ513143	AZ513143 1M0359E08
C 135	9.8	49.0	37	29	BZ383831	BZ383831 SALK_1345	C 208	9.4	47.0	33	9	AA884327	AA884327 T. brucei
C 136	9.8	49.0	37	29	AL941007	AL941007 Arabidops	C 209	9.4	47.0	34	9	AI439312	AI439312 am15e03.s
C 137	9.8	49.0	38	28	AZ643994	AZ643994 1M0507E14	C 210	9.4	47.0	34	9	AI439312	AI439312 t159e12.x
C 138	9.8	49.0	40	9	AA865290	AA865290 OG88h02.s	C 211	9.4	47.0	34	12	BJ034710	BJ034710 BJ034710
C 139	9.8	49.0	40	9	AA424850	AA424850 zw03b07.s	C 212	9.4	47.0	34	28	AZ478269	AZ478269 1M0298P09
C 140	9.8	49.0	22	28	AZ785474	AZ785474 2M0029E19	C 213	9.4	47.0	35	2	HSM003903	HSM003903 Homo sapi
C 141	9.6	48.0	24	28	AZ505513	AZ505513 1M0346B13	C 214	9.4	47.0	35	13	BQ594628	BQ594628 E012404-0
C 142	9.6	48.0	25	13	BQ592774	BQ592774 E012124-0	C 215	9.4	47.0	35	28	BH851755	BH851755 SALK_0734
C 143	9.6	48.0	25	28	AZ792087	AZ792087 2M0043L13	C 216	9.4	47.0	35	29	BZ665712	BZ665712 KG09780-5
C 144	9.6	48.0	26	9	AU256278	AU256278 AU256278	C 217	9.4	47.0	36	28	AZ372751	AZ372751 1M0124E14
C 145	9.6	48.0	26	28	AZ787019	AZ787019 2M0032B19	C 218	9.4	47.0	36	28	AZ466529	AZ466529 1M0277K18
C 146	9.6	48.0	29	9	AU257496	AU257496 AU257496	C 219	9.4	47.0	36	29	BZ380082	BZ380082 SALK_1145
C 147	9.6	48.0	29	28	AZ376581	AZ376581 1M0130E03	C 220	9.4	47.0	37	9	AI141661	AI141661 oc08a12.x
C 148	9.6	48.0	29	28	AZ596214	AZ596214 1M0409A21	C 221	9.4	47.0	37	9	AI1590572	AI1590572 tw13R052.x
C 149	9.6	48.0	29	28	AZ623273	AZ623273 1M0460M13	C 222	9.4	47.0	37	28	AZ465976	AZ465976 1M0276K13
C 150	9.6	48.0	29	28	AZ828807	AZ828807 2M0106J03	223	9.4	47.0	37	28	AZ666657	AZ666657 1M0548N22

C 224	9.4	47.0	37	28	AZ814152	2M0081C13	297	9.2	46.0	36	28	AZ354561	AZ354561	1M0093F19
C 225	9.4	47.0	37	28	BH906279	SALK 1095	298	9.2	46.0	36	28	AZ795461	AZ795461	2M0049008
C 226	9.4	47.0	37	28	AL761814	Arabidops	C 299	9.2	46.0	37	9	A1245691	qk31e05.x	
C 227	9.4	47.0	37	29	AL940347		C 300	9.2	46.0	37	28	AZ459287	AZ459287	1M0264C04
C 228	9.4	47.0	38	28	BH849979		C 301	9.2	46.0	37	29	BZ380445	SALK 1151	BZ380445
C 229	9.4	47.0	39	9	AW247770	2820018.5	C 302	9.2	46.0	37	29	DME547295	DME547295	DME547295
C 230	9.4	47.0	39	28	AZ663637	1M0543B19	C 303	9.2	46.0	38	9	AL858944	AL858944	AL858944
C 231	9.4	47.0	39	28	AZ814152	2M0079E17	C 304	9.2	46.0	38	28	BH810285	BH810285	BH810285
C 232	9.4	47.0	39	29	AA002174		C 305	9.2	46.0	39	9	AU267323	AU267323	AU267323
C 233	9.4	47.0	40	9	AA002174		C 306	9.2	46.0	39	28	AQ072927	AQ072927	AQ072927
C 234	9.4	47.0	40	9	AA002174		C 307	9.2	46.0	39	28	AQ15892	AQ15892	AQ15892
C 235	9.4	47.0	40	9	AA002174		C 308	9.2	46.0	40	9	A1097829	A1097829	A1097829
C 236	9.4	47.0	40	9	AA002174		C 309	9.2	46.0	40	9	AU257305	AU257305	AU257305
C 237	9.4	47.0	40	9	AA002174		C 310	9.2	46.0	40	14	D18218	D18218	D18218
C 238	9.4	47.0	40	28	AZ410396	1M0182N11	C 311	9.2	46.0	40	28	AZ835655	AZ835655	AZ835655
C 239	9.4	47.0	40	28	AZ759920	1M0553H11	C 312	9.2	46.0	40	28	BH917059	BH917059	BH917059
C 240	9.4	47.0	40	28	AZ772390	1M0583C17	C 313	9.2	46.0	40	28	AL951262	AL951262	AL951262
C 241	9.4	47.0	40	28	AZ979556	2M0256116	C 314	9.2	46.0	40	29	EX286458	EX286458	EX286458
C 242	9.4	47.0	40	28	BH851915	1M051915	C 315	9.2	46.0	19	28	AZ457710	AZ457710	AZ457710
C 243	9.4	47.0	40	28	BH851915	1M051915	C 316	9.2	46.0	19	28	AZ457710	AZ457710	AZ457710
C 244	9.4	47.0	40	29	BZ381549	SALK 1168	C 317	9.2	46.0	20	28	AZ969913	AZ969913	AZ969913
C 245	9.4	47.0	40	29	BZ381549	SALK 1168	C 318	9.2	46.0	21	29	TA36702P	TA36702P	TA36702P
C 246	9.2	46.0	16	9	AI000182	BZ767100	C 319	9.2	46.0	21	29	TA36702P	TA36702P	TA36702P
C 247	9.2	46.0	19	9	AI000182	BZ767100	C 320	9.2	46.0	22	28	AZ341268	AZ341268	AZ341268
C 248	9.2	46.0	20	28	AZ582821	1M0376L20	C 321	9.2	46.0	23	28	AU254186	AU254186	AU254186
C 249	9.2	46.0	20	28	AZ773525	2M0001B04	C 322	9.2	46.0	24	28	AZ476560	AZ476560	AZ476560
C 250	9.2	46.0	22	28	AZ815477	2M0083C17	C 323	9.2	46.0	24	28	AZ476560	AZ476560	AZ476560
C 251	9.2	46.0	22	28	AZ376795	1M0130N14	C 324	9.2	46.0	25	28	A1000229	A1000229	A1000229
C 252	9.2	46.0	22	28	AZ834723	2M0117L06	C 325	9.2	46.0	25	28	AZ474282	AZ474282	AZ474282
C 253	9.2	46.0	23	28	AZ376108	1M0129N14	C 326	9.2	46.0	26	28	BH904484	BH904484	BH904484
C 254	9.2	46.0	23	28	AZ381351	1M0140N08	C 327	9.2	46.0	27	28	AZ367484	AZ367484	AZ367484
C 255	9.2	46.0	24	13	BQ589506	E012561-0	C 328	9.2	46.0	28	9	AA996369	AA996369	AA996369
C 256	9.2	46.0	25	28	AZ586010	1M0391D12	C 329	9.2	46.0	28	9	AU060531	AU060531	AU060531
C 257	9.2	46.0	25	29	TA124C09P		C 330	9.2	46.0	28	28	AZ414629	AZ414629	AZ414629
C 258	9.2	46.0	26	28	BH902249	SALK 0915	C 331	9.2	46.0	28	28	AZ618471	AZ618471	AZ618471
C 259	9.2	46.0	26	28	PH303928		C 332	9.2	46.0	28	28	AZ784264	AZ784264	AZ784264
C 260	9.2	46.0	27	28	AZ473031	1M0288I12	C 333	9.2	46.0	28	29	TA192A04Q	TA192A04Q	TA192A04Q
C 261	9.2	46.0	28	28	AZ352539	1M0090J72	C 334	9.2	46.0	29	28	AZ806533	AZ806533	AZ806533
C 262	9.2	46.0	28	28	AZ875467	2M0190F10	C 335	9.2	46.0	29	29	BZ357659	BZ357659	BZ357659
C 263	9.2	46.0	29	28	AZ412411	1M0185A23	C 336	9.2	46.0	30	28	AZ784633	AZ784633	AZ784633
C 264	9.2	46.0	29	28	AZ403091	1M0185A23	C 337	9.2	46.0	30	28	BH811935	BH811935	BH811935
C 265	9.2	46.0	30	28	AZ485270	1M0312P04	C 338	9.2	46.0	30	28	BH863627	BH863627	BH863627
C 266	9.2	46.0	30	29	AL768442	Arabidops	C 339	9.2	46.0	31	28	AZ626029	AZ626029	AZ626029
C 267	9.2	46.0	31	9	AI143422	qa55b04.s	C 340	9.2	46.0	31	28	BH813637	BH813637	BH813637
C 268	9.2	46.0	31	12	B1145198	602909392	C 341	9.2	46.0	31	29	TA155G06P	TA155G06P	TA155G06P
C 269	9.2	46.0	31	28	AZ677556	1M0567C15	C 342	9.2	46.0	32	10	BFS29729	BFS29729	BFS29729
C 270	9.2	46.0	31	29	BZ767130		C 343	9.2	46.0	32	10	BFL13807	BFL13807	BFL13807
C 271	9.2	46.0	31	29	BZ767130		C 344	9.2	46.0	32	12	BG819845	BG819845	BG819845
C 272	9.2	46.0	31	29	BZ767130		C 345	9.2	46.0	32	12	BG819845	BG819845	BG819845
C 273	9.2	46.0	32	28	AZ618214	1M0449016	C 346	9.2	46.0	32	28	BH811421	BH811421	BH811421
C 274	9.2	46.0	32	28	AZ633565	1M0488F22	C 347	9.2	46.0	32	28	BH811421	BH811421	BH811421
C 275	9.2	46.0	32	29	BZ381016	1M0488F22	C 348	9.2	46.0	32	28	BH811421	BH811421	BH811421
C 276	9.2	46.0	32	29	BZ381017	1M0488F22	C 349	9.2	46.0	33	29	BZ765511	BZ765511	BZ765511
C 277	9.2	46.0	32	29	BZ381019	1M0488F22	C 350	9.2	46.0	33	29	BZ765511	BZ765511	BZ765511
C 278	9.2	46.0	32	29	TA292F10Q		C 351	9.2	46.0	34	9	AA994607	AA994607	AA994607
C 279	9.2	46.0	32	29	AZ384873	1M0143N05	C 352	9.2	46.0	34	9	AA517484	AA517484	AA517484
C 280	9.2	46.0	33	28	AZ506808	1M0348E12	C 353	9.2	46.0	34	12	BH96017	BH96017	BH96017
C 281	9.2	46.0	33	29	DR2618T		C 354	9.2	46.0	34	14	H27469	H27469	H27469
C 282	9.2	46.0	34	14	D18226		C 355	9.2	46.0	34	28	AZ621716	AZ621716	AZ621716
C 283	9.2	46.0	34	14	W85364		C 356	9.2	46.0	34	28	AZ966396	AZ966396	AZ966396
C 284	9.2	46.0	34	28	AQ026452	EP(2)0613	C 357	9.2	46.0	34	28	BH847715	BH847715	BH847715
C 285	9.2	46.0	34	29	BZ596023	SALK 0906	C 358	9.2	46.0	34	29	BZ380780	BZ380780	BZ380780
C 286	9.2	46.0	34	29	BZ765278		C 359	9.2	46.0	35	9	AL680659	AL680659	AL680659
C 287	9.2	46.0	34	29	DR321L13T		C 360	9.2	46.0	35	12	BM401165	BM401165	BM401165
C 288	9.2	46.0	35	9	AL869674		C 361	9.2	46.0	35	13	BUI98441	BUI98441	BUI98441
C 289	9.2	46.0	35	9	AL954915		C 362	9.2	46.0	35	14	T73795	T73795	T73795
C 290	9.2	46.0	35	14	D20691		C 363	9.2	46.0	35	28	AZ485619	AZ485619	AZ485619
C 291	9.2	46.0	35	28	AZ417148	1M0192N09	C 364	9.2	46.0	35	28	AZ805692	AZ805692	AZ805692
C 292	9.2	46.0	35	28	AZ493406	1M0328L06	C 365	9.2	46.0	36	9	AL752552	AL752552	AL752552
C 293	9.2	46.0	35	28	AZ780117	2M0017F12	C 366	9.2	46.0	36	28	AZ504120	AZ504120	AZ504120
C 294	9.2	46.0	35	29	BZ356774	SALK 1297	C 367	9.2	46.0	36	28	AZ610567	AZ610567	AZ610567
C 295	9.2	46.0	36	10	BF234798	602027231	C 368	9.2	46.0	36	28	AZ780177	AZ780177	AZ780177
C 296	9.2	46.0	36	10	BF234798	602027231	C 369	9.2	46.0	36	28	BH863465	BH863465	BH863465

C 370	9	45.0	36	28	BH963470	BH963470	SALK_09319	C 443	8.8	44.0	32	10	BF568357
C 371	9	45.0	36	29	BZ355000	SALK_1262		444	8.8	44.0	32	28	AQ073785
C 372	9	45.0	37	9	AI039506	Ox41f07.s		445	8.8	44.0	32	28	AQ073098
C 373	9	45.0	37	12	BI549647	603194070		446	8.8	44.0	32	28	AZ473098
C 374	9	45.0	37	12	BI550102	603192572		447	8.8	44.0	32	28	AZ656256
C 375	9	45.0	37	12	BI552796	603193771		448	8.8	44.0	32	28	AZ656256
C 376	9	45.0	37	13	BQ587909	E012339-0		449	8.8	44.0	33	28	AZ807459
C 377	9	45.0	37	28	AZ505522	1M0346D15		450	8.8	44.0	33	29	AZ290762
C 378	9	45.0	37	28	AZ595102	1M0407F03		451	8.8	44.0	33	29	AL759548
C 379	9	45.0	37	28	AZ652367	1M0525M20		452	8.8	44.0	34	9	AA857580
C 380	9	45.0	37	28	BH851228	SALK_0726		453	8.8	44.0	34	9	AA923187
C 381	9	45.0	37	28	BH853041	SALK_0759		454	8.8	44.0	34	10	BF530922
C 382	9	45.0	37	28	BH853041	SALK_0572		455	8.8	44.0	34	14	T59625
C 383	9	45.0	37	28	BH910012	SALK_1202		456	8.8	44.0	34	28	AZ486062
C 384	9	45.0	37	29	BZ353395	SALK_1295		457	8.8	44.0	34	28	AZ613348
C 385	9	45.0	37	29	BZ356684	T. brucei		458	8.8	44.0	34	28	AZ840416
C 386	9	45.0	37	29	TAl15G06P	AL462849		459	8.8	44.0	34	28	BH855732
C 387	9	45.0	37	29	TAl15H01Q	AL463801		460	8.8	44.0	34	29	BZ762432
C 388	9	45.0	38	9	AL960045	AL960045		461	8.8	44.0	35	10	BG720014
C 389	9	45.0	38	9	AU052705	AU052705		462	8.8	44.0	35	10	BG720014
C 390	9	45.0	38	13	BQ594292	E0127577-0		463	8.8	44.0	35	14	N70888
C 391	9	45.0	38	28	AZ346775	1M0082J08		464	8.8	44.0	35	14	N70888
C 392	9	45.0	38	28	BH856601	SALK_0990		465	8.8	44.0	35	28	AZ603338
C 393	9	45.0	38	29	AL946146	Arabidops		466	8.8	44.0	35	28	AZ816505
C 394	9	45.0	38	29	AL947516	Arabidops		467	8.8	44.0	35	28	AZ854098
C 395	9	45.0	39	9	AV853005	AV853005		468	8.8	44.0	35	29	BZ664130
C 396	9	45.0	39	14	T24465	EST040		469	8.8	44.0	35	29	BX292351
C 397	9	45.0	39	28	AZ462643	1M0269M10		470	8.8	44.0	36	9	AX292351
C 398	9	45.0	39	28	AZ499899	1M0337O23		471	8.8	44.0	36	12	BG297950
C 399	9	45.0	39	29	AG218881	Drosophil		472	8.8	44.0	36	28	AZ663045
C 400	9	45.0	39	29	BX534060	Arabidops		473	8.8	44.0	36	28	AZ837047
C 401	9	45.0	40	9	AA878482	oe15a01.s		474	8.8	44.0	36	29	BZ53612
C 402	9	45.0	40	9	AI074647	ox81912.s		475	8.8	44.0	37	9	AA923456
C 403	9	45.0	40	9	AI768984	wg31c06.x		476	8.8	44.0	37	9	AI119964
C 404	9	45.0	40	9	AL886409	AL886409		477	8.8	44.0	37	9	AI144860
C 405	9	45.0	40	12	BM399990	5009-0-64		478	8.8	44.0	37	9	AI601822
C 406	9	45.0	40	28	AZ974232	2M0248B18		479	8.8	44.0	37	9	AV959901
C 407	9	45.0	40	28	BH792432	SALK_0642		480	8.8	44.0	37	14	T53803
C 408	9	45.0	40	28	BH850821	SALK_0719		481	8.8	44.0	37	28	AZ794362
C 409	9	45.0	40	29	BZ377467	SALK_0828		482	8.8	44.0	37	28	AZ967846
C 410	9	45.0	40	29	BZ381343	SALK_1165		483	8.8	44.0	37	29	BZ56214
C 411	9	45.0	40	29	BZ382439	SALK_1183		484	8.8	44.0	37	29	BZ65019
C 412	9	45.0	40	29	BZ769399	SALK_1421		485	8.8	44.0	37	29	DR102U22S
C 413	8.8	44.0	21	28	AZ316011	1M0033B03		486	8.8	44.0	37	29	DR102U22S
C 414	8.8	44.0	21	28	AZ347845	1M0084L06		487	8.8	44.0	38	14	T52142
C 415	8.8	44.0	22	28	AZ836104	2M0130C17		488	8.8	44.0	38	14	T52142
C 416	8.8	44.0	24	12	BM401141	5009-0-83		489	8.8	44.0	38	29	BZ380583
C 417	8.8	44.0	24	28	AZ451705	1M0251O10		490	8.8	44.0	38	29	BZ380583
C 418	8.8	44.0	24	29	BZ356735	SALK_1296		491	8.8	44.0	39	28	BH902988
C 419	8.8	44.0	25	28	AZ587343	1M0394O22		492	8.8	44.0	39	29	BZ286258
C 420	8.8	44.0	25	28	AZ620217	1M0452B23		493	8.8	44.0	39	29	BZ353245
C 421	8.8	44.0	25	28	AZ792365	2M0046D21		494	8.8	44.0	39	29	CC180180
C 422	8.8	44.0	25	29	BZ765856	SALK_1348		495	8.8	44.0	39	29	CC458121
C 423	8.8	44.0	26	28	AZ307637	1M0009017		496	8.8	44.0	39	29	CC458121
C 424	8.8	44.0	26	28	AZ466122	1M0276003		497	8.8	44.0	39	29	CC458121
C 425	8.8	44.0	26	28	AZ820150	2M0092K11		498	8.8	44.0	39	29	CC458121
C 426	8.8	44.0	26	29	TA381C07Q	AL497666		499	8.8	44.0	39	29	CC458121
C 427	8.8	44.0	27	12	BG928138	HNC46-1-D		500	8.8	44.0	40	9	AA683589
C 428	8.8	44.0	28	9	AI649190	uk32d12.x		501	8.8	44.0	40	9	AA683589
C 429	8.8	44.0	28	28	AZ781477	2M0019H24		502	8.8	44.0	40	9	AA953211
C 430	8.8	44.0	29	9	AU255667	AU255667		503	8.8	44.0	40	9	AA953211
C 431	8.8	44.0	29	9	AU256137	AU256137		504	8.8	44.0	40	9	AA953211
C 432	8.8	44.0	29	12	BG928000	HNC45-1-H		505	8.8	44.0	40	9	AA953211
C 433	8.8	44.0	29	29	TA217F07Q	T. brucei		506	8.8	44.0	40	14	H85898
C 434	8.8	44.0	29	29	TA246H09Q	T. brucei		507	8.8	44.0	40	28	AZ501159
C 435	8.8	44.0	30	28	AZ346661	1M0082B04		508	8.8	44.0	40	28	AZ765512
C 436	8.8	44.0	30	28	AZ812357	2M0079B05		509	8.8	44.0	40	28	AZ769030
C 437	8.8	44.0	30	28	BH865507	SALK_0986		510	8.8	44.0	40	28	AZ775335
C 438	8.8	44.0	30	29	TA42E02P	AL45550		511	8.8	44.0	40	28	AZ806060
C 439	8.8	44.0	31	9	AA984702	am90a01.s		512	8.8	44.0	40	28	AZ806060
C 440	8.8	44.0	31	29	AZ609702	1M0434C07		513	8.8	44.0	40	29	CC037274
C 441	8.8	44.0	31	28	BH865607	SALK_0990		514	8.8	44.0	40	29	CC037274
C 442	8.8	44.0	32	9	AU258316	AU258316		515	8.8	44.0	40	29	CC037274
C 443	8.8	44.0	32	9	AU258316	AU258316		516	8.8	44.0	40	29	CC037274
C 444	8.8	44.0	32	9	AU258316	AU258316		517	8.8	44.0	40	29	CC037274
C 445	8.8	44.0	32	9	AU258316	AU258316		518	8.8	44.0	40	29	CC037274
C 446	8.8	44.0	32	9	AU258316	AU258316		519	8.8	44.0	40	29	CC037274
C 447	8.8	44.0	32	9	AU258316	AU258316		520	8.8	44.0	40	29	CC037274
C 448	8.8	44.0	32	9	AU258316	AU258316		521	8.8	44.0	40	29	CC037274
C 449	8.8	44.0	32	9	AU258316	AU258316		522	8.8	44.0	40	29	CC037274
C 450	8.8	44.0	32	9	AU258316	AU258316		523	8.8	44.0	40	29	CC037274
C 451	8.8	44.0	32	9	AU258316	AU258316		524	8.8	44.0	40	29	CC037274
C 452	8.8	44.0	32	9	AU258316	AU258316		525	8.8	44.0	40	29	CC037274
C 453	8.8	44.0	32	9	AU258316	AU258316		526	8.8	44.0	40	29	CC037274
C 454	8.8	44.0	32	9	AU258316	AU258316		527	8.8	44.0	40	29	CC037274
C 455	8.8	44.0	32	9	AU258316	AU258316		528	8.8	44.0	40	29	CC037274
C 456	8.8	44.0	32	9	AU258316	AU258316		529	8.8	44.0	40	29	CC037274
C 457	8.8	44.0	32	9	AU258316	AU258316		530	8.8	44.0	40	29	CC037274
C 458	8.8	44.0	32	9	AU258316	AU258316		531	8.8	44.0	40	29	CC037274
C 459	8.8	44.0	32	9	AU258316	AU258316		532	8.8	44.0	40	29	CC037274
C 460	8.8	44.0	32	9	AU258316	AU258316		533	8.8	44.0	40	29	CC037274
C 461	8.8	44.0	32	9	AU258316	AU258316		534	8.8	44.0	40	29	CC037274
C 462	8.8	44.0	32	9	AU258316	AU258316		535	8.8	44.0	40	29	CC037274
C 463	8.8	44.0	32	9	AU258316	AU258316		536	8.8	44.0	40	29	CC037274
C 464	8.8	44.0	32	9	AU258316	AU258316		537	8.8	44.0	40	29	CC037274
C 465	8.8	44.0	32	9	AU258316	AU258316		538	8.8	44.0	40	29	CC037274
C 466	8.8	44.0	32	9	AU258316	AU258316		539	8.8	44.0	40	29	CC037274
C 467	8.8	44.0	32	9	AU258316	AU258316		540	8.8	44.0	40	29	CC037274
C 468	8.8	44.0	32	9	AU258316	AU258316		541	8.8	44.0	40	29	CC037274
C 469	8.8	44.0	32	9	AU258316	AU258316		542	8.8	44.0	40	29	CC037274
C 470	8.8	44.0	32	9	AU258316	AU258316		543	8.8	44.0	40	29	CC037274
C 471	8.8	44.0	32	9	AU258316	AU258316		544	8.8	44.0	40</		

C 516 8.8 44.0 40 29 DR17124S
 C 517 8.6 43.0 19 28 AZ500335 IM0338G07
 C 518 8.6 43.0 20 9 AU266619 AU266619
 C 519 8.6 43.0 20 28 AZ775160 2M0007F14
 C 520 8.6 43.0 22 9 AA905584 ok02a11.s
 C 521 8.6 43.0 22 9 AA928512 om17g11.s
 C 522 8.6 43.0 22 9 AA991484 os91h03.s
 C 523 8.6 43.0 23 28 AZ378021 IM0132B07
 C 524 8.6 43.0 23 28 AZ479801 IM0300G16
 C 525 8.6 43.0 24 28 AZ642209 IM0505E12
 C 526 8.6 43.0 24 28 AZ657713 IM0534O05
 C 527 8.6 43.0 24 28 AZ772496 IM0583I23
 C 528 8.6 43.0 25 9 AA747047 nx65a08.s
 C 529 8.6 43.0 25 9 AI299118 qn14g07.x
 C 530 8.6 43.0 25 9 AI748295 sb50f02.y
 C 531 8.6 43.0 25 12 BM399457 IM0339A57
 C 532 8.6 43.0 26 14 HA9860 y024e12.s1
 C 533 8.6 43.0 26 28 AQ025573 IM0361O19
 C 534 8.6 43.0 26 28 AZ514619 IM0361O19
 C 535 8.6 43.0 26 29 BZ356147 SALK_1282
 C 536 8.6 43.0 26 29 TA171C11P
 C 537 8.6 43.0 27 14 L32037 HUMXP1F11B
 C 538 8.6 43.0 27 28 AQ025573 fs(3)0202
 C 539 8.6 43.0 27 28 BH840637 XG05983-5
 C 540 8.6 43.0 27 29 TA23G12Q
 C 541 8.6 43.0 28 28 AQ025025 EP(2)1081
 C 542 8.6 43.0 28 28 BZ384708 SALK_1359
 C 543 8.6 43.0 28 29 BZ765310 SALK_1299
 C 544 8.6 43.0 29 28 AZ814996 IM0083B05
 C 545 8.6 43.0 29 29 BZ290805 SALK_0915
 C 546 8.6 43.0 29 29 BZ290805 SALK_0915
 C 547 8.6 43.0 29 29 BZ356973 SALK_1300
 C 548 8.6 43.0 29 29 BZ664577 SALK_0762
 C 549 8.6 43.0 29 29 TA190B07P
 C 550 8.6 43.0 30 28 AZ489887 IM0322M03
 C 551 8.6 43.0 30 28 AZ809943 2M0074M08
 C 552 8.6 43.0 30 28 BH865098 SALK_0973
 C 553 8.6 43.0 30 29 BX285017 Arabidops
 C 554 8.6 43.0 31 29 AU243395 AU243395
 C 555 8.6 43.0 32 9 AU243395 AU243395
 C 556 8.6 43.0 32 10 BG432121 602496990
 C 557 8.6 43.0 32 10 BE729734 601562915
 C 558 8.6 43.0 32 28 AZ936721 2M0193K03
 C 559 8.6 43.0 32 28 AZ946235 2M0207O20
 C 560 8.6 43.0 32 28 BH911753 SALK_0719
 C 561 8.6 43.0 32 29 BZ593625 SALK_0749
 C 562 8.6 43.0 32 29 AL751407 Arabidops
 C 563 8.6 43.0 33 9 AW720425 LjNBST229
 C 564 8.6 43.0 33 28 AZ44218 1M0233N07
 C 565 8.6 43.0 33 28 BH846998 SALK_0125
 C 566 8.6 43.0 34 9 AA772179 ai39a07.s
 C 567 8.6 43.0 34 9 AA939151 oq07e11.s
 C 568 8.6 43.0 34 9 AA071143 zm61e06.s
 C 569 8.6 43.0 34 9 AI419301 tf27c08.x
 C 570 8.6 43.0 34 9 AI433277 t132h05.x
 C 571 8.6 43.0 34 9 AV849826 AV849826
 C 572 8.6 43.0 34 12 BM400993 5009-0-81
 C 573 8.6 43.0 34 28 AZ486062 IM0313P14
 C 574 8.6 43.0 34 28 AZ626219 IM0466B23
 C 575 8.6 43.0 34 28 AZ976169 2M0251D06
 C 576 8.6 43.0 34 29 BZ354817 SALK_1258
 C 577 8.6 43.0 34 29 BZ665002 SALK_1103
 C 578 8.6 43.0 34 29 CC053512 SALK_0444
 C 579 8.6 43.0 34 29 DMES46920 Drosophila
 C 580 8.6 43.0 35 9 AL861724 AL861724
 C 581 8.6 43.0 35 9 AL969259 AL969259
 C 582 8.6 43.0 35 28 AZ462243 1M0269M20
 C 583 8.6 43.0 35 28 AZ491991 IM0325C24
 C 584 8.6 43.0 35 28 BZ768997 IM0569F16
 C 585 8.6 43.0 35 29 BZ763637 SALK_1200
 C 586 8.6 43.0 36 9 AV832536 AV832536
 C 587 8.6 43.0 36 9 AW332206 S5E11 AGS
 C 588 8.6 43.0 36 12 BM400508 5009-0-74

C 589 8.6 43.0 36 13 BQ589315
 C 590 8.6 43.0 36 28 AZ375984
 C 591 8.6 43.0 36 28 AZ493433
 C 592 8.6 43.0 36 28 AZ868929
 C 593 8.6 43.0 36 28 BH618555 SALK_0392
 C 594 8.6 43.0 36 28 AG215408 Drosophila
 C 595 8.6 43.0 36 29 AI767851 Arabidops
 C 596 8.6 43.0 37 9 AI889881
 C 597 8.6 43.0 37 9 AV844894 AV844894
 C 598 8.6 43.0 37 9 AA584274
 C 599 8.6 43.0 37 10 BE739565
 C 600 8.6 43.0 37 12 B1524368 603052253
 C 601 8.6 43.0 37 28 AZ805885 2M0067G05
 C 602 8.6 43.0 37 28 BH610282 SALK_0085
 C 603 8.6 43.0 37 28 BH614046
 C 604 8.6 43.0 37 28 BH618374
 C 605 8.6 43.0 37 28 BZ753396 SALK_0287
 C 606 8.6 43.0 37 29 BZ53825 SALK_1222
 C 607 8.6 43.0 38 9 AV833365
 C 608 8.6 43.0 38 10 BF131353 601818845
 C 609 8.6 43.0 38 28 AZ312598 IM0028H06
 C 610 8.6 43.0 38 28 BH611643 SALK_0312
 C 611 8.6 43.0 38 28 BH809808 SALK_0060
 C 612 8.6 43.0 38 28 BH853414 SALK_0769
 C 613 8.6 43.0 38 28 BH901179 SALK_0734
 C 614 8.6 43.0 38 29 BZ377640 SALK_0986
 C 615 8.6 43.0 38 29 AG019398 Homo sapi
 C 616 8.6 43.0 39 9 AL965058
 C 617 8.6 43.0 39 10 BF038837
 C 618 8.6 43.0 39 14 N75693
 C 619 8.6 43.0 39 28 AZ490169
 C 620 8.6 43.0 39 28 AZ584738
 C 621 8.6 43.0 39 28 BH618398
 C 622 8.6 43.0 39 28 BH908729
 C 623 8.6 43.0 39 29 AG019397 Homo sapi
 C 624 8.6 43.0 39 29 AG217121 Drosophila
 C 625 8.6 43.0 39 29 CNS07EVI
 C 626 8.6 43.0 40 9 AA722106 zhi7g03.s
 C 627 8.6 43.0 40 9 AI317060
 C 628 8.6 43.0 40 9 AI747305
 C 629 8.6 43.0 40 9 AI913326
 C 630 8.6 43.0 40 9 AA428089 zw32a07.r
 C 631 8.6 43.0 40 14 CA796225 Cac BL 32
 C 632 8.6 43.0 40 28 AZ610523 1M0435B20
 C 633 8.6 43.0 40 28 AZ825890 2M0101N15
 C 634 8.6 43.0 40 28 BH618849 SALK_0398
 C 635 8.6 43.0 40 28 BH863035 SALK_0930
 C 636 8.6 43.0 40 29 CC199600 XJ193 Bay
 C 637 8.6 43.0 40 29 AI358511 qw40c04.x
 C 638 8.6 43.0 40 16 9 AI358511
 C 639 8.6 43.0 40 19 28 AZ600709 1M0418H10
 C 640 8.6 43.0 40 19 28 AZ603744 1M0423E15
 C 641 8.6 43.0 40 19 28 AZ768448 1M0568H23
 C 642 8.6 43.0 40 19 28 AZ772819 1M0584F02
 C 643 8.6 43.0 40 19 28 AZ944615 2M005H12
 C 644 8.6 43.0 40 28 AZ314252 1M0031B01
 C 645 8.6 43.0 40 20 28 AZ787173 2M0033O06
 C 646 8.6 43.0 40 21 12 BM388924 5009-0-50
 C 647 8.6 43.0 40 21 13 BQ582609 E012279-0
 C 648 8.6 43.0 40 21 28 AZ588930 1M0397L05
 C 649 8.6 43.0 40 21 28 AZ768984 1M0569C16
 C 650 8.6 43.0 40 21 28 AZ796205 2M0051O13
 C 651 8.6 43.0 40 21 28 AZ852233 2M0154D23
 C 652 8.6 43.0 40 22 9 AA908574
 C 653 8.6 43.0 40 22 9 AA912639
 C 654 8.6 43.0 40 22 28 AZ307823
 C 655 8.6 43.0 40 22 28 AZ482848 1M0308E10
 C 656 8.6 43.0 40 22 28 AZ623402 1M0461O01
 C 657 8.6 43.0 40 22 28 AZ666342 1M0548M13
 C 658 8.6 43.0 40 22 28 AZ812054 2M0078C04
 C 659 8.6 43.0 40 22 28 AZ871339 2M0184G09
 C 660 8.6 43.0 40 22 28 AZ991140 2M0275K10
 C 661 8.6 43.0 40 22 29 TA129H06P

BQ589315 S014007-0
 AZ375984 IM0129F09
 AZ493433 IM0328A12
 AZ868929 2M0180P13
 BH618555 SALK_0392
 AG215408 Drosophila
 AI767851 Arabidops
 AI889881 wme4f02.x
 AV844894 AV844894
 AA584274 nm75g02.s
 BE739565 601556525
 B1524368 603052253
 AZ805885 2M0067G05
 BH610282 SALK_0085
 BH614046 SALK_0085
 BH618374 SALK_0389
 BZ753396 SALK_0287
 BZ53825 SALK_1222
 AV833365 AV833365
 BF131353 601818845
 AZ312598 IM0028H06
 BH611643 SALK_0312
 BH809808 SALK_0060
 BH853414 SALK_0769
 BH901179 SALK_0734
 BZ377640 SALK_0986
 AG019398 Homo sapi
 AL965058 AL965058
 BF038837 601462043
 N75693 yw52a01.r1
 AZ490169 IM0323A06
 AZ584738 1M0389A07
 BH618398 SALK_0390
 BH908729 SALK_0503
 AG019397 Homo sapi
 AG217121 Drosophila
 AL670762 Anopheles
 Zhi7g03.s
 AI317060 zhi7g03.s
 AI747305 ul14909.x
 AI913326 tz76c12.x
 AA428089 zw32a07.r
 CA796225 Cac BL 32
 AZ610523 1M0435B20
 AZ825890 2M0101N15
 BH618849 SALK_0398
 BH863035 SALK_0930
 CC199600 XJ193 Bay
 AI358511 qw40c04.x
 AZ600709 1M0418H10
 AZ603744 1M0423E15
 AZ768448 1M0568H23
 AZ772819 1M0584F02
 AZ944615 2M005H12
 AZ314252 1M0031B01
 AZ787173 2M0033O06
 BM388924 5009-0-50
 BQ582609 E012279-0
 AZ588930 1M0397L05
 AZ768984 1M0569C16
 AZ796205 2M0051O13
 AZ852233 2M0154D23
 AL452378 T. brucei
 AA908574 og84c05.s
 AA912639 ol29e11.s
 AZ307823 1M010X08
 AZ482848 1M0308E10
 AZ623402 1M0461O01
 AZ666342 1M0548M13
 AZ812054 2M0078C04
 AZ871339 2M0184G09
 AZ991140 2M0275K10
 AL464015 T. brucei

C 662	8.4	42.0	22	29	TA215F02Q	AL479263 T. brucei	C 735	8.4	42.0	32	28	AZ326012	AZ326012 1M0048A19
C 663	8.4	42.0	23	9	AW063953	AW063953 DP0988 KR	C 736	8.4	42.0	32	28	AZ333224	AZ333224 1M0062P09
C 664	8.4	42.0	23	28	AZ344611	AZ344611 1M0080L10	737	8.4	42.0	32	28	AZ618503	AZ618503 1M0450F13
C 665	8.4	42.0	23	28	AZ446113	AZ446113 1M0242B21	738	8.4	42.0	32	28	AZ627984	AZ627984 1M0476O04
C 666	8.4	42.0	23	28	AZ500926	AZ500926 1M0339J01	739	8.4	42.0	32	28	AZ815330	AZ815330 2M0083D05
C 667	8.4	42.0	23	28	AZ583599	AZ583599 1M03378A11	C 740	8.4	42.0	32	28	BH858487	BH858487 B5 6383C
C 668	8.4	42.0	23	28	AZ954682	AZ954682 1M0220P23	C 741	8.4	42.0	32	29	BZ662227	BZ662227 SALK 0257
C 669	8.4	42.0	24	14	CB305252	CB305252 3-EST-NEL	C 742	8.4	42.0	32	9	AU007641	AU007641 AU007641
C 670	8.4	42.0	24	28	AZ514434	AZ514434 1M0361J17	C 743	8.4	42.0	33	9	AA91666	AA91666 ne79G09.s
C 671	8.4	42.0	24	28	AZ655394	AZ655394 1M0530C05	C 744	8.4	42.0	33	10	BG387814	BG387814 602412712
C 672	8.4	42.0	24	28	BH849969	BH849969 SALK 0706	C 745	8.4	42.0	33	10	BG387814	BG387814 602412712
C 673	8.4	42.0	25	9	AA917307	AA917307 SMOVL3CAN	C 746	8.4	42.0	33	12	BJ052224	BJ052224 BJ052224
C 674	8.4	42.0	25	12	BG927349	BG927349 HNC1-1-C4	C 747	8.4	42.0	33	12	BJ052224	BJ052224 BJ052224
C 675	8.4	42.0	25	28	AZ309919	AZ309919 1M0017C19	C 748	8.4	42.0	33	28	AZ591773	AZ591773 1M0402M06
C 676	8.4	42.0	25	28	AZ346977	AZ346977 1M0082P22	C 749	8.4	42.0	33	28	AZ766622	AZ766622 1M0545A24
C 677	8.4	42.0	25	28	AZ492371	AZ492371 1M0326P23	C 750	8.4	42.0	33	28	BH863927	BH863927 SALK 0949
C 678	8.4	42.0	25	28	BH812183	BH812183 SALK 0613	C 751	8.4	42.0	33	29	CC055061	CC055061 SALK 0806
C 679	8.4	42.0	26	28	AZ807262	AZ807262 2M0070C01	C 752	8.4	42.0	33	29	AG253538	AG253538 Lotus jap
C 680	8.4	42.0	26	28	TA82H10P	TA82H10P T. brucei	C 753	8.4	42.0	34	9	AA961906	AA961906 or68D08.s
C 681	8.4	42.0	27	28	AZ347008	AZ347008 1M0082J02	C 754	8.4	42.0	34	9	AI031843	AI031843 oy45e01.x
C 682	8.4	42.0	27	28	AZ343403	AZ343403 1M0220E15	C 755	8.4	42.0	34	9	AI181397	AI181397 uc59c02.f
C 683	8.4	42.0	27	28	AZ442177	AZ442177 1M0234K14	C 756	8.4	42.0	34	9	AI1798272	AI1798272 tr32e04.x
C 684	8.4	42.0	27	28	AZ477602	AZ477602 1M0297K11	C 757	8.4	42.0	34	9	AU255210	AU255210 AU255210
C 685	8.4	42.0	27	28	AZ797801	AZ797801 2M0054A18	C 758	8.4	42.0	34	9	AV970292	AV970292 AV970292
C 686	8.4	42.0	27	28	AZ827243	AZ827243 2M0103N04	C 759	8.4	42.0	34	10	BF580524	BF580524 602097312
C 687	8.4	42.0	27	28	AZ835413	AZ835413 2M0129E11	C 760	8.4	42.0	34	10	BG288172	BG288172 602387981
C 688	8.4	42.0	27	28	AZ966573	AZ966573 2M0237B12	C 761	8.4	42.0	34	12	BI760282	BI760282 603045345
C 689	8.4	42.0	27	29	TA202H07P	TA202H07P T. brucei	C 762	8.4	42.0	34	12	BJ060418	BJ060418 BJ060418
C 690	8.4	42.0	28	9	AI471686	AI471686 t139e04.x	C 763	8.4	42.0	34	14	CD028602	CD028602 mgap008XA
C 691	8.4	42.0	28	9	AI569493	AI569493 tn87G04.x	C 764	8.4	42.0	34	28	AZ454761	AZ454761 1M0256A24
C 692	8.4	42.0	28	9	AI699157	AI699157 tx61B09.x	C 765	8.4	42.0	34	28	AZ476549	AZ476549 1M0295P24
C 693	8.4	42.0	28	9	AI701242	AI701242 wc60B12.x	C 766	8.4	42.0	34	28	AZ481974	AZ481974 1M0306K07
C 694	8.4	42.0	28	28	AZ645934	AZ645934 1M0511N12	C 767	8.4	42.0	34	28	AZ514577	AZ514577 1M0361P11
C 695	8.4	42.0	28	28	AZ783984	AZ783984 2M0026M07	C 768	8.4	42.0	34	28	AZ787308	AZ787308 2M0033B21
C 696	8.4	42.0	28	28	AZ855627	AZ855627 2M0159D15	C 769	8.4	42.0	34	28	AZ824762	AZ824762 2M0099S02
C 697	8.4	42.0	28	28	AZ997003	AZ997003 2M0283B21	C 770	8.4	42.0	34	28	AZ825271	AZ825271 2M0100E22
C 698	8.4	42.0	29	28	AZ345803	AZ345803 1M0080J07	C 771	8.4	42.0	34	28	BH791107	BH791107 SALK 0587
C 699	8.4	42.0	29	28	AZ821985	AZ821985 2M0095B23	C 772	8.4	42.0	34	28	BH852447	BH852447 SALK 0746
C 700	8.4	42.0	29	28	AZ996661	AZ996661 2M0282J23	C 773	8.4	42.0	34	28	BZ761684	BZ761684 SALK 0750
C 701	8.4	42.0	29	28	BH910641	BH910641 SALK 0607	C 774	8.4	42.0	34	29	TA273B02Q	TA273B02Q T. brucei
C 702	8.4	42.0	29	29	BZ355020	BZ355020 SALK 1262	C 775	8.4	42.0	35	9	AV853625	AV853625 AV853625
C 703	8.4	42.0	30	28	AQ025600	AQ025600 1(2)G2839	C 776	8.4	42.0	35	14	H81781	H81781 yv82909.s1
C 704	8.4	42.0	30	28	AZ345807	AZ345807 1M0080J11	C 777	8.4	42.0	35	14	H99830	H99830 yx28612.s1
C 705	8.4	42.0	30	28	AZ579486	AZ579486 1M0367B10	C 778	8.4	42.0	35	28	AZ345880	AZ345880 1M0080O13
C 706	8.4	42.0	30	28	AZ817495	AZ817495 2M0087D05	C 779	8.4	42.0	35	28	AZ433289	AZ433289 1M0217F11
C 707	8.4	42.0	30	28	AZ827644	AZ827644 2M0104N08	C 780	8.4	42.0	35	28	AZ620930	AZ620930 1M0453B19
C 708	8.4	42.0	30	28	BH902140	BH902140 SALK 0913	C 781	8.4	42.0	35	28	AZ809028	AZ809028 2M0072A19
C 709	8.4	42.0	30	29	BZ357267	BZ357267 SALK 1304	C 782	8.4	42.0	35	28	AZ822670	AZ822670 2M0096B11
C 710	8.4	42.0	30	29	TA123E0SP	TA123E0SP T. brucei	C 783	8.4	42.0	36	9	AL797263	AL797263 AL797263
C 711	8.4	42.0	30	29	TA369C08P	TA369C08P T. brucei	C 784	8.4	42.0	36	9	AU283582	AU283582 AU283582
C 712	8.4	42.0	31	9	AI002018	AI002018 ot40f07.s	C 785	8.4	42.0	36	10	BG718554	BG718554 602696627
C 713	8.4	42.0	31	9	AI003715	AI003715 zt03c07.s	C 786	8.4	42.0	36	14	T818222	T818222 yd95906.s1
C 714	8.4	42.0	31	9	AI004493	AI004493 ot57c08.s	C 787	8.4	42.0	36	28	AZ330732	AZ330732 1M056D12
C 715	8.4	42.0	31	9	AI021154	AI021154 ub02c03.r	C 788	8.4	42.0	36	28	AZ372751	AZ372751 1M0124E14
C 716	8.4	42.0	31	9	AI140482	AI140482 ow82d12.s	C 789	8.4	42.0	36	28	AZ456786	AZ456786 1M0259P13
C 717	8.4	42.0	31	9	AI197192	AI197192 ud8a09.r	C 790	8.4	42.0	36	28	AZ514452	AZ514452 1M0361N13
C 718	8.4	42.0	31	9	AI287914	AI287914 qul3c06.x	C 791	8.4	42.0	36	28	AZ774765	AZ774765 2M0004G05
C 719	8.4	42.0	31	9	AI354521	AI354521 q44606.x	C 792	8.4	42.0	36	28	AZ794540	AZ794540 2M0048C21
C 720	8.4	42.0	31	9	AU256721	AU256721 AU256721	C 793	8.4	42.0	36	28	AZ812622	AZ812622 2M0079K21
C 721	8.4	42.0	31	9	AU258742	AU258742 AU258742	C 794	8.4	42.0	36	28	BH814646	BH814646 SALK 0667
C 722	8.4	42.0	31	9	AA245520	AA245520 ny50a02.r	C 795	8.4	42.0	37	9	AA807297	AA807297 oc37c10.s
C 723	8.4	42.0	31	9	AA486302	AA486302 ad35b07.r	C 796	8.4	42.0	37	9	AA920462	AA920462 vy53a11.r
C 724	8.4	42.0	31	9	AA619417	AA619417 v084a07.r	C 797	8.4	42.0	37	9	AA987401	AA987401 oq87g06.s
C 725	8.4	42.0	31	28	AQ025953	AQ025953 1(2)K1120	C 798	8.4	42.0	37	9	AI016852	AI016852 ou27b03.x
C 726	8.4	42.0	31	28	AZ492732	AZ492732 1M0327E06	C 799	8.4	42.0	37	9	AI016852	AI016852 ou27b03.x
C 727	8.4	42.0	31	28	AZ592386	AZ592386 1M0403H15	C 800	8.4	42.0	37	9	AI089361	AI089361 qb05h05.x
C 728	8.4	42.0	31	28	AZ945327	AZ945327 2M0206J09	C 801	8.4	42.0	37	9	AI130471	AI130471 SMOVL3CAN
C 729	8.4	42.0	31	28	AZ963641	AZ963641 2M0232D24	C 802	8.4	42.0	37	9	AI1269184	AI1269184 q125d01.x
C 730	8.4	42.0	32	9	AU011589	AU011589 AU011589	C 803	8.4	42.0	37	9	AI120693	AI120693 mp72g11.r
C 731	8.4	42.0	32	9	AU014531	AU014531 AU014531	C 804	8.4	42.0	37	9	AI581885	AI581885 as03f08.x
C 732	8.4	42.0	32	9	AU014532	AU014532 AU014532	C 805	8.4	42.0	37	9	AA161068	AA161068 z15oh07.r
C 733	8.4	42.0	32	9	AU257547	AU257547 AU257547	C 806	8.4	42.0	37	9	AA275360	AA275360 vc07d04.r
C 734	8.4	42.0	32	9	AU266374	AU266374 AU266374	C 807	8.4	42.0	37	10	BG166700	BG166700 602339211

C 808	8.4	42.0	37	12	BM396949	5009-0-27	881	8.4	42.0	40	29	TA353C08Q	AL496044	T. brucei
C 809	8.4	42.0	37	14	H98928	yx31c1l.r1	882	8.2	41.0	14	12	BM398814	BM398814	5009-0-5-
C 810	8.4	42.0	37	14	T83009	yd39a12.r1	C 883	8.2	41.0	19	9	AI049374	AI049374	ub33a03.r
C 811	8.4	42.0	37	14	W53327	md42a06.r1	C 884	8.2	41.0	19	28	AZ798955	AZ798955	2M0056K01
C 812	8.4	42.0	37	28	AZ308836	LM0012E18	C 885	8.2	41.0	20	28	AZ348287	AZ348287	1M0084D14
C 813	8.4	42.0	37	28	AZ479159	1M0299E10	C 886	8.2	41.0	20	28	AZ946089	AZ946089	2M0207A13
C 814	8.4	42.0	37	28	AZ582240	1M0374E06	C 887	8.2	41.0	20	28	AZ992240	AZ992240	2M0276M15
C 815	8.4	42.0	37	28	AZ644324	1M0508A13	C 888	8.2	41.0	21	12	BM397213	BM397213	5009-0-3-
C 816	8.4	42.0	37	28	BH759497	KG04622-5	C 889	8.2	41.0	21	28	AZ616418	AZ616418	1M0446A14
C 817	8.4	42.0	37	28	BH840538	KG04436-3	C 890	8.2	41.0	21	28	AZ638415	AZ638415	2M0134A10
C 818	8.4	42.0	37	28	BH864617	SALK_0963	C 891	8.2	41.0	22	9	AA894398	AA894398	of85h01.s
C 819	8.4	42.0	37	29	BZ661525	SALK_0249	C 892	8.2	41.0	22	9	AA985475	AA985475	oq96e09.s
C 820	8.4	42.0	37	29	BZ767403	SALK_1388	C 893	8.2	41.0	22	28	AZ333194	AZ333194	1M0156H11
C 821	8.4	42.0	37	29	AL755793	panio rer	C 894	8.2	41.0	22	28	AZ589849	AZ589849	1M0178K06
C 822	8.4	42.0	38	9	AV833036	AV833036	C 895	8.2	41.0	22	28	AZ781789	AZ781789	1M0021119
C 823	8.4	42.0	38	9	AV837883	AV837883	C 896	8.2	41.0	22	28	AZ461315	AZ461315	1M0267F09
C 824	8.4	42.0	38	9	AV839386	AV839386	C 897	8.2	41.0	23	28	AZ461315	AZ461315	1M0267F09
C 825	8.4	42.0	38	28	AQ025540	EP(X)1614	C 898	8.2	41.0	23	29	TA125F10Q	TA125F10Q	T. brucei
C 826	8.4	42.0	38	28	AZ363970	1M0109N19	C 899	8.2	41.0	24	9	AU257541	AU257541	AU257541
C 827	8.4	42.0	38	28	AZ766365	1M0563G20	C 900	8.2	41.0	24	28	AZ596086	AZ596086	1M0409E07
C 828	8.4	42.0	38	28	AZ769444	1M0570H11	C 901	8.2	41.0	24	28	AZ767824	AZ767824	1M0567K22
C 829	8.4	42.0	38	28	AZ953906	2M0219B32	C 902	8.2	41.0	25	9	AA912548	AA912548	ol36c01.s
C 830	8.4	42.0	38	28	BH792513	SALK_0646	C 903	8.2	41.0	25	9	A1000280	A1000280	ov10e04.s
C 831	8.4	42.0	38	28	BH858486	BS_6383C	C 904	8.2	41.0	25	28	AZ435187	AZ435187	1M0222E04
C 832	8.4	42.0	38	29	CC053624	SALK_0458	C 905	8.2	41.0	25	28	AZ536197	AZ536197	1M0374C11
C 833	8.4	42.0	38	29	EX004657	Arabidops	C 906	8.2	41.0	25	28	AZ599533	AZ599533	1M0414N20
C 834	8.4	42.0	38	29	DME545254	Arabidops	C 907	8.2	41.0	25	28	AZ646894	AZ646894	1M0513E10
C 835	8.4	42.0	38	29	DR40E4T	Arabidops	C 908	8.2	41.0	25	28	AZ774671	AZ774671	2M0004N11
C 836	8.4	42.0	38	29	TA110BL2Q	Arabidops	C 909	8.2	41.0	25	28	AZ779254	AZ779254	2M0015K21
C 837	8.4	42.0	39	9	AU283211	4A3A-P8C1	C 910	8.2	41.0	25	28	AZ838918	AZ838918	2M0134M13
C 838	8.4	42.0	39	9	AU961663	AU961663	C 911	8.2	41.0	25	28	BH903953	BH903953	SALK_1037
C 839	8.4	42.0	39	9	AV841757	AV841757	C 912	8.2	41.0	25	29	BZ377683	BZ377683	SALK_1060
C 840	8.4	42.0	39	28	AZ330739	1M0056F12	C 913	8.2	41.0	25	29	BZ378611	BZ378611	SALK_1083
C 841	8.4	42.0	39	28	AZ392901	1M0155B15	C 914	8.2	41.0	25	29	BZ378670	BZ378670	SALK_1086
C 842	8.4	42.0	39	28	AZ459319	1M0264K05	C 915	8.2	41.0	25	29	BZ380733	BZ380733	SALK_1155
C 843	8.4	42.0	39	28	AZ816032	2M0084A09	C 916	8.2	41.0	25	29	BZ381706	BZ381706	SALK_1171
C 844	8.4	42.0	39	28	AZ817405	2M0086H12	C 917	8.2	41.0	26	28	AQ025578	AQ025578	fs(3)0848
C 845	8.4	42.0	39	28	AZ942629	2M0202B19	C 918	8.2	41.0	26	28	AZ330746	AZ330746	1M0056I09
C 846	8.4	42.0	39	28	BH023786	BG02383-5	C 919	8.2	41.0	26	28	AZ827167	AZ827167	2M0103N22
C 847	8.4	42.0	39	28	AL757312	Arabidops	C 920	8.2	41.0	26	29	BZ377800	BZ377800	SALK_1062
C 848	8.4	42.0	39	29	TA324H05P	Arabidops	C 921	8.2	41.0	26	29	BZ378588	BZ378588	SALK_1083
C 849	8.4	42.0	40	9	AA687728	nv08c10.s	C 922	8.2	41.0	26	29	BZ378645	BZ378645	SALK_1084
C 850	8.4	42.0	40	9	AA757657	Z942f107.s	C 923	8.2	41.0	26	29	BZ378665	BZ378665	SALK_1086
C 851	8.4	42.0	40	9	AI017181	ou28c08.x	C 924	8.2	41.0	26	29	BZ378696	BZ378696	SALK_1086
C 852	8.4	42.0	40	9	AI039253	ox33b01.s	C 925	8.2	41.0	26	29	BZ383878	BZ383878	SALK_1347
C 853	8.4	42.0	40	9	AI443492	sa32d12.x	C 926	8.2	41.0	26	29	TA127E06P	TA127E06P	T. brucei
C 854	8.4	42.0	40	9	AI609582	tw28c02.x	C 927	8.2	41.0	26	28	AZ434341	AZ434341	1M0076B04
C 855	8.4	42.0	40	9	AI683349	tx66a10.x	C 928	8.2	41.0	27	28	AZ663231	AZ663231	1M0542G15
C 856	8.4	42.0	40	9	AI690571	tg02a02.x	C 929	8.2	41.0	27	28	AZ993846	AZ993846	2M0279K05
C 857	8.4	42.0	40	9	AI795097	sb76d08.y	C 930	8.2	41.0	27	28	BH757508	BH757508	SALK_0563
C 858	8.4	42.0	40	9	AI876425	uj57b04.x	C 931	8.2	41.0	27	29	BZ377643	BZ377643	SALK_0987
C 859	8.4	42.0	40	9	AA207324	mv88b05.r	C 932	8.2	41.0	27	29	BZ378558	BZ378558	SALK_1082
C 860	8.4	42.0	40	9	AV837991	AV837991	C 933	8.2	41.0	27	29	BZ381636	BZ381636	SALK_1170
C 861	8.4	42.0	40	9	AV845875	AV845875	C 934	8.2	41.0	27	29	BZ383746	BZ383746	SALK_1343
C 862	8.4	42.0	40	9	AV961768	AV961768	C 935	8.2	41.0	27	29	BZ763129	BZ763129	SALK_1137
C 863	8.4	42.0	40	10	BF343276	602015935	C 936	8.2	41.0	28	28	AZ313467	AZ313467	1M0029P06
C 864	8.4	42.0	40	14	C00565	HUMGS000810	C 937	8.2	41.0	28	28	AZ313467	AZ313467	1M0029P06
C 865	8.4	42.0	40	28	AZ480548	1M0302H12	C 938	8.2	41.0	28	28	AZ512393	AZ512393	1M0357F20
C 866	8.4	42.0	40	28	AZ575900	ASCT-722B0	C 939	8.2	41.0	28	28	AZ773089	AZ773089	1M0584J23
C 867	8.4	42.0	40	28	AZ591528	1M0401K11	C 940	8.2	41.0	28	28	AZ867377	AZ867377	2M0178N07
C 868	8.4	42.0	40	28	AZ622990	1M0460N12	C 941	8.2	41.0	28	29	BZ377671	BZ377671	SALK_0987
C 869	8.4	42.0	40	28	AZ664837	1M0545O20	C 942	8.2	41.0	28	29	BZ378654	BZ378654	SALK_1085
C 870	8.4	42.0	40	28	AZ784839	2M0028C09	C 943	8.2	41.0	28	29	BZ378727	BZ378727	SALK_1087
C 871	8.4	42.0	40	28	AZ839469	2M0134K07	C 944	8.2	41.0	28	29	BZ380171	BZ380171	SALK_1147
C 872	8.4	42.0	40	28	AZ954080	2M0219C07	C 945	8.2	41.0	28	29	BZ383909	BZ383909	SALK_1347
C 873	8.4	42.0	40	28	BH614568	2B8DC9 Su	C 946	8.2	41.0	28	29	BZ766664	BZ766664	SALK_1376
C 874	8.4	42.0	40	28	BH796423	10C8094B1	C 947	8.2	41.0	29	13	EQ0593117	EQ0593117	E012797-0
C 875	8.4	42.0	40	28	BH807499	10C8071D1	C 948	8.2	41.0	29	14	CD029249	CD029249	mgns012X0
C 876	8.4	42.0	40	29	BZ288540	Arabidops	C 949	8.2	41.0	29	28	AZ454477	AZ454477	1M0256N22
C 877	8.4	42.0	40	29	AL947087	SALK_0219	C 950	8.2	41.0	29	28	AZ494908	AZ494908	1M0330A04
C 878	8.4	42.0	40	29	EX133759	Danio rer	C 951	8.2	41.0	29	28	AZ629028	AZ629028	1M0481P12
C 879	8.4	42.0	40	29	EX197094	Danio rer	C 952	8.2	41.0	29	28	BH814913	BH814913	SALK_0672
C 880	8.4	42.0	40	29	TA253H01Q	T. brucei	C 953	8.2	41.0	29	29	BZ377673	BZ377673	SALK_0987


```

RESULT 5
AZ307649
LOCUS
DEFINITION
  AZ307649 Mouse 10kb plasmid UUGCLM library Mus musculus genomic
  clone UUGCLM0009E19 R, genomic survey sequence.
ACCESSION
  AZ307649
VERSION
  AZ307649.1 GI:10346858
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 30)
REFERENCE
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
  , M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
  and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished
JOURNAL
  Unpublished
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0009 row: E column: 19
  Seq primer: CACACAGGAACAGCTATGACC
  Class: Plasmid ends
  High quality sequence stop: 30.
  Location/Qualifiers
    1..30
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGCLM0009E19"
      /sex="Male"
      /lab_host="B. Coli strain XL10-Gold, Ti-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGCLM library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptor DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptor mouse DNA was annealed to
      adaptor vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."
      2 a 8 c 7 g 13 t
BASE COUNT
  2 a 8 c 7 g 13 t
ORIGIN
  Query Match. 58.0%; Score 11.6; DB 28; Length 30;
  Best Local Similarity 77.8%; Pred. No. 1.3e+05;
  Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  QY 2 TTCTCGCTGGTGAGTTTC 19
  ||||| ||||| |||||
  Db 8 TTCTGTGCTGATGCCTTTC 25

RESULT 6
BZ352394/c
LOCUS
DEFINITION
  BZ352394 32 bp DNA linear GSS 14-NOV-2002
  SALK_078973.15.15.x Arabidopsis thaliana TDNA insertion lines
  Arabidopsis thaliana genomic clone SALK_078973.15.15.x, genomic
  survey sequence.
ACCESSION
  BZ352394
VERSION
  BZ352394.1 GI:24943256
KEYWORDS
  GSS.
SOURCE
  Arabidopsis thaliana (thale cress)
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
  ; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
  1 (bases 1 to 32)
REFERENCE
  Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab
  , C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.
  , Zimmerman, J. and Ecker, J.R.
  A Sequence-Indexed Library of Insertion Mutations in the
  Arabidopsis Genome
  Unpublished
JOURNAL
  Unpublished
COMMENT
  Contact: Joseph R. Ecker
  Salk Institute Genomic Analysis Laboratory (SIGnAL)
  The Salk Institute for Biological Studies
  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
  Tel: 858 453 4100 x1752
  Fax: 858 558 6379
  Email: ecker@salk.edu
  This is single pass sequence recovered from the left border of
  TDNA.
  Class: TDNA tagged.
  Location/Qualifiers
    1..32
      /organism="Arabidopsis thaliana"
      /mol_type="genomic DNA"
      /strain="Columbia 0"
      /db_xref="taxon:3702"
      /clone="SALK_078973.15.15.x"
      /note="PCR was performed on Arabidopsis thaliana lines
      each of which contains one or more TDNA insertion
      elements. The resultant fragment for each line was
      directly sequenced to determine the genomic sequence at
      the site of insertion. Details of the protocols used can
      be found at http://signal.salk.edu/tdna_protocols.html"
      10 a 5 c 6 g 11 t
BASE COUNT
  10 a 5 c 6 g 11 t
ORIGIN
  Query Match. 58.0%; Score 11.6; DB 29; Length 32;
  Best Local Similarity 77.8%; Pred. No. 1.3e+05;
  Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  QY 3 TCTCGCTGGTGAGTTTCA 20
  ||||| ||||| |||||
  Db 21 TATCGCTTGAGAGTTACA 4

RESULT 7
AZ495085
LOCUS
DEFINITION
  AZ495085 34 bp DNA linear GSS 05-OCT-2000
  IM0330114R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
  clone UUGCLM0330114 R, genomic survey sequence.
ACCESSION
  AZ495085
VERSION
  AZ495085.1 GI:10670338
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 34)
REFERENCE
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
  , M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
  and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished
JOURNAL
  Unpublished
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0009 row: E column: 19
  Seq primer: CACACAGGAACAGCTATGACC
  Class: Plasmid ends
  High quality sequence stop: 30.
  Location/Qualifiers
    1..30
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGCLM0009E19"
      /sex="Male"
      /lab_host="B. Coli strain XL10-Gold, Ti-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGCLM library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptor DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptor mouse DNA was annealed to
      adaptor vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."
      2 a 8 c 7 g 13 t
BASE COUNT
  2 a 8 c 7 g 13 t
ORIGIN
  Query Match. 58.0%; Score 11.6; DB 28; Length 30;
  Best Local Similarity 77.8%; Pred. No. 1.3e+05;
  Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  QY 2 TTCTCGCTGGTGAGTTTC 19
  ||||| ||||| |||||
  Db 8 TTCTGTGCTGATGCCTTTC 25

```


Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: rdunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0330 row: 1 column: 14
 Seq primer: CACACAGGAAACAGCATGACC
 Class: plasmid ends
 High quality sequence stop: 34.

FEATURES

Location/Qualifiers
 1..34
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clones="UUGC1M0330114"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

7 a 8 c 10 g 9 t

ORIGIN

Query Match 58.0%; Score 11.6; DB 28; Length 34;
 Best Local Similarity 77.8%; Pred. No. 1.3e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TCTCGTGGTGAGTTTCA 20

|||||
 Db 8 TCTCGTGGTGAGTTTCA 25

RESULT 8

AA866679/c
 LOCUS
 DEFINITION
 ud07b12.r1 Soares NMMPu Mus musculus cDNA clone IMAGE:1434431 5' similar to SW:NUC6 BOVIN P17694 NADH-UBIQUINONE OXIDOREDUCTASE 49 KD SUBUNIT ;, mRNA sequence.
 AA866679
 VERSION
 AA866679.1 GI:2962124
 KEYWORDS
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 37)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheilenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 The WashU-HHMI Mouse EST Project
 Unpublished
 Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:918499

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1..37
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clones="IMAGE:1434431"
 /sex="female"
 /dev stage="adult"
 /lab_host="DHL0B"
 /clone_lib="Soares NMMPu"
 /note="Organ: uterus; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

12 a 9 c 10 g 6 t

BASE COUNT

ORIGIN

Query Match 58.0%; Score 11.6; DB 9; Length 37;

Best Local Similarity 77.8%; Pred. No. 1.4e+05;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 TCTCGTGGTGAGTTTCA 20

|||||
 Db 36 TCTCCCTGGGAGCTTCA 19

RESULT 9

BH840631
 LOCUS
 DEFINITION
 KG05933-Sprime Drosophila melanogaster P{SUPor-P} P element insertion lines Drosophila melanogaster genomic sequence recovered from 5' end of P element, genomic survey sequence.
 BH840631
 VERSION
 BH840631.1 GI:21264947
 KEYWORDS
 GSS.
 SOURCE
 Drosophila melanogaster (fruit fly)
 ORGANISM
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 37)
 Lewis, R., Hoskins, R., Liao, G., Mozden, N., Tsang, G., He, Y., Karpen, G., Bellien, H., Rubin, G. and Spradling, A.
 The Berkeley Drosophila Genome Project Gene Disruption Project
 Unpublished
 Contact: Gerald Rubin
 Berkeley Drosophila Genome Project

University of California, Berkeley
LSA Building Berkeley, CA 94720-3200, USA
Fax: 5106433947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P element
The P element insertion position is base 30 in the 37 bases. This insertion position refers to the first base of the 8 base target recognition sequence.
Class: transposon-tagged.

FEATURES

source
1. .37
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P(SUPor-P) P element insertion lines"
/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains one or more P(SUPor-P) P-element transposon insertion. The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at <http://www.fruitfly.org/about/methods/inverse.pcr.html>."

BASE COUNT

2 a 13 c 12 g 10 t

ORIGIN

Query Match 58.0%; Score 11.6; DB 28; Length 37;
Best Local Similarity 77.8%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCTCGCTGGTGAGTTT 18

Db 4 GTGCCGCTGGTGACATT 21

RESULT 10

BZ352489/c

LOCUS

DEFINITION BZ352489 37 bp DNA linear GSS 14-NOV-2002
Arabidopsis thaliana genomic clone SAUK_080716.25.00.n, genomic survey sequence.

ACCESSION

BZ352489

VERSION

BZ352489.1

KEYWORDS

GSS

SOURCE

Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana

REFERENCE

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab

, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.

, Zimmerman, J., and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .37

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

FEATURES

source

/db_xref="taxon:3702"

/clone="SAUK_080716.25.00.n"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html."

11 a 5 c 9 g 12 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 77.8%;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TCTCGCTGGTGAGTTTCA 20

Db 26 TATCGCTTGAGATTACA 9

RESULT 11

BH812422

LOCUS

DEFINITION BH812422

thaliana genomic clone SAUK_061751, genomic survey sequence.

33 bp DNA linear GSS 02-MAY-2002

Accession BH812422.1

Version BH812422.1

Keywords GSS

Source Arabidopsis thaliana (thale cress)

Organism Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 33)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab

, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.

, Zimmerman, J., and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At5g22690.

Class: TDNA tagged.

Location/Qualifiers

1. .33

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SAUK_061751"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html."

5 a 7 c 11 g 10 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 81.2%;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTT 17

```

Db      1  TTCTAGCTGTCGCTT 16
|||||
RESULT 12
BZ354295      36 bp      DNA      linear      GSS 14-NOV-2002
LOCUS      SALK_123484.43 15.x Arabidopsis thaliana TDNA insertion lines
DEFINITION  Arabidopsis thaliana genomic clone SALK_123484.43.15.x, genomic
survey sequence.
ACCESSION  BZ354295
VERSION    BZ354295.1 GI:24945157
KEYWORDS   GSS.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE  1 (bases 1 to 36)
AUTHORS    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
,Zimmerman,J. and Ecker,J.R.
TITLE      A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL    Unpublished
COMMENT    Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source           1..36
     /organism="Arabidopsis thaliana"
     /mol_type="genomic DNA"
     /db_xref="taxon:3702"
     /clone_lib="SALK_123484.43.15.x"
     /note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"
BASE COUNT          10 a      8 c      5 g      13 t
ORIGIN

Query Match      56.0%; Score 11.2; DB 29; Length 36;
Best Local Similarity 81.2%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2  TTCTCGCTGTCGCTT 17
|||||
Db      21  TTCTCGCTGTCGCTT 36
|||||
RESULT 13
AQ026356
LOCUS      AQ026356      18 bp      DNA      linear      GSS 08-JUL-1998
DEFINITION  1(3)RG554 Drosophila melanogaster P lethal line Drosophila
melanogaster genomic Sequence recovered from 5' end of P element,
genomic survey sequence.
ACCESSION  AQ026356
VERSION    AQ026356.1 GI:3293769
KEYWORDS   GSS.
SOURCE     Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Spradling,A.C., Stern,D., Beaton,A., Rehm,E.J., Lavery,T., Mozden
,N., Misra,S. and Rubin,G.M.
TITLE      The BDGP gene disruption project: Single P element insertions
mutating 30% of Drosophila autosomal genes
JOURNAL    Unpublished
COMMENT    On Jul 7, 1998 this sequence version replaced gi:3266641.
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
USA Building, Berkeley, CA 94720-3200, USA
Fax: 5106433947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element

The P element insertion position is base 011 in the 149 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
FEATURES             Location/Qualifiers
     source           1..18
     /organism="Drosophila melanogaster"
     /mol_type="genomic DNA"
     /db_xref="taxon:7227"
     /clone_lib="Drosophila melanogaster P lethal line"
     /note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains a single P
transposable element insertion that is thought to cause
either lethality or sterility. The resultant fragment for
each strain was directly sequenced to determine the
genomic sequence at the site of insertion. Details of the
protocols used can be found at
http://fruitfly.berkeley.edu/p\_disrupt/inverse\_pcr.html."
BASE COUNT          2 a      5 c      7 g      4 t
ORIGIN

Query Match      55.0%; Score 11; DB 28; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6  CGCTGGTGAGT 16
|||||
Db      2  CGCTGGTGAGT 12
|||||
RESULT 14
AZ776659
LOCUS      AZ776659      24 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION  2M0010C02R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC2M0010C02 R, genomic survey sequence.
ACCESSION  AZ776659
VERSION    AZ776659.1 GI:12904456
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,R., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

```

The p element insertion position is base 11 in the 27 bases. This

insertion position refers to the first base of the 8 base target recognition sequence.

Class: transposon-tagged.

Location/Qualifiers

1. .27
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone_lib="Drosophila melanogaster EP line"

/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains a single EP transposable element insertion. (The generation of these insertion strains is described in Rorth P, Szabo K, Bailey A, Laverty T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function genetics in Drosophila. Development 6:1049-1057.) The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."

BASE COUNT 5 a 7 c 11 g 4 t

ORIGIN

Query Match 55.0%; Score 11; DB 28; Length 27;
Best Local Similarity 100.0%; Pred.No. 2.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGGTGAGT 16

Db 2 CGCTGGTGAGT 12

RESULT 17

AQ073845

LOCUS

DEFINITION EP(3)3236 Drosophila melanogaster EP line Drosophila melanogaster genomic sequence recovered from Both 5' and 3' ends of P element, genomic survey sequence.

ACCESSION AQ073845

VERSION 1

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 27)

Liaw, G.-C., Rehm, E.J. and Rubin, G.M.

Insertion site preferences of the P transposable element in

Drosophila melanogaster

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)

20202638

10716700

CONTACT: Gerald Rubin

Berkeley Drosophila Genome Project

University of California, Berkeley

USA Building, Berkeley, CA 94720-3200, USA

Fax: 5106439947

Email: germy@fruitfly.berkeley.edu

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P element

The P element insertion position is base 11 in the 27 bases. This insertion position refers to the first base of the 8 base target recognition sequence.

Class: transposon-tagged.

Location/Qualifiers

1. .27

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/db_xref="taxon:7227"

/clone_lib="Drosophila melanogaster EP line"
/note="Inverse PCR was performed on Drosophila melanogaster strains each of which contains a single EP transposable element insertion. (The generation of these insertion strains is described in Rorth P, Szabo K, Bailey A, Laverty T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function genetics in Drosophila. Development 6:1049-1057.) The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."

BASE COUNT 5 a 7 c 11 g 4 t

ORIGIN

Query Match 55.0%; Score 11; DB 28; Length 27;

Best Local Similarity 100.0%; Pred.No. 2.4e+05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGGTGAGT 16

Db 2 CGCTGGTGAGT 12

RESULT 18

AZ788334

LOCUS

DEFINITION

clone UUGC2M0035B19 F, genomic survey sequence.

ACCESSION AZ788334

VERSION 1

KEYWORDS

SOURCE

ORGANISM

Mus musculus

(house mouse)

Eukaryota; Chordata; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: rdunn@genetics.utah.edu

Insert Length: 10000

Std Error: 0.00

Plate: 0035

row: B

column: 19

Seq primer: CGTTCTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

1. .30

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0035B19"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:1164508"
/dev_stage="7 day juvenile"
/lab_host="DH10B"
/clone_lib="Barstead mouse"

```

was hydrodynamically sheared by repeated passage through a
(<http://www.jax.org/resources/documents/updates/>). The DNA

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
AUTHORS

1 (bases 1 to 34)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project

TITLE
JOURNAL
COMMENT

Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu

GENOME SYSTEMS CLONE ID: Gm-cl004-297
Possible reversed clone: similarity on wrong strand This clone is
available through: ResGen, Invitrogen Corp. 2130 South Memorial
Parkway Huntsville, AL 35801 For further information call: (800
)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gbco
High quality sequence stop: 1
POLYA=No.

Location/Qualifiers

1. .34

/organism="Glycine max"

/mol_type="mRNA"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl004-297"

/tissue_type="root"

/lab_host="Xt10-Gold"

/clone_lib="Gm-cl004"

/notes="Vector: pBluescript II Xr; Site 1: EcoRI; Site 2:
XhoI; Root cDNA. The mRNA was isolated from entire roots
of 8 day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize the
cDNA. First-strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is hemimethylated.
Stratagene's first-strand synthesis primer was used
[GAGAGAGAGAGAGAGAGACTGCTCGAG(T)-18]. After
second-strand synthesis, the cDNA ends were 'polished'
with clone Pfu DNA polymerase, ligated to EcoRI adapters,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by digestion with XhoI;
all XhoI sites in the cDNA would be protected by their
hemimethylated status. The cDNA constructs were
size-fractionated with a 500bp cutoff, using GibcoBRL Life
Technologies' cDNA Size Fractionation column. The column
eluent was then ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+)) that had been
digested with EcoRI and XhoI, and phosphorylated. Both
the white and blue colonies appear to contain recombinant
plasmids with cDNA inserts. Blue colonies 9n=15) have been
sequenced, and possess putative cDNA inserts. This library
was constructed by Dr. Paul Keim & Virginia H. Coryell,
Department of Biology, Box5640, Northern Arizona
University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
520-523-7500, email: paul.keim@naau.edu,
virginia.coryell@naau.edu"

FEATURES

Source

1. .34

/organism="Glycine max"

/mol_type="mRNA"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-cl004-297"

/tissue_type="root"

/lab_host="Xt10-Gold"

/clone_lib="Gm-cl004"

/notes="Vector: pBluescript II Xr; Site 1: EcoRI; Site 2:
XhoI; Root cDNA. The mRNA was isolated from entire roots
of 8 day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize the
cDNA. First-strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is hemimethylated.
Stratagene's first-strand synthesis primer was used
[GAGAGAGAGAGAGAGACTGCTCGAG(T)-18]. After
second-strand synthesis, the cDNA ends were 'polished'
with clone Pfu DNA polymerase, ligated to EcoRI adapters,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by digestion with XhoI;
all XhoI sites in the cDNA would be protected by their
hemimethylated status. The cDNA constructs were
size-fractionated with a 500bp cutoff, using GibcoBRL Life
Technologies' cDNA Size Fractionation column. The column
eluent was then ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+)) that had been
digested with EcoRI and XhoI, and phosphorylated. Both
the white and blue colonies appear to contain recombinant
plasmids with cDNA inserts. Blue colonies 9n=15) have been
sequenced, and possess putative cDNA inserts. This library
was constructed by Dr. Paul Keim & Virginia H. Coryell,
Department of Biology, Box5640, Northern Arizona
University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
520-523-7500, email: paul.keim@naau.edu,
virginia.coryell@naau.edu"

FEATURES

Source

1. .34

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4555280"

/tissue_type="leiomyosarcoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 46"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 14 a 9 c 9 g 2 t

ORIGIN

Query Match 55.0%; Score 11; DB 10; Length 34;

Best Local Similarity 73.7%; Pred. No. 2.6e+05;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGGATTCA 20

|||||

Db 27 TTCTCGCTGGTGGATTCA 9

|||||

RESULT 25

BG340055/c

LOCUS

DEFINITION

602438218F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4556092 5',

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

Homo sapiens

Chordata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 GTTCTCGCTGGTGGATTTC 19

Query Match 55.0%; Score 11; DB 9; Length 34;

Best Local Similarity 73.7%; Pred. No. 2.6e+05;

Matches 14; Conservative 0; Mismatches 5; Indels 3; Gaps 0;

QY 1 GTTCTCGCTGGTGGATTTC 19

Db 19 GGTCTTCCGGTGAGGTC 1

|||||

RESULT 24

BG339578/c

LOCUS

DEFINITION

602437433F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4555280 5',

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

Homo sapiens

Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 34)

NIH-MGC http://mgi.nhl.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLC1256 row: a column: 09

High quality sequence stop: 34.

Location/Qualifiers

1. .34

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4555280"

/tissue_type="leiomyosarcoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 46"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 14 a 9 c 9 g 2 t

ORIGIN

Query Match 55.0%; Score 11; DB 10; Length 34;

Best Local Similarity 73.7%; Pred. No. 2.6e+05;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGGATTCA 20

|||||

Db 27 TTCTCGCTGGTGGATTCA 9

|||||

RESULT 25

BG340055/c

LOCUS

DEFINITION

602438218F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4556092 5',

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

Homo sapiens

Chordata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


```

REFERENCE
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1258 row: c column: 05
High quality sequence stop: 34.
Location/Qualifiers
1. 34
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4556092"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 46"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 14 a 9 c 9 g 2 t
ORIGIN
Query Match 55.0%; Score 11; DB 10; Length 34;
Best Local Similarity 73.7%; Pred. No. 2.6e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTTTCA 20
|||||
Db 27 TTCTGCTTGTGGTTCA 9

RESULT 26
AI766095/c
LOCUS wh70a04.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2386062 3'
DEFINITION similar to TR:008837 O08837 CDC-LIKE PROTEIN ; mRNA sequence.
ACCESSION AI766095
VERSION AI766095.1 GI:5232504
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennor, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

```

```

Trace considered overall poor quality
Insert Length: 865 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. 37
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2386062"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo. "
BASE COUNT 10 a 14 c 6 g 7 t
ORIGIN
Query Match 55.0%; Score 11; DB 9; Length 37;
Best Local Similarity 73.7%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TTCTCGCTGGTGAGTTTCA 20
|||||
Db 33 TTCTGCTGGGGTTTCA 15

RESULT 27
TA11C07P/c
LOCUS TA11C07P 37 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 11c07, forward sequence,
genomic survey sequence.
ACCESSION AL451655
VERSION AL451655.1 GI:11831678
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1. (bases 1 to 37)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1. 37
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"

```

FEATURES

source

FEATURES

source


```

BASE COUNT      9 a      9 c      9 g      10 t
ORIGIN
Query Match      55.0%; Score 11; DB 29; Length 37;
Best Local Similarity 73.7%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCTCGCTGGTGAGTTTCA 20
    ||| ||||| |||||
Db 30 TGCTCAATGGTGAAGTTCA 12

RESULT 28
LOCUS BZ768960/c
DEFINITION SALK_141393.29.40.x Arabidopsis thaliana TDNA insertion lines
          Arabidopsis thaliana genomic clone SALK_141393.29.40.x, genomic
          survey sequence.
ACCESSION BZ768960
VERSION BZ768960.1 GI:28942644
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
          ; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 39)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
        , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
        Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL Arabidopsis Genome
COMMENT Contact: Joseph R. Ecker
        Salk Institute Genomic Analysis Laboratory (SIGnAL)
        The Salk Institute for Biological Studies
        10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
        Tel: 858 453 4100 x1752
        Fax: 858 558 6379
        Email: ecker@salk.edu
        This is single pass sequence recovered from the left border of
        TDNA. This sequence lies within an annotated intron of At3g18165.
        Class: TDNA tagged.
FEATURES             location/Qualifiers
     source          1..39
                    /organism="Arabidopsis thaliana"
                    /mol_type="genomic DNA"
                    /strain="Columbia 0"
                    /db_xref="taxon:3702"
                    /clone="SALK_141393.29.40.x"
                    /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                    /note="PCR was performed on Arabidopsis thaliana lines
                    each of which contains one or more TDNA insertion
                    elements. The resultant fragment for each line was
                    directly sequenced to determine the genomic sequence at
                    the site of insertion. Details of the protocols used can
                    be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT      20 a      6 c      6 g      7 t
ORIGIN
Query Match      55.0%; Score 11; DB 29; Length 39;
Best Local Similarity 73.7%; Pred. No. 2.8e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TTCTCGCTGGTGAGTTTCA 20
    ||| ||||| |||||
Db 29 TTTTGGTTTGAGTTTCA 11

RESULT 29
LOCUS AZ514463
DEFINITION LM0361A19F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
          clone UUGCIM0361A19 F, genomic survey sequence.
ACCESSION AZ514463
VERSION AZ514463.1 GI:10695875
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
        Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
        , M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
        and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SL/C, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert length: 10000 Std Error: 0.00
          Plate: 0361 row: A column: 19
          Seq primer: CGTTGTAACACGACGCCAGT
          Class: plasmid ends
          High quality sequence stop: 23.
FEATURES             location/Qualifiers
     source          1..23
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUGCIM0361A19"
                    /sex="Male"
                    /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
                    /clone_lib="Mouse 10kb plasmid UUGCIM library"
                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a
                    0.005 inch orifice at constant velocity. The sheared DNA
                    was blunt end-repaired with T4 DNA polymerase and T4
                    polynucleotide kinase. Adaptor oligonucleotides were
                    ligated to the blunt ends in high molar excess. The
                    adaptor DNA was purified and size-selected for a 9.5 to
                    10.5 kb range using preparative agarose gel
                    electrophoresis. Vector DNA was prepared from a derivative
                    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                    inducible derivative of plasmid R1. The vector was ligated
                    with adaptors complementary to the insert adaptors and
                    purified. The sheared, adaptor mouse DNA was annealed to
                    adaptor vector DNA, and transformed into
                    chemically-competent E. coli XL10-Gold (Stratagene) cells
                    and selected for ampicillin resistance."
BASE COUNT      5 a      3 c      7 g      8 t
ORIGIN
Query Match      54.0%; Score 10.8; DB 28; Length 23;
Best Local Similarity 85.7%; Pred. No. 2.9e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTCTCGCTGGTGA 14
    ||||| |||||
Db 2 GTTCTCTCTGGGA 15

RESULT 30
LOCUS AZ764581

```

LOCUS AZ764581 24 bp DNA linear GSS 16-FEB-2001
 DEFINITION 1M0561103F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0561103 F, genomic survey sequence.
 ACCESSION AZ764581
 VERSION AZ764581.1 GI:12879689
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0561 row: 1 column: 03
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0561103"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 3 a 8 c 8 g 5 t
 ORIGIN
 Query Match 54.0%; Score 10.8; DB 28; Length 24;
 Best Local Similarity 85.7%; Pred. No. 2.9e+05;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TTCTCGCTGGTGAG 15
 |||||
 Db 7 TTCTCGCTGGTGAG 20
 |||||

RESULT 31

AZ352257 33 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0090G1LR Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0090G11 R, genomic survey sequence.
 ACCESSION AZ352257
 VERSION AZ352257.1 GI:10431494
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 33)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0090 row: G column: 11
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 33.
 Location/Qualifiers
 1..33
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0090G11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 5 a 10 c 10 g 8 t
 ORIGIN

Query Match 54.0%; Score 10.6; DB 28; Length 33;
 Best Local Similarity 85.7%; Pred. No. 3.3e+05;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TTCTCGCTGGTGAGT 16
 |||||
 Db 19 TCTCCTCGGAGAGT 32
 |||||

```

RESULT 32
BZ661620
LOCUS
DEFINITION
  SALK_025093.42.05.x Arabidopsis thaliana TDNA insertion lines
  Arabidopsis thaliana genomic clone SALK_025093.42.05.x, genomic
  survey sequence.
ACCESSION
  BZ661620
VERSION
  BZ661620.1 GI:28174767
KEYWORDS
  GSS.
SOURCE
  Arabidopsis thaliana (thale cress)
ORGANISM
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
  ; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
  1 (bases 1 to 40)
REFERENCE
  Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
  ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
  , Zimmerman,J. and Ecker,J.R.
  A Sequence-Indexed Library of Insertion Mutations in the
  Arabidopsis Genome
JOURNAL
  Unpublished
COMMENT
  Contact: Joseph R. Ecker
  Salk Institute Genomic Analysis Laboratory (SIGNAL)
  The Salk Institute for Biological Studies
  10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
  Tel: 858 453 4100 x1752
  Fax: 858 558 6379
  Email: eckersalk.edu
  This is single pass sequence recovered from the left border of
  TDNA. This sequence lies within an annotated exon of At3g29170.
  Class: TDNA tagged.
FEATURES
  source
  1..40
  /organism="Arabidopsis thaliana"
  /mol_type="genomic DNA"
  /strain="Columbia 0"
  /db_xref="taxon:3702"
  /clone="SALK_025093.42.05.x"
  /clone_lib="Arabidopsis thaliana TDNA insertion lines"
  /note="PCR was performed on Arabidopsis thaliana lines
  each of which contains one or more TDNA insertion
  elements. The resultant fragment for each line was
  directly sequenced to determine the genomic sequence at
  the site of insertion. Details of the protocols used can
  be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT
  7 a 9 c 8 g 16 t
ORIGIN
  Query Match 54.0%; Score 10.8; DB 29; Length 40;
  Best Local Similarity 85.7%; Pred. No. 3.5e+05;
  Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  Qy 2 TTCTCGCTGGTGAG 15
  |||||
  Db 17 TTCTCCCTGGTAA 30
  |||||

RESULT 33
AI338568
LOCUS
DEFINITION
  Q99803.x1 Soares Total fetus Nb2HF8 9w Homo sapiens cDNA clone
  IMAGE:1939444 3' Similar to RF:Q33563 Q33563 EATRO 164 KINETOPLAST
  ;, mRNA sequence.
ACCESSION
  AI338568
VERSION
  AI338568.1 GI:4075495
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 28)
REFERENCE
  NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  TITLE

```

```

Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: rcgaps@remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 948 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
  source
  1..28
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:1939444"
  /dev stage="8-9 weeks"
  /lab_host="DH10B"
  /clone_lib="Soares total fetus Nb2HF8 9w"
  /note="Vector: pT7TD-Fac (Pharmacia) with a modified
  polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
  was prepared from mRNA obtained from pooled 8-9 week
  (total) fetus material with a Not I - oligo(dT) primer [5'
  TGTACCAATCTGAGTGGGAGCGCGCTTAATTTTTTT 3'].
  Double-stranded cDNA was ligated to Eco RI adaptors
  (Pharmacia), digested with Not I and cloned into the Not I
  and Eco RI sites of the modified pT7T3 vector. Library
  went through one round of normalization, and was
  constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT
  2 a 1 c 5 g 20 t
ORIGIN
  Query Match 53.0%; Score 10.6; DB 9; Length 28;
  Best Local Similarity 76.5%; Pred. No. 3.9e+05;
  Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  Qy 2 TTCTCGCTGGTGAGTT 18
  |||||
  Db 11 TTTTGGTTGGTTAGTT 27
  |||||

RESULT 34
AZ344319
LOCUS
DEFINITION
  1X0078G16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
  clone UUGCIM0078G16 F, genomic survey sequence.
ACCESSION
  AZ344319
VERSION
  AZ344319.1 GI:10423434
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 31)
REFERENCE
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,I., Reilly
  ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
  and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0078 row: G column: 16
  Seq primer: CGTTGTAAACGACGCCACT
  Class: plasmid ends

```


Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..31
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="238c03"

BASE COUNT 12 a 11 c 5 g 3 t

ORIGIN

Query Match 53.0%; Score 10.6; DB 29; Length 31;

Best Local Similarity 76.5%; Pred. No. 4e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TTCTGCTGGTGAGTTT 18

Db 22 TCGCGCTGGGATTT 6

RESULT 37

AZ780156

LOCUS

DEFINITION 33 bp DNA linear GSS 16-FEB-2001
 clone UUGC2M0017B15 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

UNPUBLISHED

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0017 row: B column: 15

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 33.

Location/Qualifiers

1..33

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0017B15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 3 a 6 c 7 g 17 t

ORIGIN

Query Match 53.0%; Score 10.6; DB 28; Length 33;

Best Local Similarity 76.5%; Pred. No. 4.1e+05;

Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 TCTGCTGGTGAGTTTC 19

Db 2 TGCTCTGTTAGTTTC 18

RESULT 38

AZ946219

LOCUS

DEFINITION

33 bp DNA linear GSS 27-APR-2001
 clone UUGC2M0207K24 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

UNPUBLISHED

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0207 row: K column: 24

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 33.

Location/Qualifiers

1..33

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0207K24"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 5 c 10 g 16 t
 ORIGIN
 Query Match 53.0%; Score 10.6; DB 28; Length 33;
 Best Local Similarity 76.5%; Pred. No. 4.1e+05;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 TTCTCGCTGGTGAGTT 18
 ||||| ||||| |||||
 Db 15 TTCTACTGGTCTGTTT 31

RESULT 39
 AL675283/c
 LOCUS
 DEFINITION AL675283 XGC-gastrula silurana tropicalis cDNA clone TGas063121 5',
 mRNA sequence.

ACCESSION AL675283.1 GI:19531657
 VERSION
 KEYWORDS
 ORGANISM Silurana tropicalis (western clawed frog)

Silurana tropicalis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Silurana.

1 (bases 1 to 35)
 Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.
 Sanger Xenopus tropicalis EST project 2002

Unpublished
 Contact: Taylor R
 Sanger Centre
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE ID: TGas063121.plcSP6
 Sequencing primer: PICSP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.

FEATURES
 source.
 1..35
 /organism="Silurana tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TGas063121"
 /dev_stage="gastrula (stages 10.5-13 mixed)"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-gastrula"
 /notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dt primed from 5ug of poly A+ RNA from stages
 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
 into pCS107 with EcoRI at the 5' end and NotI at the 3'
 end."

BASE COUNT 7 a 11 c 12 g 5 t
 ORIGIN
 Query Match 53.0%; Score 10.6; DB 9; Length 35;
 Best Local Similarity 76.5%; Pred. No. 4.2e+05;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTT 17
 ||||| ||||| |||||

Db 17 GTTCTCCCCGGGAATT 1
 RESULT 40
 AL678369/c
 LOCUS
 DEFINITION AL678369 XGC-gastrula silurana tropicalis cDNA clone TGas064121 5',
 mRNA sequence.

ACCESSION AL678369.1 GI:19534743
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Silurana tropicalis (western clawed frog)

Silurana tropicalis
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 Xenopodinae; Silurana.

1 (bases 1 to 35)
 Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.
 Sanger Xenopus tropicalis EST project 2002

Unpublished
 Contact: Taylor R
 Sanger Centre
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE ID: TGas064121.plcSP6
 Sequencing primer: PICSP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.

FEATURES
 source
 1..35
 /organism="Silurana tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TGas064121"
 /dev_stage="gastrula (stages 10.5-13 mixed)"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-gastrula"
 /notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dt primed from 5ug of poly A+ RNA from stages
 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
 into pCS107 with EcoRI at the 5' end and NotI at the 3'
 end."

BASE COUNT 7 a 11 c 12 g 5 t
 ORIGIN
 Query Match 53.0%; Score 10.6; DB 9; Length 35;
 Best Local Similarity 76.5%; Pred. No. 4.2e+05;
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTTCTCGCTGGTGAGTT 17
 ||||| ||||| |||||
 Db 17 GTTCTCCCCGGGAATT 1

Search completed: January 24, 2004, 15:36:46
 Job time : 1886 secs